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| 09/617,747   | 17 July 2000 (17.07.2000)      | US                        |    |            |                             |    |            |                                |    |            |                           |    |            |                           |    |   |
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*[Continued on next page]*

**(54) Title:** COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

11729.1 conto

TTAGAGAGGCCACAGAAGGAAGAAGAGTTAAAGCAGCAAAAGCGGGTTTTTGTGTTTGTTTGTTGTTTGTGTTTGT  
TTTGTAGATGAGGTCTCACTCTGTTGCCAAGCTGGAGTACAAGCGGATGATCTCAGGTCGGTGCACATCCGCTCCGCT  
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11729-45.21.21.cons1

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GCTACATAGTAAAGAAAGGCGACAGCGAAAGAAATGGACTGAAGAAGTGTGTGTGATCAAAACCAACATAAT  
TCTTACTATGTGTAGTGAGGATCTGAAGGTAAGAAGGAGACATCTCTTGGAGAAAATTGTGTGTAGAGT  
CTTTCTGTGCAAGAGTGTGAAGAA

11729-45.21.21.cons2

TTAGAGAGGCACAGAAAGGAAGAAGATTTAAAGCAGCAAGCGGGTTTTTGTGTTGTTTGTGTTTGTGTTTGTGTTGAGATGAGATCTCACTCTCTGTTGCCAAGCTGGAGTACAAAGCATGATCTCAGCTGCGTGCACACTTCGCTCTCCAGATCTAAAGTATTTCTCTGCTCAGCTCCCGAACTGCTGGAGTACAGGGCGGCCAGCTCACTGACTAACTGTAATTTTTTTGTTGTTATTTTACAGCAAGGGTTTTACCAAGTTGGCCACAGCTCTCTTGAACCTCTGCACTCAGTTGATCTACCGCGCTCGGCTCCCAAGTGTGGAGTACAGGCTGAGGCCACAGCTCGCGGCCGCCAAAGCTGTGTTTCTTTGTCTTTAGGCTAAAGCTCTCTCTGCCATGCAATATCATATAACTGAGCTGACTGCCAAGCTCAGCTCAGCTGCTGCTC

11731.1cont1g

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**(57) Abstract:** Compositions and methods for the therapy and diagnosis of cancer, such as ovarian cancer, are disclosed. Compositions may comprise one or more ovarian carcinoma proteins, immunogenic portions thereof, polynucleotides that encode such portions or antibodies or immune system cells specific for such proteins. Such compositions may be used, for example, for the prevention and treatment of diseases such as ovarian cancer. Methods are further provided for identifying tumor antigens that are secreted from ovarian carcinomas and/or other tumors. Polypeptides and polynucleotides as provided herein may further be used for the diagnosis and monitoring of ovarian cancer.

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## COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

### Technical Field

The present invention relates generally to ovarian cancer therapy. The  
5 invention is more specifically related to polypeptides comprising at least a portion of an  
ovarian carcinoma protein, and to polynucleotides encoding such polypeptides, as well  
as antibodies and immune system cells that specifically recognize such polypeptides.  
Such polypeptides, polynucleotides, antibodies and cells may be used in vaccines and  
pharmaceutical compositions for treatment of ovarian cancer.

### 10 Background of the Invention

Ovarian cancer is a significant health problem for women in the United  
States and throughout the world. Although advances have been made in detection and  
therapy of this cancer, no vaccine or other universally successful method for prevention  
or treatment is currently available. Management of the disease currently relies on a  
15 combination of early diagnosis and aggressive treatment, which may include one or  
more of a variety of treatments such as surgery, radiotherapy, chemotherapy and  
hormone therapy. The course of treatment for a particular cancer is often selected based  
on a variety of prognostic parameters, including an analysis of specific tumor markers.  
However, the use of established markers often leads to a result that is difficult to  
20 interpret, and high mortality continues to be observed in many cancer patients.

Immunotherapies have the potential to substantially improve cancer  
treatment and survival. Such therapies may involve the generation or enhancement of  
an immune response to an ovarian carcinoma antigen. However, to date, relatively few  
ovarian carcinoma antigens are known and the generation of an immune response  
25 against such antigens has not been shown to be therapeutically beneficial.

Accordingly, there is a need in the art for improved methods for  
identifying ovarian tumor antigens and for using such antigens in the therapy of ovarian  
cancer. The present invention fulfills these needs and further provides other related  
advantages.



## SUMMARY OF THE INVENTION

Briefly stated, this invention provides compositions and methods for the therapy of cancer, such as ovarian cancer. In one aspect, the present invention provides polypeptides comprising an immunogenic portion of an ovarian carcinoma protein, or a  
5 variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished. Within certain embodiments, the ovarian carcinoma protein comprises a sequence that is encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NO:456-457, 460-477 and 512-  
10 570 and complements of such polynucleotides.

The present invention further provides polynucleotides that encode a polypeptide as described above or a portion thereof, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

The present invention further provides polypeptide compositions  
15 comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596.

Within other aspects, the present invention provides pharmaceutical compositions and vaccines. Pharmaceutical compositions may comprise a physiologically acceptable carrier or excipient in combination with one or more of: (i) a  
20 polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence encoded by a polynucleotide that comprises a  
25 sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570 or (ii) a polynucleotide encoding such a polypeptide; (iii) an antibody that specifically binds to such a polypeptide; (iv) an antigen-presenting cell that expresses such a polypeptide and/or (v) a T cell that specifically reacts with such a polypeptide. Vaccines may  
30 comprise a non-specific immune response enhancer in combination with one or more of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions

and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence set forth in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596 or an amino acid sequence encoded by a polynucleotide that  
5 comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570 or (ii) a polynucleotide encoding such a polypeptide; (iii) an anti-idiotypic antibody that is specifically bound by an antibody that specifically binds to such a polypeptide; (iv) an antigen-presenting cell that expresses such a polypeptide and/or (v) a T cell that specifically reacts with such a polypeptide.

10           The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

          Within related aspects, pharmaceutical compositions comprising a fusion protein or polynucleotide encoding a fusion protein in combination with a  
15 physiologically acceptable carrier are provided.

          Vaccines are further provided, within other aspects, comprising a fusion protein or polynucleotide encoding a fusion protein in combination with a non-specific immune response enhancer.

          Within further aspects, the present invention provides methods for  
20 inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

          The present invention further provides, within other aspects, methods for stimulating and/or expanding T cells, comprising contacting T cells with (a) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a  
25 variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence set forth in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596 or an amino acid sequence encoded by a polynucleotide that comprises a  
30 sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570; (b) a polynucleotide encoding such a polypeptide and/or (c) an antigen presenting cell that

expresses such a polypeptide under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Such polypeptide, polynucleotide and/or antigen presenting cell(s) may be present within a pharmaceutical composition or vaccine, for use in stimulating and/or expanding T cells in a mammal.

5                Within other aspects, the present invention provides methods for inhibiting the development of ovarian cancer in a patient, comprising administering to a patient T cells prepared as described above.

              Within further aspects, the present invention provides methods for inhibiting the development of ovarian cancer in a patient, comprising the steps of: (a)  
10 incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein  
15 comprises an amino acid sequence encoded by a polynucleotide that comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570; (ii) a polynucleotide encoding such a polypeptide; or (iii) an antigen-presenting cell that expresses such a polypeptide; such that T cells proliferate; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the  
20 development of ovarian cancer in the patient. The proliferated cells may be cloned prior to administration to the patient.

              The present invention also provides, within other aspects, methods for identifying secreted tumor antigens. Such methods comprise the steps of: (a) implanting tumor cells in an immunodeficient mammal; (b) obtaining serum from the  
25 immunodeficient mammal after a time sufficient to permit secretion of tumor antigens into the serum; (c) immunizing an immunocompetent mammal with the serum; (d) obtaining antiserum from the immunocompetent mammal; and (e) screening a tumor expression library with the antiserum, and therefrom identifying a secreted tumor antigen. A preferred method for identifying a secreted ovarian carcinoma antigen  
30 comprises the steps of: (a) implanting ovarian carcinoma cells in a SCID mouse; (b) obtaining serum from the SCID mouse after a time sufficient to permit secretion of

ovarian carcinoma antigens into the serum; (c) immunizing an immunocompetent mouse with the serum; (d) obtaining antiserum from the immunocompetent mouse; and (e) screening an ovarian carcinoma expression library with the antiserum, and therefrom identifying a secreted ovarian carcinoma antigen.

5           The present invention also discloses antibody epitopes recognized by the O8E polyclonal anti-sera which epitopes are presented herein as SEQ ID NO: 394-415.

Further disclosed by the present invention are 10-mer and 9-mer peptides predicted to bind HLA-0201 which peptides are disclosed herein as SEQ ID NO:416-435 and SEQ ID NO:436-455, respectively.

10           These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

          In another aspect of the present invention, the applicants have  
15           unexpectedly identified a series of novel repeating sequence elements in the 5' end of the gene encoding O772P. Therefore, the present invention provides O772P polypeptides having structures represented by  $X_n$ -Y, wherein X comprises a sequence having at least 50% identity, preferably at least 70% identity, and more preferably at least 90% identity with an O772P repeat sequence set forth in SEQ ID NO: 596. Y will  
20           typically comprise a sequence having at least 80% identity, preferably at least 90% identity and more preferably at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 594. According to this embodiment, n will generally be an integer from 1 to 35, preferably an integer from 15 to 25, and X can be the same or different.

25           In one preferred embodiment, X comprises a sequence selected from the group consisting of any one of SEQ ID NOs: 574-593 and Y comprises the sequence set forth in SEQ ID NO: 594.

          In another preferred embodiment, an illustrative O772P polypeptide comprises the sequence set forth in SEQ ID NO: 595, containing 20 repeating sequence  
30           elements (i.e.,  $X_{20}$ ) wherein the X elements are arranged in the following order (moving from N-terminal to C-terminal in the O772P repeat region): SEQ ID NO: 574 - SEQ ID

NO: 575 - SEQ ID NO: 576 - SEQ ID NO: 577 - SEQ ID NO: 578 - SEQ ID NO: 579 -  
SEQ ID NO: 580 - SEQ ID NO: 581 - SEQ ID NO: 582 - SEQ ID NO: 583 - SEQ ID  
NO: 584 - SEQ ID NO: 585 - SEQ ID NO: 586 - SEQ ID NO: 587 - SEQ ID NO: 588 -  
SEQ ID NO: 589 - SEQ ID NO: 590 - SEQ ID NO: 591 - SEQ ID NO: 592 - SEQ ID  
5 NO: 593.

According to another aspect of the present invention, an O772P polynucleotide is provided having the structure  $X_n$ -Y, wherein X comprises an O772P repeat sequence element selected from the group consisting of any one of SEQ ID NOs: 512-540, 542-546 and 548-567. Y will generally comprise a sequence having at least  
10 80% identity, preferably at least 90% identity, and more preferably at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 568. In this embodiment, n is typically an integer from 1 to 35, preferably from 15 to 25 and X can be the same or different.

In another embodiment, an illustrative O772P polynucleotide comprises  
15 the sequence set forth in SEQ ID NO: 569, containing 20 repeating sequence elements (i.e.,  $X_{20}$ ).

According to another aspect of the present invention, O772 polypeptides are provided comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 490-511.

20 According to another aspect of the present invention, O8E polypeptides are provided comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 394-415.

#### BRIEF DESCRIPTION OF THE SEQUENCE IDENTIFIERS AND DRAWINGS

SEQ ID NO:1-71 are ovarian carcinoma antigen polynucleotides shown  
25 in Figures 1A-1S.

SEQ ID NO:72-74 are ovarian carcinoma antigen polynucleotides shown in Figures 2A-2C.

SEQ ID NO:75 is the ovarian carcinoma polynucleotide 3g (Figure 4).

SEQ ID NO:76 is the ovarian carcinoma polynucleotide 3f (Figure 5).

30 SEQ ID NO:77 is the ovarian carcinoma polynucleotide 6b (Figure 6).

SEQ ID NO:78 is the ovarian carcinoma polynucleotide 8e (Figure 7A).

SEQ ID NO:79 is the ovarian carcinoma polynucleotide 8h (Figure 7B).

SEQ ID NO:80 is the ovarian carcinoma polynucleotide 12e (Figure 8).

SEQ ID NO:81 is the ovarian carcinoma polynucleotide 12h (Figure 9).

5       SEQ ID NO:82-310 are ovarian carcinoma antigen polynucleotides shown in Figures 15A-15EEE.

SEQ ID NO:311 is a full length sequence of ovarian carcinoma polynucleotide O772P.

SEQ ID NO:312 is the O772P amino acid sequence.

10       SEQ ID NO:313-384 are ovarian carcinoma antigen polynucleotides.

SEQ ID NO:385 represents the cDNA sequence of a form of the clone O772P, designated 21013.

SEQ ID NO:386 represents the cDNA sequence of a form of the clone O772P, designated 21003.

15       SEQ ID NO:387 represents the cDNA sequence of a form of the clone O772P, designated 21008.

SEQ ID NOs:388 is the amino acid sequence corresponding to SEQ ID NO:385.

20       SEQ ID NOs:389 is the amino acid sequence corresponding to SEQ ID NO:386. SEQ ID NOs:390 is the amino acid sequence corresponding to SEQ ID NO:387.

SEQ ID NO:391 is a full length sequence of ovarian carcinoma polynucleotide O8E.

SEQ ID NO:392-393 are protein sequences encoded by O8E.

25       SEQ ID NO:394-415 are peptide sequences corresponding to the OE8 antibody epitopes.

SEQ ID NO:416-435 are potential HLA-A2 10-mer binding peptides predicted using the full length open-reading frame from OE8.

30       SEQ ID NO:436-455 are potential HLA-A2 9-mer binding peptides predicted using the full length open-reading frame from OE8.

SEQ ID NO:456 is a truncated nucleotide sequence of the full length Genbank sequence showing homology to O772P

SEQ ID NO:457 is the full length Genbank sequence showing significant homology to O772P

5 SEQ ID NO:458 is a protein encoding a truncated version of the full length Genbank sequence showing homology to O772P

SEQ ID NO:459 is the full length protein sequence from Genbank showing significant homology to the protein sequence for O772P

10 SEQ ID NO:460 encodes a unique N-terminal portion of O772P contained in residues 1-70.

SEQ ID NO:461 contains unique sequence and encodes residues 1-313 of SEQ ID NO: 456.

SEQ ID NO:462 is the hypothetical sequence for clone O772P.

SEQ ID NO:463 is the cDNA sequence for clone FLJ14303.

15 SEQ ID NO:464 is a partial cDNA sequence for clone O772P.

SEQ ID NO:465 is a partial cDNA sequence for clone O772P.

SEQ ID NO:466 is a partial cDNA sequence for clone O772P.

SEQ ID NO:467 is a partial cDNA sequence for clone O772P.

SEQ ID NO:468 is a partial cDNA sequence for clone O772P.

20 SEQ ID NO:469 is a partial cDNA sequence for clone O772P.

SEQ ID NO:470 is a partial cDNA sequence for clone O772P.

SEQ ID NO:471 is a partial cDNA sequence for clone O772P.

SEQ ID NO:472 is a partial cDNA sequence for clone O772P.

SEQ ID NO:473 is a partial cDNA sequence for clone O772P.

25 SEQ ID NO:474 is a partial cDNA sequence for clone O772P.

SEQ ID NO:475 is a partial cDNA sequence for clone O772P.

SEQ ID NO:476 is a partial cDNA sequence for clone O772P.

SEQ ID NO:477 represents the novel 5'-end of the ovarian tumor antigen O772P.

30 SEQ ID NO:478 is the amino acid sequence encoded by SEQ ID NO:462.

SEQ ID NO:479 is the amino acid sequence encoded by SEQ ID NO:463.

SEQ ID NO:480 is a partial amino acid sequence encoded by SEQ ID NO:472.

5 SEQ ID NO:481 is a partial amino acid sequence encoded by a possible open reading frame of SEQ ID NO:471.

SEQ ID NO:482 is a partial amino acid sequence encoded by a second possible open reading frame of SEQ ID NO:471.

10 SEQ ID NO:483 is a partial amino acid sequence encoded by SEQ ID NO:467.

SEQ ID NO:484 is a partial amino acid sequence encoded by a possible open reading frame of SEQ ID NO:466.

SEQ ID NO:485 is a partial amino acid sequence encoded by a second possible open reading frame of SEQ ID NO:466.

15 SEQ ID NO:486 is a partial amino acid sequence encoded by SEQ ID NO:465.

SEQ ID NO:487 is a partial amino acid sequence encoded by SEQ ID NO:464.

20 SEQ ID NO:488 represents the extracellular, transmembrane and cytoplasmic regions of O772P.

SEQ ID NO:489 represents the predicted extracellular domain of O772P.

SEQ ID NO:490 represents the amino acid sequence of peptide #2 which corresponds to an O772P specific antibody epitope.

25 SEQ ID NO:491 represents the amino acid sequence of peptide #6 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:492 represents the amino acid sequence of peptide #7 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:493 represents the amino acid sequence of peptide #8 which corresponds to an O772P specific antibody epitope.

30 SEQ ID NO:494 represents the amino acid sequence of peptide #9 which corresponds to an O772P specific antibody epitope.



SEQ ID NO:495 represents the amino acid sequence of peptide #11, which corresponds to an O772P specific antibody epitope.

SEQ ID NO:496 represents the amino acid sequence of peptide #13 which corresponds to an O772P specific antibody epitope.

5        SEQ ID NO:497 represents the amino acid sequence of peptide #22 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:498 represents the amino acid sequence of peptide #24 which corresponds to an O772P specific antibody epitope.

10       SEQ ID NO:499 represents the amino acid sequence of peptide #27 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:500 represents the amino acid sequence of peptide #40 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:501 represents the amino acid sequence of peptide #41 which corresponds to an O772P specific antibody epitope.

15       SEQ ID NO:502 represents the amino acid sequence of peptide #47 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:503 represents the amino acid sequence of peptide #50 which corresponds to an O772P specific antibody epitope.

20       SEQ ID NO:504 represents the amino acid sequence of peptide #51 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:505 represents the amino acid sequence of peptide #52 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:506 represents the amino acid sequence of peptide #53 which corresponds to an O772P specific antibody epitope.

25       SEQ ID NO:507 represents the amino acid sequence of peptide #58 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:508 represents the amino acid sequence of peptide #59 which corresponds to an O772P specific antibody epitope.

30       SEQ ID NO:509 represents the amino acid sequence of peptide #60 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:510 represents the amino acid sequence of peptide #61 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:511 represents the amino acid sequence of peptide #71 which corresponds to an O772P specific antibody epitope.

5        SEQ ID NO:512 (O772P repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:513 (O772P repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

10       SEQ ID NO:514 (O772P repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:515 (O772P repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:516 (O772P repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

15       SEQ ID NO:517 (HB repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:518 (HB repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

20       SEQ ID NO:519 (HB repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:520 (HB repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:521 (HB repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

25       SEQ ID NO:522 (HB repeat6 5'-end) represents an example of a cDNA sequence corresponding to repeat number 16 from the 5' variable region of O772P.

SEQ ID NO:523 (1043400.1 repeat1) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

30       SEQ ID NO:524 (1043400.1 repeat2) represents an example of a cDNA sequence corresponding to repeat number 10 from the 5' variable region of O772P.

SEQ ID NO:525 (1043400.1 repeat3) represents an example of a cDNA sequence corresponding to repeat number 10/11 from the 5' variable region of O772P.

SEQ ID NO:526 (1043400.1 repeat4) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

5        SEQ ID NO:527 (1043400.1 repeat5) represents an example of a cDNA sequence corresponding to repeat number 14 from the 5' variable region of O772P.

SEQ ID NO:528 (1043400.1 repeat6) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

10       SEQ ID NO:529 (1043400.3 repeat1) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

SEQ ID NO:530 (1043400.3 repeat2) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:531 (1043400.5 repeat1) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

15       SEQ ID NO:532 (1043400.5 repeat2) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P, in addition containing intron sequence.

SEQ ID NO:533 (1043400.5 repeat2) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

20       SEQ ID NO:534 (1043400.8 repeat1) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

SEQ ID NO:535 (1043400.8 repeat2) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

25       SEQ ID NO:536 (1043400.8 repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:537 (1043400.9 repeat1) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:538 (1043400.9 repeat2) represents an example of a cDNA sequence corresponding to repeat number 5 from the 5' variable region of O772P.

30       SEQ ID NO:539 (1043400.9 repeat3) represents an example of a cDNA sequence corresponding to repeat number 7 from the 5' variable region of O772P.

SEQ ID NO:540 (1043400.9 repeat4) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:541 (1043400.11 repeat1) represents an example of a cDNA sequence corresponding to repeat number 1 from the 5' variable region of O772P.

5        SEQ ID NO:542 (1043400.11 repeat2) represents an example of a cDNA sequence corresponding to repeat number 2 from the 5' variable region of O772P.

SEQ ID NO:543 (1043400.11 repeat3) represents an example of a cDNA sequence corresponding to repeat number 3 from the 5' variable region of O772P.

10       SEQ ID NO:544 (1043400.11 repeat4) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

SEQ ID NO:545 (1043400.11 repeat5) represents an example of a cDNA sequence corresponding to repeat number 12 from the 5' variable region of O772P.

SEQ ID NO:546 (1043400.12 repeat1) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

15       SEQ ID NO:547 (PB repeatA) represents an example of a cDNA sequence corresponding to repeat number 1 from the 5' variable region of O772P.

SEQ ID NO:548 (PB repeatB) represents an example of a cDNA sequence corresponding to repeat number 2 from the 5' variable region of O772P.

20       SEQ ID NO:549 (PB repeatE) represents an example of a cDNA sequence corresponding to repeat number 3 from the 5' variable region of O772P.

SEQ ID NO:550 (PB repeatG) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:551 (PB repeatC) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

25       SEQ ID NO:552 (PB repeatH) represents an example of a cDNA sequence corresponding to repeat number 6 from the 5' variable region of O772P.

SEQ ID NO:553 (PB repeatJ) represents an example of a cDNA sequence corresponding to repeat number 7 from the 5' variable region of O772P.

30       SEQ ID NO:554 (PB repeatK) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:555 (PB repeatD) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

SEQ ID NO:556 (PB repeatI) represents an example of a cDNA sequence corresponding to repeat number 10 from the 5' variable region of O772P.

5 SEQ ID NO:557 (PB repeatM) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

SEQ ID NO:558 (PB repeat9) represents an example of a cDNA sequence corresponding to repeat number 12 from the 5' variable region of O772P.

10 SEQ ID NO:559 (PB repeat8.5) represents an example of a cDNA sequence corresponding to repeat number 13 from the 5' variable region of O772P.

SEQ ID NO:560 (PB repeat8) represents an example of a cDNA sequence corresponding to repeat number 14 from the 5' variable region of O772P.

SEQ ID NO:561 (PB repeat7) represents an example of a cDNA sequence corresponding to repeat number 15 from the 5' variable region of O772P.

15 SEQ ID NO:562 (PB repeat6) represents an example of a cDNA sequence corresponding to repeat number 16 from the 5' variable region of O772P.

SEQ ID NO:563 (PB repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

20 SEQ ID NO:564 (PB repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:565 (PB repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:566 (PB repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

25 SEQ ID NO:567 (PB repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:568 represents the cDNA sequence form the 3' constant region.

30 SEQ ID NO:569 represents a cDNA sequence containing the consensus sequences of the 21 repeats, the 3' constant region and the 3' untranslated region.

SEQ ID NO:570 represents the cDNA sequence of the consensus repeat sequence.

SEQ ID NO:571 represents the consensus amino acid sequence of one potential open reading frame of repeat number 1 from the 5' variable region of O772P.

5        SEQ ID NO:572 represents the consensus amino acid sequence of a second potential open reading frame of repeat number 1 from the 5' variable region of O772P.

SEQ ID NO:573 represents the consensus amino acid sequence of a third potential open reading frame of repeat number 1 from the 5' variable region of O772P.

10        SEQ ID NO:574 represents the consensus amino acid sequence of repeat number 2 from the 5' variable region of O772P.

SEQ ID NO:575 represents the consensus amino acid sequence of repeat number 3 from the 5' variable region of O772P.

15        SEQ ID NO:576 represents the consensus amino acid sequence of repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:577 represents the consensus amino acid sequence of repeat number 5 from the 5' variable region of O772P.

SEQ ID NO:578 represents the consensus amino acid sequence of repeat number 6 from the 5' variable region of O772P.

20        SEQ ID NO:579 represents the consensus amino acid sequence of repeat number 7 from the 5' variable region of O772P.

SEQ ID NO:580 represents the consensus amino acid sequence of repeat number 8 from the 5' variable region of O772P.

25        SEQ ID NO:581 represents the consensus amino acid sequence of repeat number 9 from the 5' variable region of O772P.

SEQ ID NO:582 represents the consensus amino acid sequence of repeat number 10 from the 5' variable region of O772P.

SEQ ID NO:583 represents the consensus amino acid sequence of repeat number 11 from the 5' variable region of O772P.

30        SEQ ID NO:584 represents the consensus amino acid sequence of repeat number 12 from the 5' variable region of O772P.

SEQ ID NO:585 represents the consensus amino acid sequence of repeat number 13 from the 5' variable region of O772P.

SEQ ID NO:586 represents the consensus amino acid sequence of repeat number 14 from the 5' variable region of O772P.

5        SEQ ID NO:587 represents the consensus amino acid sequence of repeat number 15 from the 5' variable region of O772P.

SEQ ID NO:588 represents the consensus amino acid sequence of repeat number 16 from the 5' variable region of O772P.

10       SEQ ID NO:589 represents the consensus amino acid sequence of repeat number 17 from the 5' variable region of O772P.

SEQ ID NO:590 represents the consensus amino acid sequence of repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:591 represents the consensus amino acid sequence of repeat number 19 from the 5' variable region of O772P.

15       SEQ ID NO:592 represents the consensus amino acid sequence of repeat number 20 from the 5' variable region of O772P.

SEQ ID NO:593 represents the consensus amino acid sequence of repeat number 21 from the 5' variable region of O772P.

20       SEQ ID NO:594 represents the amino acid sequence of the 3' constant region.

SEQ ID NO:595 represents an amino acid sequence containing the consensus sequences of the 21 repeats and the 3' constant region.

SEQ ID NO:596 represents the amino acid sequence of the consensus repeat sequence.

25       Figures 1A-1S (SEQ ID NO:1-71) depict partial sequences of polynucleotides encoding representative secreted ovarian carcinoma antigens.

Figures 2A-2C depict full insert sequences for three of the clones of Figure 1. Figure 2A shows the sequence designated O7E (11731; SEQ ID NO:72), Figure 2B shows the sequence designated O9E (11785; SEQ ID NO:73) and Figure 2C  
30       shows the sequence designated O8E (13695; SEQ ID NO:74).

Figure 3 presents results of microarray expression analysis of the ovarian carcinoma sequence designated O8E.

Figure 4 presents a partial sequence of a polynucleotide (designated 3g; SEQ ID NO:75) encoding an ovarian carcinoma sequence that is a splice fusion  
5 between the human T-cell leukemia virus type I oncoprotein TAX and osteonectin.

Figure 5 presents the ovarian carcinoma polynucleotide designated 3f (SEQ ID NO:76).

Figure 6 presents the ovarian carcinoma polynucleotide designated 6b (SEQ ID NO:77).

10 Figures 7A and 7B present the ovarian carcinoma polynucleotides designated 8e (SEQ ID NO:78) and 8h (SEQ ID NO:79).

Figure 8 presents the ovarian carcinoma polynucleotide designated 12c (SEQ ID NO:80).

15 Figure 9 presents the ovarian carcinoma polynucleotide designated 12h (SEQ ID NO:81).

Figure 10 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 3f.

Figure 11 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 6b.

20 Figure 12 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 8e.

Figure 13 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 12c.

25 Figure 14 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 12h.

Figures 15A-15EEE depict partial sequences of additional polynucleotides encoding representative secreted ovarian carcinoma antigens (SEQ ID NO:82-310).

30 Figure 16 is a diagram illustrating the location of various partial O8E sequences within the full length sequence.



Figure 17 is a graph illustrating the results of epitope mapping studies on O8E protein.

Figure 18 is graph of a fluorescence activated cell sorting (FACS) analysis of O8E cell surface expression.

5 Figure 19 is graph of a FACS analysis of O8E cell surface expression.

Figure 20 shows FACS analysis results for O8E transfected HEK293 cells demonstrating cell surface expression of O8E.

Figure 21 shows FACS analysis results for SKBR3 breast tumor cells demonstrating cell surface expression of O8E.

10 Figure 22 shows O8E expression in HEK 293 cells. The cells were probed with anti-O8E rabbit polyclonal antisera #2333L.

Figure 23 shows the ELISA analysis of anti-O8E rabbit sera.

Figure 24 shows the ELISA analysis of affinity purified rabbit anti-O8E polyclonal antibody.

15 Figure 25 is a graph determining antibody internalization of anti-O8E mAb showing that mAbs against amino acids 61-80 induces ligand internalization.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy of cancer, such as ovarian cancer. The  
20 compositions described herein may include immunogenic polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies that bind to a polypeptide, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells).

Polypeptides of the present invention generally comprise at least an immunogenic portion of an ovarian carcinoma protein or a variant thereof. Certain  
25 ovarian carcinoma proteins have been identified using an immunoassay technique, and are referred to herein as ovarian carcinoma antigens. An "ovarian carcinoma antigen" is a protein that is expressed by ovarian tumor cells (preferably human cells) at a level that is at least two fold higher than the level in normal ovarian cells. Certain ovarian carcinoma antigens react detectably (within an immunoassay, such as an ELISA or  
30 Western blot) with antisera generated against serum from an immunodeficient animal

implanted with a human ovarian tumor. Such ovarian carcinoma antigens are shed or secreted from an ovarian tumor into the sera of the immunodeficient animal. Accordingly, certain ovarian carcinoma antigens provided herein are secreted antigens. Certain nucleic acid sequences of the subject invention generally comprise a DNA or  
5 RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence.

The present invention further provides ovarian carcinoma sequences that are identified using techniques to evaluate altered expression within an ovarian tumor. Such sequences may be polynucleotide or protein sequences. Ovarian carcinoma  
10 sequences are generally expressed in an ovarian tumor at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal ovarian tissue, as determined using a representative assay provided herein. Certain partial ovarian carcinoma polynucleotide sequences are presented herein. Proteins encoded by genes comprising such polynucleotide sequences (or complements thereof) are also  
15 considered ovarian carcinoma proteins.

Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to at least a portion of an ovarian carcinoma polypeptide as described herein. T cells that may be employed within the compositions provided herein are generally T cells (*e.g.*, CD4<sup>+</sup> and/or CD8<sup>+</sup>) that are  
20 specific for such a polypeptide. Certain methods described herein further employ antigen-presenting cells (such as dendritic cells or macrophages) that express an ovarian carcinoma polypeptide as provided herein.

#### Ovarian Carcinoma Polynucleotides

Any polynucleotide that encodes an ovarian carcinoma protein or a  
25 portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 45 consecutive nucleotides, that encode a portion of an ovarian carcinoma protein. More preferably, a polynucleotide encodes an immunogenic portion of an ovarian carcinoma  
30 protein, such as an ovarian carcinoma antigen. Polynucleotides complementary to any

such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a  
5 polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes an ovarian carcinoma protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity  
10 of the encoded polypeptide is not diminished, relative to a native ovarian carcinoma protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native ovarian carcinoma protein or  
15 a portion thereof.

The percent identity for two polynucleotide or polypeptide sequences may be readily determined by comparing sequences using computer algorithms well known to those of ordinary skill in the art, such as Megalign, using default parameters. Comparisons between two sequences are typically performed by comparing the  
20 sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, or 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment of sequences for  
25 comparison may be conducted, for example, using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. Preferably, the percentage of sequence identity is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the  
30 window may comprise additions or deletions (*i.e.*, gaps) of 20 % or less, usually 5 to 15 %, or 10 to 12%, relative to the reference sequence (which does not contain additions or

deletions). The percent identity may be calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

5 Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native ovarian carcinoma protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 10 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode 15 a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous 20 genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

25 Polynucleotides may be prepared using any of a variety of techniques. For example, an ovarian carcinoma polynucleotide may be identified, as described in more detail below, by screening a late passage ovarian tumor expression library with antisera generated against sera of immunocompetent mice after injection of such mice with sera from SCID mice implanted with late passage ovarian tumors. Ovarian carcinoma polynucleotides may also be identified using any of a variety of techniques 30 designed to evaluate differential gene expression. Alternatively, polynucleotides may

be amplified from cDNA prepared from ovarian tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

5           An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, an ovarian carcinoma cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for  
10 identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured  
15 bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using  
20 a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be  
25 generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed  
30 using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target

sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding portions of ovarian carcinoma antigens are provided in Figures 1A-1S (SEQ ID NO:1 to 71) and Figures 15A to 15EEE (SEQ ID NO:82 to 310). The sequences provided in Figures 1A-1S appear to be novel. For sequences in Figures 15A-15EEE, database searches revealed matches having substantial identity. These polynucleotides were isolated by serological screening of an ovarian tumor cDNA expression library, using a technique designed to identify secreted tumor antigens. Briefly, a late passage ovarian tumor expression library was prepared from a SCID-derived human ovarian tumor (OV9334) in the vector  $\lambda$ -screen (Novagen). The sera used for screening were obtained by

injecting immunocompetent mice with sera from SCID mice implanted with one late passage ovarian tumors. This technique permits the identification of cDNA molecules that encode immunogenic portions of secreted tumor antigens.

5 The polynucleotides recited herein, as well as full length polynucleotides comprising such sequences, other portions of such full length polynucleotides, and sequences complementary to all or a portion of such full length molecules, are specifically encompassed by the present invention. It will be apparent to those of ordinary skill in the art that this technique can also be applied to the identification of antigens that are secreted from other types of tumors.

10 Other nucleic acid sequences of cDNA molecules encoding portions of ovarian carcinoma proteins are provided in Figures 4-9 (SEQ ID NO:75-81), as well as SEQ ID NO:313-384. These sequences were identified by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in an ovarian tumor than in normal ovarian tissue, as determined using a representative  
15 assay provided herein). Such screens were performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). SEQ ID NO:311 and 391 provide full length sequences incorporating certain of these nucleic acid sequences.

20 Any of a variety of well known techniques may be used to evaluate tumor-associated expression of a cDNA. For example, hybridization techniques using labeled polynucleotide probes may be employed. Alternatively, or in addition, amplification techniques such as real-time PCR may be used (*see* Gibson et al., *Genome Research* 6:995-1001, 1996; Heid et al., *Genome Research* 6:986-994, 1996). Real-  
25 time PCR is a technique that evaluates the level of PCR product accumulation during amplification. This technique permits quantitative evaluation of mRNA levels in multiple samples. Briefly, mRNA is extracted from tumor and normal tissue and cDNA is prepared using standard techniques. Real-time PCR may be performed, for example, using a Perkin Elmer/Applied Biosystems (Foster City, CA) 7700 Prism instrument.  
30 Matching primers and fluorescent probes may be designed for genes of interest using, for example, the primer express program provided by Perkin Elmer/Applied Biosystems

(Foster City, CA). Optimal concentrations of primers and probes may be initially determined by those of ordinary skill in the art, and control (e.g.,  $\beta$ -actin) primers and probes may be obtained commercially from, for example, Perkin Elmer/Applied Biosystems (Foster City, CA). To quantitate the amount of specific RNA in a sample, a  
5 standard curve is generated alongside using a plasmid containing the gene of interest. Standard curves may be generated using the Ct values determined in the real-time PCR, which are related to the initial cDNA concentration used in the assay. Standard dilutions ranging from  $10^{-10}$  to  $10^{-6}$  copies of the gene of interest are generally sufficient. In addition, a standard curve is generated for the control sequence. This permits  
10 standardization of initial RNA content of a tissue sample to the amount of control for comparison purposes.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced  
15 using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding an ovarian carcinoma antigen, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain  
20 portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo*.

A portion of a sequence complementary to a coding sequence (i.e., an antisense polynucleotide) may also be used as a probe or to modulate gene expression.  
25 cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells or tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of an ovarian carcinoma protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to  
30 open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., In Huber and Carr, *Molecular and Immunologic Approaches*,



Futura Publishing Co. (Mt. Kisco, NY; 1994). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

5           Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and  
10 other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of  
15 particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

20           Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For  
25 example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of  
30 transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also

be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

#### Ovarian Carcinoma Polypeptides

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of an ovarian carcinoma protein or a variant thereof, as described herein. As noted above, certain ovarian carcinoma proteins are ovarian carcinoma antigens that are expressed by ovarian tumor cells and react detectably within an immunoassay (such as an ELISA) with antisera generated against serum from an immunodeficient animal implanted with an ovarian tumor. Other ovarian carcinoma proteins are encoded by ovarian carcinoma polynucleotides recited herein. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of an antigen that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of an ovarian carcinoma protein or a variant thereof. Preferred immunogenic portions are encoded by cDNA molecules isolated as described herein. Further immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with ovarian carcinoma protein-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "ovarian carcinoma protein-

specific" if they specifically bind to an ovarian carcinoma protein (*i.e.*, they react with the ovarian carcinoma protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera, antibodies and T cells may be prepared as described herein, and using well known techniques. An immunogenic portion of a native ovarian carcinoma protein is a portion that reacts with such antisera, antibodies and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length protein. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

As noted above, a composition may comprise a variant of a native ovarian carcinoma protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native ovarian carcinoma protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with ovarian carcinoma protein-specific antisera may be enhanced or unchanged, relative to the native ovarian carcinoma protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native ovarian carcinoma protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with ovarian carcinoma protein-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the native polypeptide. Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells

include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available  
5 filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic  
10 means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is  
15 commercially available from suppliers such as Applied BioSystems, Inc. (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises one polypeptide as described herein and a known tumor antigen, such as an ovarian  
20 carcinoma protein or a variant of such a protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion  
25 partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques,  
30 including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused

protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred  
10 embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen present cells. Other  
15 fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is  
20 derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been  
25 exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at  
30 residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

#### Binding Agents

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to an ovarian carcinoma protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to an ovarian carcinoma protein if it reacts at a detectable level (within, for example, an ELISA) with an ovarian carcinoma protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a "complex" is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as ovarian cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to an ovarian carcinoma antigen will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological



samples (e.g., blood, sera, leukophoresis, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the

desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include

methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

5           A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-  
10   containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

          Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker  
15   group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

          It will be evident to those skilled in the art that a variety of bifunctional  
20   or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

25           Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction  
30   of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of

derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one  
5 embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for  
10 attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may  
15 also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be  
20 formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and  
25 immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Also provided herein are anti-idiotypic antibodies that mimic an  
30 immunogenic portion of an ovarian carcinoma protein. Such antibodies may be raised against an antibody, or antigen-binding fragment thereof, that specifically binds to an

immunogenic portion of an ovarian carcinoma protein, using well known techniques. Anti-idiotypic antibodies that mimic an immunogenic portion of an ovarian carcinoma protein are those antibodies that bind to an antibody, or antigen-binding fragment thereof, that specifically binds to an immunogenic portion of an ovarian carcinoma protein, as described herein.

### T Cells

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for an ovarian carcinoma protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be present within (or isolated from) bone marrow, peripheral blood or a fraction of bone marrow or peripheral blood of a mammal, such as a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human animals, cell lines or cultures.

T cells may be stimulated with an ovarian carcinoma polypeptide, polynucleotide encoding an ovarian carcinoma polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, an ovarian carcinoma polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for an ovarian carcinoma polypeptide if the T cells kill target cells coated with an ovarian carcinoma polypeptide or expressing a gene encoding such a polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be

accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with an ovarian carcinoma polypeptide  
5 (200 ng/ml - 100 µg/ml, preferably 100 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells and/or contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., Current  
10 Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998). T cells that have been activated in response to an ovarian carcinoma polypeptide, polynucleotide or ovarian carcinoma polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Ovarian carcinoma polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient or a related or  
15 unrelated donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to an ovarian carcinoma polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be  
20 accomplished in a variety of ways. For example, the T cells can be re-exposed to an ovarian carcinoma polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize an ovarian carcinoma polypeptide. Alternatively, one or more T cells that proliferate in the presence of an ovarian carcinoma polypeptide can be expanded in number by cloning. Methods for  
25 cloning cells are well known in the art, and include limiting dilution. Following expansion, the cells may be administered back to the patient as described, for example, by Chang et al., *Crit. Rev. Oncol. Hematol.* 22:213, 1996.

#### Pharmaceutical Compositions and Vaccines

Within certain aspects, polypeptides, polynucleotides, binding agents  
30 and/or immune system cells as described herein may be incorporated into

pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds or cells and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds or cells and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance  
5 that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and  
10 adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound within the composition or vaccine.

15 A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid  
20 expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox  
25 virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651;  
30 EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al.,

PNAS 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 5 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier 10 will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. 15 For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for 20 example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) 25 and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. 30 Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune



responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ), alum, biodegradable  
5 microspheres, monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , IL-2 and IL-12) tend to favor the  
10 induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- $\beta$ ) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly  
15 Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type  
20 response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). Also preferred is AS-2 (SmithKline Beecham). CpG-containing oligonucleotides (in which the CpG  
25 dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the  
30 combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO

96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination  
5 of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example,  
10 oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant  
15 level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific  
20 immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se*  
25 and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic  
30 cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to

be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a ovarian carcinoma antigen (or portion or other variant thereof) such that the antigen, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells  
5 may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun  
10 approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently  
15 conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

#### Cancer Therapy

In further aspects of the present invention, the compositions described  
20 herein may be used for immunotherapy of cancer, such as ovarian cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a  
25 cancer or to treat a patient afflicted with a cancer. Within certain preferred embodiments, a patient is afflicted with ovarian cancer. Such cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration  
30 of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immuno response-modifying agents (such as tumor vaccines, bacterial adjuvants and/or  
5 cytokines).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host  
10 immune system. Examples of effector cells include T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides  
15 recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for  
20 adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above,  
25 immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example,  
30 antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system.

Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., 5 *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into stem cells taken from a patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

Routes and frequency of administration, as well as dosage, will vary 10 from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration), orally or in the bed of a resected tumor. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are 15 administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level.. Such response can be monitored by measuring 20 the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for 25 pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the 30 active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical

outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to an ovarian carcinoma antigen generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated  
5 using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

#### Screens for Identifying Secreted Ovarian Carcinoma Antigens

The present invention provides methods for identifying secreted tumor antigens. Within such methods, tumors are implanted into immunodeficient animals  
10 such as SCID mice and maintained for a time sufficient to permit secretion of tumor antigens into serum. In general, tumors may be implanted subcutaneously or within the gonadal fat pad of an immunodeficient animal and maintained for 1-9 months, preferably 1-4 months. Implantation may generally be performed as described in WO 97/18300. The serum containing secreted antigens is then used to prepare antisera in  
15 immunocompetent mice, using standard techniques and as described herein. Briefly, 50-100  $\mu$ L of sera (pooled from three sets of immunodeficient mice, each set bearing a different SCID-derived human ovarian tumor) may be mixed 1:1 (vol:vol) with an appropriate adjuvant, such as RIBI-MPL or MPL + TDM (Sigma Chemical Co., St. Louis, MO) and injected intraperitoneally into syngeneic immunocompetent animals at  
20 monthly intervals for a total of 5 months. Antisera from animals immunized in such a manner may be obtained by drawing blood after the third, fourth and fifth immunizations. The resulting antiserum is generally pre-cleared of *E. coli* and phage antigens and used (generally following dilution, such as 1:200) in a serological expression screen.

25 The library is typically an expression library containing cDNAs from one or more tumors of the type that was implanted into SCID mice. This expression library may be prepared in any suitable vector, such as  $\lambda$ -screen (Novagen). cDNAs that encode a polypeptide that reacts with the antiserum may be identified using standard techniques, and sequenced. Such cDNA molecules may be further characterized to

evaluate expression in tumor and normal tissue, and to evaluate antigen secretion in patients.

The methods provided herein have advantages over other methods for tumor antigen discovery. In particular, all antigens identified by such methods should  
5 be secreted or released through necrosis of the tumor cells. Such antigens may be present on the surface of tumor cells for an amount of time sufficient to permit targeting and killing by the immune system, following vaccination.

#### Methods for Detecting Cancer

In general, a cancer may be detected in a patient based on the presence of  
10 one or more ovarian carcinoma proteins and/or polynucleotides encoding such proteins in a biological sample (such as blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as ovarian cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein  
15 generally permit detection of the level of protein that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, an ovarian carcinoma-associated sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

20 There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b)  
25 detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection  
30 reagent that contains a reporter group and specifically binds to the binding



agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length ovarian carcinoma proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports  
5 having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.  
10 This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a  
15 different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically  
20 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact  
25 time (*i.e.,* incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with ovarian cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve  
30 equilibrium may be readily determined by assaying the level of binding that occurs over

a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second  
5 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of  
10 binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups  
15 and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

20 To determine the presence or absence of a cancer, such as ovarian cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with  
25 samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985,  
30 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity)

that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use  
5 ovarian carcinoma polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such ovarian carcinoma protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with an ovarian carcinoma protein in a biological sample.  
10 Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with an ovarian carcinoma protein, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated  
15 T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with an ovarian carcinoma protein (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of ovarian carcinoma protein to serve as a control. For  
20 CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

25 As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding an ovarian carcinoma protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of an ovarian carcinoma protein cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is  
30 specific for (*i.e.*, hybridizes to) a polynucleotide encoding the ovarian carcinoma protein. The amplified cDNA is then separated and detected using techniques well

known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding an ovarian carcinoma protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

5           To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding an ovarian carcinoma protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably,  
10 oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous  
15 nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence provided herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

20           One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample such as a biopsy tissue and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification  
25 may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered  
30 positive.

In another embodiment, ovarian carcinoma proteins and polynucleotides encoding such proteins may be used as markers for monitoring the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple ovarian carcinoma protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

#### Diagnostic Kits

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to an ovarian carcinoma protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain

a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding an ovarian carcinoma protein in a biological sample. Such kits generally  
5 comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding an ovarian carcinoma protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second  
10 oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding an ovarian carcinoma protein.

The following Examples are offered by way of illustration and not by way of limitation.



## EXAMPLES

## EXAMPLE 1

## IDENTIFICATION OF REPRESENTATIVE OVARIAN CARCINOMA PROTEIN CDNAS

This Example illustrates the identification of cDNA molecules encoding  
5 ovarian carcinoma proteins.

Anti-SCID mouse sera (generated against sera from SCID mice carrying  
late passage ovarian carcinoma) was pre-cleared of E. coli and phage antigens and used  
at a 1:200 dilution in a serological expression screen. The library screened was made  
from a SCID-derived human ovarian tumor (OV9334) using a directional RH oligo(dT)  
10 priming cDNA library construction kit and the  $\lambda$ Screen vector (Novagen). A  
bacteriophage lambda screen was employed. Approximately 400,000 pfu of the  
amplified OV9334 library were screened.

196 positive clones were isolated. Certain sequences that appear to be  
novel are provided in Figures 1A-1S and SEQ ID NO:1 to 71. Three complete insert  
15 sequences are shown in Figures 2A-2C (SEQ ID NO:72 to 74). Other clones having  
known sequences are presented in Figures 15A-15EEE (SEQ ID NO:82 to 310).  
Database searches identified the following sequences that were substantially identical to  
the sequences presented in Figures 15A-15EEE.

These clones were further characterized using microarray technology to  
20 determine mRNA expression levels in a variety of tumor and normal tissues. Such  
analyses were performed using a Synteni (Palo Alto, CA) microarray, according to the  
manufacturer's instructions. PCR amplification products were arrayed on slides, with  
each product occupying a unique location in the array. mRNA was extracted from the  
tissue sample to be tested, reverse transcribed and fluorescent-labeled cDNA probes  
25 were generated. The microarrays were probed with the labeled cDNA probes and the  
slides were scanned to measure fluorescence intensity. Data was analyzed using  
Synteni's provided GEMtools software. The results for one clone (13695, also referred  
to as O8E) are shown in Figure 3.

## EXAMPLE 2

## IDENTIFICATION OF OVARIAN CARCINOMA cDNAs USING MICROARRAY TECHNOLOGY

This Example illustrates the identification of ovarian carcinoma polynucleotides by PCR subtraction and microarray analysis. Microarrays of cDNAs  
5 were analyzed for ovarian tumor-specific expression using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997).

A PCR subtraction was performed using a tester comprising cDNA of  
10 four ovarian tumors (three of which were metastatic tumors) and a driver of cDNA from five normal tissues (adrenal gland, lung, pancreas, spleen and brain). cDNA fragments recovered from this subtraction were subjected to DNA microarray analysis where the fragments were PCR amplified, adhered to chips and hybridized with fluorescently labeled probes derived from mRNAs of human ovarian tumors and a variety of normal  
15 human tissues. In this analysis, the slides were scanned and the fluorescence intensity was measured, and the data were analyzed using Synteni's GEMtools software. In general, sequences showing at least a 5-fold increase in expression in tumor cells (relative to normal cells) were considered ovarian tumor antigens. The fluorescent results were analyzed and clones that displayed increased expression in ovarian tumors  
20 were further characterized by DNA sequencing and database searches to determine the novelty of the sequences.

Using such assays, an ovarian tumor antigen was identified that is a splice fusion between the human T-cell leukemia virus type I oncoprotein TAX (*see* Jin et al., *Cell* 93:81-91, 1998) and an extracellular matrix protein called osteonectin. A  
25 splice junction sequence exists at the fusion point. The sequence of this clone is presented in Figure 4 and SEQ ID NO:75. Osteonectin, unspliced and unaltered, was also identified from such assays independently.

Further clones identified by this method are referred to herein as 3f, 6b, 8e, 8h, 12c and 12h. Sequences of these clones are shown in Figures 5 to 9 and SEQ ID  
30 NO:76 to 81. Microarray analyses were performed as described above, and are presented in Figures 10 to 14. A full length sequence encompassing clones 3f, 6b, 8e

and 12h was obtained by screening an ovarian tumor (SCID-derived) cDNA library. This 2996 base pair sequence (designated O772P) is presented in SEQ ID NO:311, and the encoded 914 amino acid protein sequence is shown in SEQ ID NO:312. PSORT analysis indicates a Type 1a transmembrane protein localized to the plasma membrane.

- 5 In addition to certain of the sequences described above, this screen identified the following sequences which are described in detail in Table 1:

Table 1

| Sequence                | Comments                                  |
|-------------------------|---|
| OV4vG11 (SEQ ID NO:313) | human clone 1119D9 on chromosome 20p12    |
| OV4vB11 (SEQ ID NO:314) | human UWGC:y14c094 from chromosome 6p21   |
| OV4vD9 (SEQ ID NO:315)  | human clone 1049G16 chromosome 20q12-13.2 |
| OV4vD5 (SEQ ID NO:316)  | human KIAA0014 gene                       |
| OV4vC2 (SEQ ID NO:317)  | human KIAA0084 gene                       |
| OV4vF3 (SEQ ID NO:318)  | human chromosome 19 cosmid R31167         |
| OV4VC1 (SEQ ID NO:319)  | novel                                     |
| OV4vH3 (SEQ ID NO:320)  | novel                                     |
| OV4vD2 (SEQ ID NO:321)  | novel                                     |
| O815P (SEQ ID NO:322)   | novel                                     |
| OV4vC12 (SEQ ID NO:323) | novel                                     |
| OV4vA4 (SEQ ID NO:324)  | novel                                     |
| OV4vA3 (SEQ ID NO:325)  | novel                                     |
| OV4v2A5 (SEQ ID NO:326) | novel                                     |
| O819P (SEQ ID NO:327)   | novel                                     |
| O818P (SEQ ID NO:328)   | novel                                     |
| O817P (SEQ ID NO:329)   | novel                                     |
| O816P (SEQ ID NO:330)   | novel                                     |
| Ov4vC5 (SEQ ID NO:331)  | novel                                     |
| 21721 (SEQ ID NO:332)   | human lumican                             |
| 21719 (SEQ ID NO:333)   | human retinoic acid-binding protein II    |
| 21717 (SEQ ID NO:334)   | human 26S proteasome ATPase subunit       |
| 21654 (SEQ ID NO:335)   | human copine I                            |
| 21627 (SEQ ID NO:336)   | human neuron specific gamma-2 enolase     |

| Sequence   | Comments  |
|--|---|
| 21623 (SEQ ID NO:337)                            | human geranylgeranyl transferase II                   |
| 21621 (SEQ ID NO:338)                            | human cyclin-dependent protein kinase                 |
| 21616 (SEQ ID NO:339)                            | human prepro-megakaryocyte potentiating factor        |
| 21612 (SEQ ID NO:340)                            | human UPH1  |
| 21558 (SEQ ID NO:341)                            | human RalGDS-like 2 (RGL2)                            |
| 21555 (SEQ ID NO:342)                            | human autoantigen P542                                |
| 21548 (SEQ ID NO:343)                            | human actin-related protein (ARP2)                    |
| 21462 (SEQ ID NO:344)                            | human huntingtin interacting protein                  |
| 21441 (SEQ ID NO:345)                            | human 90K product (tumor associated antigen)          |
| 21439 (SEQ ID NO:346)                            | human guanine nucleotide regulator protein (tim1)     |
| 21438 (SEQ ID NO:347)                            | human Ku autoimmune (p70/p80) antigen                 |
| 21237 (SEQ ID NO:348)                            | human S-laminin                                       |
| 21436 (SEQ ID NO:349)                            | human ribophorin I                                    |
| 21435 (SEQ ID NO:350)                            | human cytoplasmic chaperonin hTRiC5                   |
| 21425 (SEQ ID NO:351)                            | humanEMX2   |
| 21423 (SEQ ID NO:352)                            | human p87/p89 gene                                    |
| 21419 (SEQ ID NO:353)                            | human HPBR11-7  |
| 21252 (SEQ ID NO:354)                            | human T1-227H   |
| 21251 (SEQ ID NO:355)                            | human cullin I  |
| 21247 (SEQ ID NO:356)                            | kunitz type protease inhibitor (KOP)                  |
| 21244-1 (SEQ ID NO:357)                          | human protein tyrosine phosphatase receptor F (PTPRF) |
| 21718 (SEQ ID NO:358)                            | human LTR repeat                                      |
| OV2-90 (SEQ ID NO:359)                           | novel   |
| Human zinc finger (SEQ ID NO:360)                |   |
| Human polyA binding protein (SEQ ID NO:361)      |   |
| Human pleitrophin (SEQ ID NO:362)                |   |
| Human PAC clone 278C19 (SEQ ID NO:363)           |   |
| Human LLRep3 (SEQ ID NO:364)                     |   |
| Human Kunitz type protease inhib (SEQ ID NO:365) |   |
| Human KIAA0106 gene (SEQ ID NO:366)              |   |
| Human keratin (SEQ ID NO:367)                    |   |
| Human HIV-1TAR (SEQ ID NO:368)                   |   |
| Human glia derived nexin (SEQ ID NO:369)         |   |

| Sequence  | Comments |
|---|----------|
| Human fibronectin (SEQ ID NO:370)                         |          |
| Human ECMproBM40 (SEQ ID NO:371)                          |          |
| Human collagen (SEQ ID NO:372)                            |          |
| Human alpha enolase (SEQ ID NO:373)                       |          |
| Human aldolase (SEQ ID NO:374)                            |          |
| Human transf growth factor BIG H3 (SEQ ID NO:375)         |          |
| Human SPARC osteonectin (SEQ ID NO:376)                   |          |
| Human SLP1 leucocyte protease (SEQ ID NO:377)             |          |
| Human mitochondrial ATP synth (SEQ ID NO:378)             |          |
| Human DNA seq clone 461P17 (SEQ ID NO:379)                |          |
| Human dbpB pro Y box (SEQ ID NO:380)                      |          |
| Human 40 kDa keratin (SEQ ID NO:381)                      |          |
| Human arginosuccinate synth (SEQ ID NO:382)               |          |
| Human acidic ribosomal phosphoprotein (SEQ ID NO:383)     |          |
| Human colon carcinoma laminin binding pro (SEQ ID NO:384) |          |

This screen further identified multiple forms of the clone O772P, referred to herein as 21013, 21003 and 21008. PSORT analysis indicates that 21003 (SEQ ID NO:386; translated as SEQ ID NO:389) and 21008 (SEQ ID NO:387; translated as SEQ ID NO:390) represent Type 1a transmembrane protein forms of

5 O772P. 21013 (SEQ ID NO:385; translated as SEQ ID NO:388) appears to be a truncated form of the protein and is predicted by PSORT analysis to be a secreted protein.

Additional sequence analysis resulted in a full length clone for O8E (2627 bp, which agrees with the message size observed by Northern analysis; SEQ ID

10 NO:391). This nucleotide sequence was obtained as follows: the original O8E sequence (OrigO8Econs) was found to overlap by 33 nucleotides with a sequence from an EST clone (IMAGE#1987589). This clone provided 1042 additional nucleotides upstream of the original O8E sequence. The link between the EST and O8E was confirmed by sequencing multiple PCR fragments generated from an ovary primary tumor library

15 using primers to the unique EST and the O8E sequence (ESTxO8EPCR). Full length status was further indicated when anchored PCR from the ovary tumor library gave

several clones (AnchoredPCR cons) that all terminated upstream of the putative start methionine, but failed to yield any additional sequence information. Figure 16 presents a diagram that illustrates the location of each partial sequence within the full length O8E sequence.

5 Two protein sequences may be translated from the full length O8E. For "a" (SEQ ID NO:393) begins with a putative start methionine. A second form "b" (SEQ ID NO:392) includes 27 additional upstream residues to the 5' end of the nucleotide sequence.

### EXAMPLE 3

10 This example discloses the identification and characterization of antibody epitopes recognized by the O8E polyclonal anti-sera.

Rabbit anti-sera was raised against E. coli derived O8E recombinant protein and tested for antibody epitope recognition against 20 or 21 mer peptides that correspond to the O8E amino acid sequence. Peptides spanning amino acid regions 31  
15 to 65, 76 to 110, 136 to 200 and 226 to 245 of the full length O8E protein were recognized by an acid eluted peak and/or a salt eluted peak from affinity purified anti-O8E sera. Thus, the corresponding amino acid sequences of the above peptides constitute the antibody epitopes recognized by affinity purified anti-O8E antibodies.

ELISA analysis of anti-O8E rabbit sera is shown in Figure 23, and ELISA  
20 analysis of affinity purified rabbit anti-O8E polyclonal antibody is shown in Figure 24.

For epitope mapping, 20 or 21 mer peptides corresponding to the O8E protein were synthesized. For antibody affinity purification, rabbit anti-O8E sera was run over an O8E-sepharose column, then antibody was eluted with a salt buffer containing 0.5 M NaCl and 20 mM PO<sub>4</sub>, followed by an acid elution step using 0.2 M  
25 Glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8 and buffer exchanged into phosphate buffered saline (PBS). For enzyme linked immunosorbant assay (ELISA) analysis, O8E peptides and O8E recombinant protein were coated onto 96 well flat bottom plates at 2 µg/ml for 2 hours at room temperature (RT). Plates were then washed 5 times with PBS + 0.1 % Tween 20 and blocked with  
30 PBS + 1 % bovine serum albumin (BSA) for 1 hour. Affinity purified anti-O8E antibody, either an acid or salt eluted fraction, was then added to the wells at 1 µg/ml

and incubated at RT for 1 hr. Plates were again washed, followed by the addition of donkey anti-rabbit-Ig-horseradish peroxidase (HRP) antibody for 1 hour at RT. Plates were washed, then developed by the addition of the chromagenic substrate 3, 3', 5, 5'-tetramethylbenzidine (TMB) (described by Bos *et al.*, *J. of Immunoassay* 2:187-204 (1981); available from Sigma (St. Louis, MO)). The reaction was incubated 15 minutes at RT and then stopped by the addition of 1 N H<sub>2</sub>SO<sub>4</sub>. Plates were read at an optical density of 450 (OD450) in an automated plate reader. The sequences of peptides corresponding to the O8E antibody epitopes are disclosed herein as SEQ ID NO: 394-415. Antibody epitopes recognized by the O8E polyclonal anti-sera are disclosed herein in Figure 17.

#### EXAMPLE 4

This example discloses IHC analysis of O8E expression in ovarian cancer tissue samples.

For immunohistochemistry studies, paraffin-embedded formalin fixed ovarian cancer tissue was sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody (anti-O8E rabbit affinity purified polyclonal antibody) was added to each section for 25 min followed by a 25 min incubation with an anti-rabbit biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 min incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase system was used along with DAB chromogen to visualize antigen expression. Slides were counterstained with hematoxylin. One (papillary serous carcinoma) of six ovarian cancer tissue sections displayed O8E immunoreactivity. Upon optimization of the staining conditions, 4/5 ovarian cancer samples stained positive using the O8E polyclonal antibody. O8E expression was localized to the plasma membrane.

Six ovarian cancer tissues were analyzed with the anti-O8E rabbit polyclonal antibody. One (papillary serous carcinoma) of six ovarian cancer tissue samples stained positive for O8E expression. O8E expression was localized to the surface membrane.

## EXAMPLE 5

This example discloses O8E peptides that are predicted to bind HLA-A2 and to be immunogenic for CD8 T cell responses in humans.

Potential HLA-A2 binding peptides of O8E were predicted by using the full-length open-reading frame (ORF) from O8E and running it through "Episeek," a program used to predict MHC binding peptides. The program used is based on the algorithm published by Parker, K.C. *et al.*, *J. Immunol.* 152(1):163-175 (1994) (incorporated by reference herein in its entirety). 10-mer and 9-mer peptides predicted to bind HLA-0201 are disclosed herein as SEQ ID NO: 416-435 and SEQ ID NO: 436-455, respectively.

## EXAMPLE 6

This example discloses O8E cell surface expression measured by fluorescence activated cell sorting.

For FACS analysis, cells were washed with ice cold staining buffer (PBS/1% BSA/azide). Next, the cells were incubated for 30 minutes on ice with 10 micrograms/ml of affinity purified rabbit anti-B305D polyclonal antibody. The cells were washed 3 times with staining buffer and then incubated with a 1:100 dilution of a goat anti-rabbit Ig (H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice. Following 3 washes, the cells were resuspended in staining buffer containing prodium iodide, a vital stain that allows for identification of permeable cells, and analyzed by FACS. O8E surface expression was confirmed on SKBR3 breast cancer cells and HEK293 cells that stably overexpress the cDNA for O8E. Neither MB415 cells nor HEK293 cells stably transfected with a control irrelevant plasmid DNA showed surface expression of O8E (Figures 18 and 19).

## EXAMPLE 7

This example further evaluates the expression and surface localization of O8E.

For expression and purification of antigen used for immunization, O8E expressed in an *E. coli* recombinant expression system was grown overnight in LB Broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning,



10 ml of the overnight culture was added to 500 ml of 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nanometers) of the culture reached 0.4-0.6 the cells were induced with IPTG (1 mM). 4 hours after induction with IPTG the cells were harvested by centrifugation. The cells  
5 were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed. To break open the E. coli cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and  
10 pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For protein that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0 , 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM  
15 imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using  
20 8M urea, 10 mM tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin such as Hi-Prep Q (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off of the column with an increasing  
25 salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. This material was then evaluated for acceptable purity as determined by SDS-PAGE or HPLC, concentration as determined by Lowry assay or Amino Acid Analysis, identity as determined by amino terminal  
30 protein sequence, and endotoxin level as determined by the Limulus (LAL) assay. The

proteins were then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

For generation of polyclonal anti-sera, 400 micrograms of each prostate antigen was combined with 100 micrograms of muramyl dipeptide (MDP). Equal  
5 volume of Incomplete Freund's Adjuvant (IFA) was added and then mixed. Every four weeks animals were boosted with 100 micrograms of antigen mixed with an equal volume of IFA. Seven days following each boost the animal was bled. Sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

For characterization of polyclonal antisera, 96 well plates were coated  
10 with antigen by incubating with 50 microliters (typically 1 microgram) at 4°C for 20 hrs. 250 microliters of BSA blocking buffer was added to the wells and incubated at RT for 2 hrs. Plates were washed 6 times with PBS/0.01% tween. Anti-O8E rabbit sera or affinity purified anti-O8e antibody was diluted in PBS. Fifty microliters of diluted antibody was added to each well and incubated at RT for 30 min. Plates were washed as  
15 described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at RT for 30 min. Plates were washed as described above and 100 microliters of TMB microwell Peroxidase Substrate was added to each well. Following a 15 minute incubation in the dark at room temperature the colorimetric reaction was stopped with 100 microliters of 1N H<sub>2</sub>SO<sub>4</sub> and read  
20 immediately at 450 nm. All polyclonal antibodies showed immunoreactivity to the O8E antigen.

For recombinant expression in mammalian HEK293 cells, full length O8E cDNA was subcloned into the mammalian expression vectors pcDNA3.1+ and pCEP4 (Invitrogen) which were modified to contain His and FLAG epitope tags,  
25 respectively. These constructs were transfected into HEK293 cells (ATCC) using Fugene 6 reagent (Roche). Briefly, HEK293 cells were plated at a density of 100,000 cells/ml in DMEM (Gibco) containing 10% FBS (Hyclone) and grown overnight. The following day, 2 ul of Fugene6 was added to 100 ul of DMEM containing no FBS and incubated for 15 minutes at room temperature. The Fugene6/DMEM mixture was then  
30 added to 1ug of O8E/pCEP4 or O8E/pcDNA3.1 plasmid DNA and incubated for 15 minutes at room temperature. The Fugene/DNA mix was then added to the HEK293

cells and incubated for 48-72 hrs at 37°C with 7% CO<sub>2</sub>. Cells were rinsed with PBS then collected and pelleted by centrifugation. For Western blot analysis, whole cell lysates were generated by incubating the cells in Triton-X100 containing lysis buffer for 30 minutes on ice. Lysates were then cleared by centrifugation at 10,000rpm for 5 minutes at 4 C. Samples were diluted with SDS-PAGE loading buffer containing beta-mercaptoethanol, then boiled for 10 minutes prior to loading the SDS-PAGE gel. Protein was transferred to nitrocellulose and probed using anti-O8E rabbit polyclonal sera #2333L at a dilution of 1:750. The blot was revealed with a goat anti-rabbit Ig coupled to HRP followed by incubation in ECL substrate.

For FACS analysis, cells were washed further with ice cold staining buffer (PBS+1%BSA+Azide). Next, the cells were incubated for 30 minutes on ice with 10ug/ml of Protein A purified anti-O8E polyclonal sera. The cells were washed 3 times with staining buffer and then incubated with a 1:100 dilution of a goat anti-rabbit Ig(H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice. Following 3 washes, the cells were resuspended in staining buffer containing Propidium Iodide (PI), a vital stain that allows for the identification of permeable cells, and analyzed by FACS.

From these experiments, the results of which are illustrated in Figures 20-21, O8E expression was detected on the surface of transfected HEK293 cells and SKBR3 cells by FACS analysis using rabbit anti-O8E sera. Expression was also detected in transfected HEK293 cell lysates by Western blot analysis (Figure 22).

## EXAMPLE 8

### GENERATION AND CHARACTERIZATION OF ANTI-O8E MABS.

Mouse monoclonal antibodies were raised against E. coli derived O8E proteins as follows. A/J mice were immunized intraperitoneally (IP) with Complete Freund's Adjuvant (CFA) containing 50 µg recombinant O8E, followed by a subsequent IP boost with Incomplete Freund's Adjuvant (IFA) containing 10µg recombinant O8E protein. Three days prior to removal of the spleens, the mice were immunized intravenously with approximately 50µg of soluble O8E recombinant protein. The spleen of a mouse with a positive titer to O8E was removed, and a single-cell suspension made and used for fusion to SP2/0 myeloma cells to generate B cell

hybridomas. The supernatants from the hybrid clones were tested by ELISA for specificity to recombinant O8E, and epitope mapped using peptides that spanned the entire O8E sequence. The mAbs were also tested by flow cytometry for their ability to detect O8E on the surface of cells stably transfected with O8E and on the surface of a breast tumor cell line.

For ELISA analysis, 96 well plates were coated with either recombinant O8E protein or overlapping 20-mer peptides spanning the entire O8E molecule at a concentration of either 1-2 $\mu$ g/ml or 10 $\mu$ g/ml, respectively. After coating, the plates were washed 5 times with washing buffer (PBS + 0.1% Tween-20) and blocked with PBS containing 0.5% BSA, 0.4% Tween-20. Hybrid supernatants or purified mAbs were then added and the plates incubated for 60 minutes at room temperature. The plates were washed 5 times with washing buffer and the secondary antibody, donkey-anti mouse Ig linked to horseradish peroxidase (HRP)(Jackson ImmunoResearch), was added for 60 minutes. The plates were again washed 5 times in washing buffer, followed by the addition of the peroxidase substrate. Of the hybridoma clones generated, 15 secreted mAbs that recognized the entire O8E protein. Epitope mapping revealed that of these 15 clones, 14 secreted mAbs that recognized the O8E amino acid residues 61-80 and one clone secreted a mAb that recognized amino acid residues 151-170.

For flow cytometric analysis, HEK293 cells which had been stably transfected with O8E and SKBR3 cells which express O8E mRNA, were harvested and washed in flow staining buffer (PBS+1%BSA+Azide). The cells were incubated with the supernatant from the mAb hybrids for 30 minutes on ice followed by 3 washes with staining buffer. The cells were incubated with goat-anti mouse Ig-FITC for 30 minutes on ice, followed by three washes with staining buffer before being resuspended in wash buffer containing propidium iodide. Flow cytometric analysis revealed that 15/15 mAbs were able to detect O8E protein expressed on the surface of O8E-transfected HEK293 cells. 6/6 mAbs tested on SKBR3 cells were able to recognize surface expressed O8E.

## EXAMPLE 9

## EXTENDED DNA AND PROTEIN SEQUENCE ANALYSIS OF SEQUENCE O772P

A full-length sequence encompassing clones 3f, 6b, 8e, and 12 was obtained by screening an ovarian tumor (SCID-derived) cDNA library described in detail in Example 2. This 2996 base pair sequence, designated O772P, is presented in SEQ ID NO: 311, and the encoded 914 amino acid protein sequence is shown in SEQ ID NO: 312. The DNA sequence O772P was searched against public databases including Genbank and showed a significant hit to Genbank Accession number AK024365 (SEQ ID NO: 457). This Genbank sequence was found to be 3557 base pairs in length and encodes a protein 1156 amino acids in length (SEQ ID NO: 459). A truncated version of this sequence, residues 25-3471, in which residue 25 corresponds to the first ATG initiation codon in the Genbank sequence, (SEQ ID NO: 456), encodes a protein that is 1148 amino acids in length (SEQ ID NO: 458). The published DNA sequence (SEQ ID NO: 457) differs from O772P in that it has a 5 base pair insertion corresponding to bases 958-962 of SEQ ID NO: 457. This insertion results in a frame shift such that SEQ ID NO: 457 encodes an additional N-terminal protein sequence relative to O772P (SEQ ID NO: 312). In addition, O772P encodes a unique N-terminal portion contained in residues 1-79 (SEQ ID NO: 460). The N-terminal portion of SEQ ID NO: 456, residues 1-313, also contains unique sequence and is listed as SEQ ID NO: 461.

## EXAMPLE 10

THE GENERATION OF POLYCLONAL ANTIBODIES FOR IMMUNOHISTOCHEMISTRY  
AND FLOW CYTOMETRIC ANALYSIS OF THE CELL ASSOCIATED EXPRESSION  
PATTERN OF MOLECULE O772P

The O772P molecule was identified in Examples 2 and 9 of this application. To evaluate the subcellular localization and specificity of antigen expression in various tissues, polyclonal antibodies were generated against O772P. To produce these antibodies, O772P-1 (amino acids 44-772 of SEQ ID NO:312) and O772P-2 (477-914 of SEQ ID NO:312) were expressed in an E. coli recombinant expression system and grown overnight at 37°C in LB Broth. The following day, 10ml

of the overnight culture was added to 500ml of 2xYT containing the appropriate antibiotics. When the optical density of the cultures (560 nanometers) reached 0.4-0.6 the cells were induced with IPTG. Following induction, the cells were harvested, washed, lysed and run through a French Press at a pressure of 16000 psi. The cells were  
5 then centrifuged and the pellet checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localize to the cell pellet, the pellet was resuspended in 10mM Tris, pH 8.0, 1% CHAPS and the inclusion body pellet washed and centrifuged. The washed inclusion body was solubilized with either 8M urea or 6M guanidine HCL containing 10mM Tris, pH 8.0, plus 10mM imidazole. The solubilized  
10 protein was then added to 5ml of nickel-chelate resin (Qiagen) and incubated for 45 minutes at room temperature.

Following the incubation, the resin and protein mixture was poured through a column and the flow through collected. The column was washed with 10-20 column volumes of buffer and the antigen eluted using 8M urea, 10mM Tris, pH 8.0,  
15 and 300 mM imidazole and collected in 3ml fractions. SDS-PAGE was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin was equilibrated with the appropriate buffer and the pooled fractions were loaded onto the column. Each antigen was eluted from the column with an increasing salt gradient. Fractions were collected and analyzed by a SDS-PAGE to  
20 determine which fractions from the column to pool. The pooled fractions were dialyzed against 10mM Tris, pH 8.0, and the resulting protein was submitted for quality control for final release. The release criteria were: (a) purity as determined by SDS-PAGE or HPLC, (b) concentration as determined by Lowry assay or Amino Acid Analysis, (c) identity as determined by amino terminal protein, and (d) endotoxin levels as  
25 determined by the Limulus (LAL) assay. The proteins were then filtered through a 0.22µM filter and frozen until needed for immunizations.

To generate polyclonal antisera, 400µg of O772P-1 or O772P-2 was combined with 100µg of muramyl dipeptide (MDP). The rabbits were immunized every 4 weeks with 100µg of antigen mixed with an equal volume of Incomplete Freund's  
30 Adjuvant (IFA). Seven days following each boost, the animals were bled and sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

To characterize the antisera, 96 well plates were coated with antigen followed by blocking with BSA. Rabbit sera was diluted in PBS and added to each well. The plates were then washed, and goat anti-rabbit horseradish peroxidase (HRP). The plates were again washed and TMB microwell Peroxidase Substrate was added.

5 Following this incubation, the colormetric reaction was stopped and the plates read immediately at 450nm. All polyclonal antibodies showed immunoreactivity to the appropriate antigen.

Immunohistochemistry analysis of O772P expression was performed on paraffin-embedded formalin fixed tissue. O772P was found to be expressed in normal

10 ovary and ovarian tumor, but not in normal heart, kidney, colon, lung or liver. Additionally, immunohistochemistry and flow cytometric analysis indicates that O772P is a plasma membrane-associated molecule. O772P contains 1 plasma transmembrane domain predicted to be encoded by amino acids 859-880. The N-terminus of O772P is extracellular and is encoded by amino acids 1-859, while the C-terminus is intracellular.

15 Sequence analysis shows that there are 17 potential N-linked glycosylation sites.

#### EXAMPLE 11

##### O772P IS EXPRESSED ON THE SURFACE OF PRIMARY OVARIAN TUMOR CELLS

For recombinant expression in mammalian cells, the O772P-21008 (SEQ ID NO:387) and O772P full length cDNA (SEQ ID NO:311 encoding the protein of

20 SEQ ID NO:312) were subcloned into mammalian expression vectors pBIB or pCEP4 respectively. These constructs were transfected into HEK293 cells using Fugene 6 (Roche). The HEK cells were then plated at a density of 100,000 cells/ml in DMEM containing fetal bovine serum (FBS) and grown overnight. The following day, 2µl of Fugene 6 was added to 100µl of DMEM, which contained no FBS, and incubated for 15

25 minutes at room temperature. The Fugene 6/DMEM mixture was then added to 1µg of O772P/pBIB or O772P/pCEP4 plasmid DNA and incubated for an additional 15 minutes at room temperature. The Fugene 6/DNA mix was then added to the HEK293 cells and incubated for 48-72 hours at 37°C with 7% CO<sub>2</sub>. The cells were rinsed and pelleted by centrifugation.

For Western Blot analysis, whole cell lysates were generated by incubating the cells in lysis buffer followed by clarification by centrifugation. The samples were diluted and run on SDS-PAGE. The gel was then transferred to nitrocellulose and probed using purified anti-O772P-2 rabbit polyclonal antibody. The blot was revealed with a goat anti-rabbit Ig coupled to HRP followed by incubation in ECL substrate. Western Blot analysis revealed that O772P-21008 could be detected in HEK293 cells that had been transfected with O772P.

To determine the cell expression profile of O772P in cells, primary ovarian tumor cells were grown in SCID mice. The cells were retrieved from the mice and analyzed by flow cytometry. Briefly, cells washed in cold staining buffer containing PBS, 1% BSA, and Na Azide. The cells were incubated for 30 minutes with 10µg/ml of purified anti-O772P-1 and O772P-2 polyclonal sera. Following this incubation, the cells were washed three times in staining buffer and incubated with goat anti-rabbit Ig (H+L) conjugated to FITC (Southern Biotechnology). The cells were washed and resuspended in staining buffer containing Propidium Iodide (PI), a vital stain that identifies non-viable cells. The cells were then analyzed using Fluorescence Activated Cell Sorting (FACS). FACS analysis revealed that O772P was present on the cells surface. Surface expression of O772P on tumor cells allows for immune targeting by therapeutic antibodies.

## EXAMPLE 12

### FUNCTIONAL CHARACTERIZATION OF ANTI-O8E MONOCLONAL ANTIBODIES

Mouse monoclonal antibodies (mAb) raised against E. coli derived O8E, as described in Example 8, were tested for their ability to promote O8E antigen internalization. Internalization of the antibody was determined using an in vitro cytotoxicity assay. Briefly, HEK293 and O8E/HEK transfected cells were plated into 96 well plates containing DME plus 10% heat-inactivated FBS in the presence of 50ng/well of purified anti-O8E or control antibodies. The isotype of the anti-O8E mAbs are as follows: 11A6-IgG1/kappa, 15C6-IgG2b/kappa, 18A8-IgG2b/kappa, and 14F1-IgG2a/kappa. W6/32 is a pan anti-human MHC class I mouse monoclonal antibody that serves as a positive control, and two irrelevant mAbs, Ir-Pharm and Ir-



Crxa were included as negative controls. Following incubation with the O8E specific antibodies or the relevant controls antibodies, the mAb-zap, a goat anti-mouse Ig-saporin conjugated secondary antibody (Advanced Targeting Systems) was added at a concentration of 100ng/ml to half of the wells, and the plates were incubated for 48 to 5 72 hours at 37°C in a 7% CO<sub>2</sub> incubator. This assay takes advantage of the toxic nature of saporin, a ribozyme inactivating protein, which when internalized has a cytotoxic effect. Following incubation with the mAb-zap, internalization was quantitated by the addition of MTS reagent, followed by reading the OD490 of the plate on a microplate ELISA reader. Figure 25 depicts the results from these assays. The top panel represents 10 HEK cells that have not been transfected with O8E and therefore O8E antibody should not bind and be internalized. Levels of proliferation were the same in all samples whether they were incubated with or without the mAb-zap, with the exception of the positive control Ab, W6/32. The lower panel represents cells that have been transfected with O8E and therefore should bind O8E specific antibodies. Antibodies from the 15 hybridomas 11H6, 14F1, and 15C6, which recognize the amino acids 61-80 of O8E were able to promote internalization of the O8E surface protein as measured by decreased levels of proliferation due to the toxic nature of the mAb-zap (See Figure 25). The antibody generated by the hybridoma 18A8, which recognizes amino acids 151-170 of O8E, was unable to promote internalization as determined by normal levels of 20 proliferation either in the absence or presence of the mAb-zap.

### EXAMPLE 13

#### CHARACTERIZATION OF THE OVARIAN TUMOR ANTIGEN, O772P

The cDNA and protein sequences for multiple forms of the ovarian tumor antigen O772P have been described in the above (e.g., Examples 2 and 9). A 25 Genbank search indicated that O772P has a high degree of similarity with FLJ14303 (Accession # AK024365; SEQ ID NO:457 and 463). Protein sequences corresponding to O772P and FLJ14303 are disclosed in SEQ ID NO:478 and 479, respectively. FLJ14303 was identical to the majority of O772P, with much of the 3'-end showing 100% homology. However, the 5'-end of FLJ14303 was found to extend further 5' than 30 O772P. In addition, FLJ14303 contained a 5 bp insert (SEQ ID NO:457) resulting in a

frame shift of the amino-terminus protein sequence such that FLJ14303 utilizes a different starting methionine than O772P and therefore encodes a different protein. This insertion was present in the genomic sequence and seen in all EST clones that showed identity to this region, suggesting that FLJ14303 (SEQ ID NO:457) represents a splice variant of O772P, with an ORF that contains an extended and different amino-terminus. The additional 5'-nucleotide sequence included repeat sequences that were identified during the genomic mapping of O772P. The 5'-end of O772P and the corresponding region of FLJ14303 showed between 90-100% homology. Taken together, this suggests that O772P and FLJ14303 are different splice variants of the same gene, with different unique repeat sequences being spliced into the 5'-end of the gene.

The identification of an additional ten or more repeat sequences within the same region of chromosome 19, indicates that there may be many forms of O772P, each with a different 5'-end, due to differential splicing of different repeat sequences. Northern blot analysis of O772P demonstrated multiple O772P-hybridizing transcripts of different sizes, some in excess 10kb.

Upon further analysis, 13 additional O772P-related sequences were identified, the cDNA and amino acid sequences of which are described in Table 2.

Table 2

| SEQ ID NO: | Description           | Transmembrane Domains |
|------------|-----------------------|-----------------------|
| 464        | LS #1043400.1 (cDNA)  | nd                    |
| 465        | LS #1043400.10 (cDNA) | 0                     |
| 466        | LS #1043400.11 (cDNA) | 2                     |
| 467        | LS #1043400.12 (cDNA) | 2                     |
| 468        | LS #1043400.2 (cDNA)  | nd                    |
| 469        | LS #1043400.3 (cDNA)  |                       |
| 470        | LS #1043400.5 (cDNA)  | nd                    |
| 471        | LS #1043400.8 (cDNA)  | 1                     |
| 472        | LS #1043400.9 (cDNA)  | 0                     |

|     |   |    |
|-----|---|----|
| 473 | LS #1043400.6 (cDNA)  | nd |
| 474 | LS #1043400.7 (cDNA)  | nd |
| 475 | LS #1043400.4 (cDNA)  | nd |
| 476 | LS #1397610.1 (cDNA)  | 0  |
| 477 | 1043400.10 Novel 5' (cDNA)                                      | -  |
| 480 | LS #1043400.9 (amino acid)                                      | -  |
| 481 | LS #1043400.8B (amino acid)<br>Contains a transmembrane domain  | -  |
| 482 | LS #1043400.8A (amino acid)                                     | -  |
| 483 | LS #1043400.12 (amino acid)<br>Contains a transmembrane domain  | -  |
| 484 | LS #1043400.11B (amino acid)<br>Contains a transmembrane domain | -  |
| 485 | LS #1043400.11A (amino acid)                                    | -  |
| 486 | LS #1043400.10 (amino acid)                                     | -  |
| 487 | LS #1043400.1 (amino acid)                                      | -  |

nd=not determined

Initially it appeared that these sequences represented overlapping and/or discrete sequences of O772P splice forms that were capable of encoding polypeptides unique to the specific splice forms of O772P. However, nucleotide alignment of these sequences failed to identify any identical regions within the repeat elements. This indicates that the sequences may represent different specific regions of a single O772P gene, one that contains 16 or more repeat domains, all of which form a single linear transcript. The 5'-end of sequence LS #1043400.10 (Table 2; SEQ ID NO:465) is unique to both O772P and FLJ14303 and contains no repeat elements, indicating that this sequence may represent the 5'-end of O772P.

Previously, transmembrane prediction analysis had indicated that O772P contained between 1 and 3 transmembrane spanning domains. This was verified by the

use of immunohistochemistry and flow cytometry, which demonstrated the existence of a plasma membrane-associated molecule representing O772P. However, immunohistochemistry also indicated the presence of secreted form(s) of O772P, possibly resulting from an alternative splice form of O772P or from a post-translational cleavage event. Analysis of several of the sequences presented in Table 2 showed that sequences 1043400B.12, 1043400.8B, and 1043400.11B all contained transmembrane regions, while 1043400.8A, 1043400.10, 1043400.1, 1043400.11A, and 1043400.9 were all lacking transmembrane sequences, suggesting that these proteins may be secreted.

Analysis indicates a part of O772P is expressed and/or retained on the plasma membrane, making O772P an attractive target for directing specific immunotherapies, e.g., therapeutic antibodies, against this protein. The predicted extracellular domain of O772P is disclosed in SEQ ID NO:489 and secretion of O772P is likely to occur as a result of a cleavage event within the sequence:

SLVEQVFLDK<sup>1</sup>TLNASFHWLGSTYQLVDIHVTEMESSVYQP.

Proteolytic cleavage is most likely to occur at the Lysine (K) at position 10 of SEQ ID NO:489. The extracellular, transmembrane, and cytoplasmic regions of O772P are all disclosed in SEQ ID NO:488:

Extracellular:

SLVEQVFLDK<sup>1</sup>TLNASFHWLGSTYQLVDIHVTEMESSVYQPTSSSS  
TQHFYLNFTTTNLPYSQDKAQP<sup>15</sup>GT<sup>16</sup>TNYQRNKR<sup>17</sup>NIEDALNQ<sup>18</sup>FRNSSIK<sup>19</sup>SYFSDCQ  
VSTFR<sup>20</sup>SVPNRHHTGVDSLCNFSPLARRV<sup>21</sup>DRVAIYEEFLRMTRNGTQLQNFTLDR  
SSVLVDGYFPNRNEPLTGNS<sup>24</sup>DL<sup>25</sup>PF<sup>26</sup>

Transmembrane:

WAVILIGLAGLLGLITCLICGVLVTT

Cytoplasmic:

RRRKKEGEYNVQQQCPGY<sup>30</sup>YQSHLDLEDLQ

**EXAMPLE 14****IMMUNOHISTOCHEMISTRY (IHC) ANALYSIS OF O8E EXPRESSION IN OVARIAN CANCER  
AND NORMAL TISSUES**

In order to determine which tissues express the ovarian cancer antigen O8E, IHC analysis was performed on a diverse range of tissue sections using both polyclonal and monoclonal antibodies specific for O8E. The generation of O8E specific polyclonal antibodies is described in detail in Example 8. The monoclonal antibodies used for staining were 11A6 and 14F1, both of which are specific for amino acids 61-80 of O8E and 18A8, which recognizes amino acids 151-170 of O8E (see Example 12 for details on generation).

To perform staining, tissue samples were fixed in formalin solution for 12-24 hours and embedded in paraffin before being sliced into 8 micron sections. Steam heat induced epitope retrieval (SHEIR) in 0.1M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody was then added to each section for 25 minutes followed by 25 minutes of incubation with either anti-rabbit or anti-mouse biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize the antigen expression. Slides were counterstained with hematoxylin to visualize the cell nuclei.

Results using rabbit affinity purified polyclonal antibody to O8E (a.a. 29-283; for details on the generation of this Ab, see Example 3) are presented in Table 3. Results using the three monoclonal antibodies are presented in Table 4.

Table 3

Immunohistochemistry analysis of O8E using polyclonal antibodies

| Tissue         | O8E Expression |
|----------------|----------------|
| Ovarian Cancer | Positive       |
| Breast Cancer  | Positive       |

|               |          |
|---------------|----------|
| Normal Ovary  | Positive |
| Normal Breast | Positive |
| Blood Vessel  | Positive |
| Kidney        | Negative |
| Lung          | Negative |
| Colon         | Negative |
| Liver         | Negative |
| Heart         | Negative |

Table 4Immunohistochemistry analysis of O8E using monoclonal antibodies

| Normal<br>Tissue         | 11A6            |            | 18A8        |            | 14F1        |            |
|--------------------------|-----------------|------------|-------------|------------|-------------|------------|
|                          | Endothelia<br>1 | Epithelial | Endothelial | Epithelial | Endothelial | Epithelial |
| Skin                     | 2               | 2          | 0           | 0          | 1           | 1          |
| Skin                     | 1               | 1          | 0           | 0          | 1           | 1          |
| Breast                   | 0               | 1          | n/a         | n/a        | 1           | 1          |
| Colon                    | 0               | 0          | 0           | 0          | 0           | 0          |
| Jejunum                  | 0               | 0          | 0           | 0          | 0           | 0          |
| Colon                    | 0               | 0          | 0           | 0          | 0           | 0          |
| Colon                    | 0               | 0          | 0           | 0          | 0           | 0          |
| Ovary                    | 0               | 0          | 0           | 0          | 1           | 0          |
| Colon                    | 0               | 0          | 0           | 0          | 0           | 1          |
| Liver                    | 0               | 0          | 0           | 0          | 1           | 2          |
| Skin                     | 0               | 0          | 0           | 0          | 1           | 0          |
| Duodenum<br>and Pancreas | 0               | 0          | 0           | 0          | 0           | 0          |
| Appendix                 | 0               | 0          | 0           | 0          | 0           | 0          |
| Ileum                    | 0               | 0          | 0           | 0          | 0           | 0          |

0=no staining, 1=light staining, 2=moderate staining, n/a=not available

## EXAMPLE 15

## EPIOTOPE MAPPING OF O772P POLYCLONAL ANTIBODIES

To perform epitope mapping of O772P, peptides were generated, the sequences of which were derived from the sequence of O772P. These peptides were 15mers that overlapped by 5 amino acids and were generated via chemical synthesis on membrane supports. The peptides were covalently bound to Whatman 50 cellulose support by their C-terminus with the N-terminus unbound. In order to determine epitope specificity, the membranes were wet with 100% ethanol for 1 minute, and then blocked for 16 hours in TBS/Tween/Triton buffer (50mM Tris, 137 mM NaCl, 2.7 mM KCl, 0.5% BSA, 0.05% Tween 20, 0.05% Triton X-100, pH 7.5). The peptides were then probed with 2 O772P specific antibodies, O772P-1 (amino acids 44-772 of SEQ ID NO:312) and O772P-2 (477-914 of SEQ ID NO:312; see Example 10 for details of antibody generation), as well as irrelevant rabbit antibodies for controls. The antibodies were diluted to 1µg/ml and incubated with the membranes for 2 hours at room temperature. The membranes were then washed for 30 minutes in TBS/Tween/Triton buffer, prior to being incubated with a 1:10,000 dilution of HRP-conjugated anti-rabbit secondary antibody for 2 hours. The membranes were again washed for 30 minutes in TBS/Tween/Triton and anti-peptide reactivity was visualized using ECL. Specific epitope binding specificity for each of the O772P-polyclonal antibodies is described in Table 5.

Table 5

| SEQ ID NO: | Peptide # | Anti-O772P1 | Anti-O772P2 | Peptide Sequence |
|------------|-----------|-------------|-------------|------------------|
| 490        | 2         | ***         | -           | TCGMRRTCSTLAPGS  |
| 491        | 6         | *           | */-         | CRLTLLRPEKDGTAT  |
| 492        | 7         | *           | -           | DGTATGVDAICTHHP  |
| 493        | 8         | -           | -           | CTHHPDPKSPRLDRE  |
| 494        | 9         | ***         | ***         | RLDREQLYWELSQLT  |
| 495        | 11        | */-         | -           | LGPYALDNDLSLFVNG |
| 496        | 13        | ****        | -           | SVSTTSTPGIPTVYL  |
| 497        | 22        | -           | -           | LRPEKDGEATGVDAI  |
| 498        | 24        | **          | */-         | DPTGPGLDREQLYLE  |
| 499        | 27        | */-         | -           | LDRDSLYVNGFTHRS  |
| 500        | 40        | */-         | -           | GPYSLDKDSLYLNGY  |
| 501        | 41        | -           | -           | YLNQYNEPGPDEPPT  |
| 502        | 47        | ***         | ***         | ATFNSTEGVLQHLLR  |

|     |    |   |     |                   |
|-----|----|---|-----|-------------------|
| 503 | 50 | - | *** | QLISLRPEKDGAATG   |
| 504 | 51 | - | **  | GAATGVDTTCTYHPD   |
| 505 | 52 | - | */- | TYHPDPVGPGLDIQQ   |
| 506 | 53 | - | *   | LDIQQLYWELSOLTH   |
| 507 | 58 | - | *   | HIVNWNLSNPDPTSS   |
| 508 | 59 | - | *   | DPTSSEYITLLRDIQ   |
| 509 | 60 | - | *   | LRDIQDKVTTLYKGS   |
| 510 | 61 | - | *** | LYKGSQ LHD TFRFCL |
| 511 | 71 | - | **  | DKAQPGTTNYQRNKR   |

\*= relative reactive level, -; no binding, \*\*\*\*; maximal binding

### EXAMPLE 16

#### IDENTIFICATION OF A NOVEL N-TERMINAL REPEAT STRUCTURE ASSOCIATED WITH O772P

5 Various O772P cDNA and protein forms have been identified and characterized as detailed above (e.g., Examples 1, 2, 9, and 14). Importantly, O772P RNA and protein have been demonstrated to be over-expressed in ovarian cancer tissue relative to normal tissues and thus represents an attractive target for ovarian cancer diagnostic and therapeutic applications.

10 Using bioinformatic analysis of open reading frames (ORFs) from genomic nucleotide sequence identified previously as having homology with O772P, multiple nucleotide repeat sequences were identified in the 5' region of the gene encoding the O772P protein. A number of these repeat sequences were confirmed by RT-PCR using primers specific for the individual repeats. Fragments which contained  
15 multiple repeats were amplified from cDNA, thus confirming the presence of specific repeats and allowing an order of these repeats to be established.

Unexpectedly, when various sets of O772P sequences derived from different database and laboratory sources were analyzed, at least 20 different repeat structures, each having substantial levels of identity with each other (see Table 6), were  
20 identified in the 5' region of the O772P gene and the corresponding N-terminal region of the O772P protein. Each repeat comprises a contiguous open reading frame encoding a polypeptide unit that is capable of being spliced to one or more other repeats such that concatomers of the repeats are formed in differing numbers and orders. Interestingly, other molecules have been described in the scientific literature that have repeating  
25 structural domains analogous to those described herein for O772P. For example, the



mucin family of proteins, which are the major glycoprotein component of the mucous which coats the surfaces of cells lining the respiratory, digestive and urogenital tracts, have been shown to be composed of tandemly repeated sequences that vary in number, length and amino acid sequence from one mucin to another (Perez-Vilar and Hill, *J. Biol. Chem.* 274(45):31751-31754, 1999).

The various identified repeat structures set forth herein are expected to give rise to multiple forms of O772P, most likely by alternative splicing. The cDNA sequences of the identified repeats are set forth in SEQ ID NOs:513-540, 542-546, and 548-567. The encoded amino acid sequences of the repeats are set forth in SEQ ID NOs:574-593. In many instances these amino acid sequences represent consensus sequences that were derived from the alignment of more than one experimentally derived sequence.

Each of these splice forms is capable of encoding a unique O772P protein with multiple repeat domains attached to a constant carboxy terminal protein portion of O772P that contains a trans membrane region. The cDNA sequence of the O772P constant region is set forth in SEQ ID NO:568 and the encoded amino acid sequence is set forth in SEQ ID NO:594.

All of the available O772P sequences that were obtained were broken down into their identifiable repeats and these sequences were compared using the Clustal method with weighted residue weight table (MegAlign software within DNASTAR sequence analysis package) to identify the relationship between the repeat sequences. Using this information, the ordering data provided by the RT-PCR, and sequence alignments (automatic and manual) using SeqMan (DNASTAR), one illustrative consensus full length O772P contig was identified comprising 20 distinct repeat units. The cDNA for this O772P cDNA contig is set forth in SEQ ID NO:569 and the encoded amino acid sequence is set forth in SEQ ID NO:595. This form of the O772P protein includes the following consensus repeat structures in the following order:

SEQ ID NO:572- SEQ ID NO:574- SEQ ID NO:575-SEQ ID NO:576-  
SEQ ID NO:577- SEQ ID NO:578- SEQ ID NO:579- SEQ ID NO:580- SEQ ID  
NO:581- SEQ ID NO:582- SEQ ID NO:583- SEQ ID NO:584- SEQ ID NO:585- SEQ

ID NO:586- SEQ ID NO:587- SEQ ID NO:588- SEQ ID NO:589- SEQ ID NO:590-  
SEQ ID NO:591- SEQ ID NO:592- SEQ ID NO:593.

SEQ ID NO:595, therefore, represents one illustrative full-length  
consensus sequence for the O772P protein. As discussed above, however, based on  
5 current knowledge of this protein and based upon scientific literature describing  
proteins containing analogous repeating structures, many other forms of O772P are  
expected to exist with either more or less repeats. In addition, many forms of O772P  
are expected to have differing arrangements, e.g., different orders, of these N-terminal  
repeat structures. The existence of multiple forms of O772P having differing numbers  
10 of repeats is supported by Northern analysis of O772P. In this study, Northern  
hybridization of a O772P-specific probe resulted in a smear of multiple O772P-  
hybridizing transcripts, some in excess 10kb.

Thus, the variable repeat region of the O772 protein can be illustratively  
represented by the structure  $X_n - Y$ , wherein X comprises a repeat structure having at  
15 least 50% identity with the consensus repeat sequence set forth in SEQ ID NO:596; n is  
the number of repeats present in the protein and is expected to typically be a integer  
from 1 to about 35; Y comprise the O772P constant region sequence set forth in SEQ  
ID NO:594 or sequences having at least 80% identity with SEQ ID NO:594. Each X  
present in the  $X_n$  repeat region of the O772 molecule is different.

20 To determine the consensus sequences of each of the 20 repeat regions,  
sequences that were experimentally determined for a discrete repeat region were aligned  
and a consensus sequence determined. In addition to determining the consensus  
sequences for individual repeat regions, a consensus repeat sequence was also  
determined. This sequence was obtained by aligning the 20 individual consensus  
25 sequences. Variability of the repeats was determined by aligning the consensus amino  
acid sequences from each of the individual repeat regions with the over all repeat  
consensus sequence. Identity data is presented in Table 6.

Table 6

Percent identities of Repeat Sequences with Reference to the Consensus Repeat Sequence

| Repeat Number<br>(amino acid) | SEQ ID NO: | Percent Identity to<br>Consensus Repeat<br>Sequence |
|-------------------------------|------------|---|
| 2                             | 574        | 88  |
| 3                             | 575        | 84  |
| 4                             | 576        | 88  |
| 5                             | 577        | 89  |
| 6                             | 578        | 93  |
| 7                             | 579        | 90  |
| 8                             | 580        | 91  |
| 9                             | 581        | 88  |
| 10                            | 582        | 85  |
| 11                            | 583        | 86  |
| 12                            | 584        | 87  |
| 13                            | 585        | 87  |
| 14                            | 586        | 89  |
| 15                            | 587        | 89  |
| 16                            | 588        | 89  |
| 17                            | 589        | 83  |
| 18                            | 590        | 84  |
| 19                            | 591        | 83  |
| 20                            | 592        | 57  |
| 21                            | 593        | 68  |

5 From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration,

various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

## CLAIMS

What is Claimed:

1. An O772P polypeptide having the structure:  
 $X_n$ -Y  
wherein X comprises a sequence having at least 50% identity with the consensus O772P repeat sequence set forth in SEQ ID NO: 596;  
Y comprises a sequence having at least 80% identity with the O772P constant region sequence set forth in SEQ ID NO: 594;  
n is an integer from 1 to 35;  
wherein each X present in said polypeptide is different.
2. The polypeptide of claim 1, wherein X comprises a sequence selected from the group consisting of any one of SEQ ID NOs: 574-593.
3. The polypeptide of claim 1, wherein Y comprises the sequence set forth in SEQ ID NO: 594.
4. The polypeptide of claim 1, wherein n is an integer from 15 to 25.
5. The polypeptide of claim 1, wherein n is 20.
6. The polypeptide of claim 1, wherein said polypeptide comprises SEQ ID NO: 595.
7. The polypeptide of claim 1, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.
8. An O772P polypeptide having the structure:  
 $X_n$ -Y

wherein X comprises an O772P repeat sequence selected from the group consisting of any one of SEQ ID NOs: 574-593;

Y comprises a sequence having at least 90% identity with the O772P constant region sequence set forth in SEQ ID NO: 594;

n is an integer from 15 to 25;

wherein each X present in said polypeptide is different.

9. The polypeptide of claim 8, wherein n is 20.
10. The polypeptide of claim 8, wherein said polypeptide comprises SEQ ID NO: 595.
11. The polypeptide of claim 8, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.
12. An O772P polypeptide having the structure:  
 $X_n$ -Y  
wherein n is 20 and X comprises the following O772P repeat sequences:  
SEQ ID NO: 574 - SEQ ID NO: 575 - SEQ ID NO: 576 - SEQ ID NO: 577 - SEQ ID NO: 578 - SEQ ID NO: 579 - SEQ ID NO: 580 - SEQ ID NO: 581 - SEQ ID NO: 582 - SEQ ID NO: 583 - SEQ ID NO: 584 - SEQ ID NO: 585 - SEQ ID NO: 586 - SEQ ID NO: 587 - SEQ ID NO: 588 - SEQ ID NO: 589 - SEQ ID NO: 590 - SEQ ID NO: 591 - SEQ ID NO: 592 - SEQ ID NO: 593; and  
Y comprises the sequence set forth in SEQ ID NO: 594.
13. The polypeptide of claim 12, wherein said polypeptide comprises SEQ ID NO: 595.
14. The polypeptide of claim 12, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.

15. An O772P polynucleotide having the structure:

$X_n$ -Y

wherein X comprises an O772P repeat sequence selected from the group consisting of any one of SEQ ID NOs: 512-540, 542-546 and 548-567;

Y comprises a sequence having at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 568;

n is an integer from 1 to 35;

wherein each X present in said polypeptide is different.

16. The polynucleotide of claim 15, wherein said polynucleotide comprises SEQ ID NO: 569.

17. The polynucleotide of claim 15, wherein n is from 15 to 25.

18. The polynucleotide of claim 15, wherein n is 20.

19. The polynucleotide of claim 15, wherein said polynucleotide is overexpressed in ovarian cancer cells compared with normal tissues.

20. An isolated polynucleotide comprising a sequence selected from the group consisting of:

- (a) sequences provided in SEQ ID NOs: 464-477 and 512-569;
- (b) complements of the sequences provided in SEQ ID NOs: 464-477 and 512-569;
- (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NOs: 464-477 and 512-569;
- (d) sequences that hybridize to a sequence provided in SEQ ID NOs: 464-477 and 512-569, under highly stringent conditions;
- (e) sequences having at least 75% identity to a sequence of SEQ ID NOs: 464-477 and 512-569;

(f) sequences having at least 90% identity to a sequence of SEQ ID NOs: 464-477 and 512-569; and

(g) degenerate variants of a sequence provided in SEQ ID NOs: 464-477 and 512-569.

21. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences encoded by a polynucleotide of claim 20; and

(b) sequences having at least 80% identity to a sequence encoded by a polynucleotide of claim 20; and

(c) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 20.

22. An expression vector comprising a polynucleotide of claim 20 operably linked to an expression control sequence.

23. A host cell transformed or transfected with an expression vector according to claim 22.

24. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 21.

25. A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 21;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.



26. A fusion protein comprising at least one polypeptide according to claim 21.

27. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) polypeptides according to claim 21;
- (b) polynucleotides according to claim 20; and
- (c) antigen-presenting cells that express a polynucleotide according to claim 20,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

28. An isolated T cell population, comprising T cells prepared according to the method of claim 27.

29. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 21;
- (b) polynucleotides according to claim 20;
- (c) antibodies according to claim 24;
- (d) fusion proteins according to claim 26;
- (e) T cell populations according to claim 28; and
- (f) antigen presenting cells that express a polypeptide according to claim 21.

30. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 29.

31. A method for the treatment of a ovarian cancer in a patient, comprising administering to the patient a composition of claim 29.

32. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide that hybridizes to a polynucleotide sequence according to claim 21 under moderately stringent conditions;
- (c) detecting in the sample an amount of said polynucleotide that hybridizes to the oligonucleotide; and
- (d) comparing the amount of said polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

33. An O772 polypeptide comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 490-511.

34. An O8E polypeptide comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 394-415.

35. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 1.

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11729.1 contg

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTGTTTTGTTTTGTTTTGTTTTG  
TTTTGAGATGGAGTCTCACTCTGTTGCCAAGCTGGAGTACAACGGCATGATCTCAGCTCGCTGCAACCTCCGC  
CTCCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCGCCACCACGCTCA  
GCTAATTTTTTTGTATTTTAGTAGAGACAGGTTTACCAGGTTGGCCAGGCTGCTCTTGAACCTCTGACCT  
CAGGTGATCCACCCGCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCCAAAG  
CTGTTTCTTTGTCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGC  
TCAGTCACTCCGTGGTC

11729-45.21.21.cons1

TAGGATGTGTTGGACCCTCTGTGTCAAAAAAACCTCACAAAGAATCCCCTGCTCATTACAGAAGAAGATGCAT  
TAAAAATATGGGTATTTTCAACTTTTTATCTGAGGACAAGTATCCATTATTGTGTGAGAAGAGATTGAA  
TACCTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAATCAA  
CTTTGATGACAGTAAAAATGGCCTTCTGCATGGGAACCTATTGAGCTTATTGGAAATGGACAGTTTAGCAAAG  
GCATGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTTAATGAACCTATATTAGATGTGTTAAAGCAG  
GGTTACATGATGAAAAAGGGCCACAGACGGAAGAACTGGACTGAAAGATGGTTTGTACTAAACCCAACATAAT  
TTCTTACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTGGATGAAAATTGCTGTGTAGAGT  
CCTTGCTGACAAAGATGGAAA

11729-45.21.21.cons2

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTGTTTTGTTTTGTTTTGTTTTG  
TTTTGAGATGGAGTCTCACTCTGTTGCCAAGCTGGAGTACAACGGCATGATCTCAGCTCGCTGCAACCTCCGC  
CTCCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCGCCACCACGCTCA  
GCTAATTTTTTTGTATTTTAGTAGAGACAGGTTTACCAGGTTGGCCAGGCTGCTCTTGAACCTCTGACCT  
CAGGTGATCCACCCGCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCCAAAG  
CTGTTTCTTTGTCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGC  
TCAGTCACTCCGTGGTC

11731.1contig

TCTTTTCTTTGATTTCTTCAATTTGTACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTAT  
TATAGCTTTCTCTGAGTTCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTT  
TCAAGAGCATCTAATTGTTCTTTAAGTCTTTGGCATAATCTTCTTTCTGATGACTTTTTATGAAGTAACT  
GATCCCTGAATCAGGTGTGTTACTGAGCTGCATGTTTTAATTCTTTCTGTTAATAGCTGCTTCTCAGGGACCA  
GATAGATAAGCTTATTTGATATTCCTTAAGCTCTTGTTGAAGTTGTTTGATTTCATAATTTCCAGGTCACAC  
TGTTTATCCAAACTTCTAGCTCAGTCTTTGTGTTTGCTTTCTGATTGGACATCTGTAGTCTGCCGAGAT  
CTGCTGATGXTTCCATTCACTGCTTCCAGTTCAGGTGGAGACTTTCCTTCTGGAGCTCAGCCTGACAATGC  
CTTCTTGXTCCCT

**Fig. 1A**

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11731.2contig

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGG  
CCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGG  
AGGTTACATAACAGGTGATCAAGCCCGTACTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAA  
TATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATC  
AAGTTAAAGTTGCAGGGCCAACAGCTGCCTGTAGTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCC  
ACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCAATCTGTCCATTCATCAGCCATTGCCTCCAGTTGCAC  
CTATAGCAACACCCTTGTCTTCTGCTACTTCAGGGACCAGTATTCCTCCCTAATGATGCCTGCTCCCTAGTG  
CCTTCTGTAGTA

11734.1contig

AATAGATTTAATGCAGAGTGTCAACTTCAATTGATTGATAGTGGCTGCCTAGAGTGCTGTGTTGAGTAGGTTTC  
TGAGGATGCACCCTGGCTTGAAGAGAAAGACTGGCAGGATTAACAATATCTAAAATCTCACTTGTAGGAGAAAC  
CACAGGCACCAGAGCTGCCACTGGTGCTGGCACCAGCTCCACCAAGGCCAGCGAAGAGCCCAAATGTGAGAGTG  
GCGGTGAGGCTGGCACCAGCACTGAAGCCACCCTGGTGCTGGCACTGGCACTGGCACTGTTATTGGTACTGGT  
ACTGGCACCAGTGCTGGCACTGCCACTCTCTTGGGCTTTGGCTTTAGCTTCTGCTCCCGCCTGGATCCGGGCTT  
TGGCCAGGGTCCGATATCAGCTTCGTCCAGTTGCAAGGCCCGGCAGCATTCTCGAGCCGAGCCCAATGCC  
ATTCGAGCTCTAATCTCGGCCCTAGCCTTGGCTTCAGCTGCAGCCTCAGCTGCAGCCTTCAAATCCGCTTCCAT  
CGCCTCTCGGTAC

11734.2contig

GCCAAGAAAGCCCGAAAGGTGAAGCATCTGGATGGGGAAGAGGATGGCAGCAGTGATCAGAGTCAGGCTTCTGG  
AACCACAGGTGGCCGAAGGGTCTCAAAGGCCCTAATGGCCTCAATGGCCCGCAGGGCTTCAAGGGGTCCCATAG  
CCTTTTGGGCCCCGAGGGCATCAAGGACTCGGTTGGCTGCTTGGGCCCCGAGAGCCTTGCTCTCCCTGAGATCA  
CCTAAAGCCCGTAGGGGCAAGGCTCGCGTAGAGCTGCCAAGCTCCAGTCATCCAAGAGCCTGAAGCACCACC  
ACCTCGGGATGTGGCCCTTTTGCAAGGGAGGGCAAATGATTTGGTGAAGTACCTTTTGGCTAAAGACCAGACGA  
AGATTCCCATCAAGCGCTCGGACATGCTGAAGGACATCATCAAAGAATACTGATGTGTACCCCGAAATCATT  
GAACGAGCAGGCTATTCCTTGGAGAAGGTATTTGGGATTCAATTGAAGGAAATTGATAAGAATGACCACTTGTA  
CATTCTTCTCAGC

11736.1contg

GAGGTCTCACTATGTTGCCAGGCTGTTCTTGAACCTCTGGGATCAAGCAATCCACCCATGTTGGTCTCCAAAA  
GTGCTGGGATCATAGCGTGAGCCACCTCAGCCAGCCACCAATTTTCAATCAGGAAGACTTTTTCTTCTTCAA  
GAAGTGAAGGGTTTCCAGAGTATAGCTACACTATTGCTTGCCTGAGGGTGACTACAAAATTGCTTGCTAAAAGG  
TTAGGATGGGTAAGAATTAGATTTTCTGAATGCAAAAATAAAATGTGAACCTAATGAACCTTAGGTAATACATA  
TTCATAAAATAATTATTCACATATTTCTGATTTATCACAGAAATAATGTATGAAATGCTTTGAGTTTCTTGA  
GTAACTCCATTACTCATCCAAGAAACCATATTATAAGTATCACTGATAATAAGAACACAGGACCTTGTCTAT  
AAATTCGGATAAGAGAAATAGTCTCTGGGTGTTGXTCTTAATTGATAAAATTTACTTGTCCATCTTTAGTT  
CAGAATCACAAA

**Fig. 1B**

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11736.2contig

AAGCGGAAATGAGAAAGGAGGGGAAAATCATGTGGTATTGAGCGGAAAACCTGCTGGATGACAGGGCTCAGTCCTG  
TTGGAGAACTCTGGGTGGTGTGTAGAACAGGGCCACTCACAGTGGGGTGCACAGACCAGCACGGCTCTGTGAC  
CTGTTTGTTACAGGTCCATGATGAGGTAAACAATACTGAGTATAAGGGTTGGTTTAGAACTCTTACAGCAA  
TTTGACAAAGTAATCTTCTGTGCAGTGAATCTAAGAAAAAATTGGGGCTGTATTTGTATGTTCCCTTTTTTCA  
TTTCATGTTCTGAGTTACCTATTTTTATTGCATTTTACAAAAGCATCCTTCCATGAAGGACCGGAAGTTAAAAA  
CAAAGCAGGTCTTTATCACAGCACTGTCGTAGAACACAGTTTCAGAGTTATCCACCCAAGGAGCCAGGGAGCTG  
GGCTAAACCAAAGAATTTTGCTTTTGTTAATCATCAGGTACTTGAGTTGGAATTGTTTAAATCCCATCATTAC  
CAGGCTGGAXGTG

11739-1&amp;2

CCGCGGCTCCTGTCCAGACCCTGACCCTCCCTCCCAAGGCTCAACCGTCCCCAACAACCGCCAGCCTTGACT  
GATGTCGGCTGCGAGAGCCTGTGCTTAAGTAAGAATCAGGCCTTATTGGAGACATTCAAGCAAAGGTTGGACAA  
CTACTTTTCCAGAACAGAAAGGAACTCATGCATCAGAAAAGGTGACTAATAAAGGTACCAGAAGAATATGGCT  
GCACAAATACCAGAATCTGATCAGATAAACAGTTTAAGGAATTTCTGGGGACCTACAATAAACTTACAGAGAC  
CTGCTTTTTGGACTGTGTTAGAGACTTCACAACAAGAGAAGTAAACCTGAAGAGACCACCTGTTCAGAACATT  
GCTTACAGAAATATTTAAAAATGACACAAAGAATATCCATGAGATTTCAGGAATATCATATTCAGCAGAATGAA  
GCCCTGGCAGCCAAAGCAGGACTCCTTGGCCAACCCAGATAGAGAAGTCTGATGGATGAACTTTTGATGAAAG  
ATTGCCAACAGCTGCTTTATTGGAAATGAGGACTCATCTGATAGAATCCCTGAAAGCAGTAGCCACCATGTTT  
AACCATCTGTGATGACTGTTTGGCAAATGGAACCGCTGGAGAAACAAAATTGCTATTTACCAGGAATAATCAC  
AATAGAAGGTCTTATTGTTCAAGTGAATAATAAGATGCAACATTTGTTGAGGCCTTATGATTCAGCAGCTTGGT  
CACTTGATTAGAAAAATAAACCATTTGTTCTTCAATTGTGACTGTTAATTTTAAAGCAACTTATGTGTTGATC  
ATGTATGAGATAGAAAAATTTTATTACTCAAAGTAAATAAATGGA

11740.1.contig

GAAAAAAATATAAAACACACTTTTGCGAAAACGGTGGCCCTAAAAGAGGAAAAGAATTCACCAATATAAATC  
CAATTTTATGAAAACGACAATTTAATCCAAGAAATCACTTTTGTAATGAAGCTAGCAAGTGATGATATGATAA  
AATAAACGTGGAGGAAATAAAAACACAAGACTTGGCATAAGATATATCCACTTTTGATATTAACCTTGTAAGC  
ATATTTCTCGACAAATTGTGAAAGCGTTCCTGATCTTGCTTGTTCTCCATTTCAAATAAGGAGGCATATCACAT  
CCCAAGAGTAACAGAAAAAGAAAAAGACATTTTTGCATTTTGAGATGAACCAAAGACACAAAACAAACGAAC  
AAAGTGTGATGTTAATTTAGCCTCTGAAATAAACCTTGAACATCTCCTACAAGGCACCGTGATTTTTGTAAT  
TCTAACCTGAAGAAATGTGATGACTTTTGTGGACATGAAAATCAGATGAGAAAACCTGTGGTCTTTCCAAAGCCT  
GAACTCCCTGAAAACCTTTGCA

*Fig. 1C*

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## 11766.1.contig

CTGGGATCATTTCTCTTGATGTCATAAAAGACTCTTCTTCTCCTCTTCATCCTCTTCTTCATCCTCTTCTGTA  
CAGTGCTGCCGGGTACAACGGCTATCTTTGTCTTTATCCTGAGATGAAGATGATGCTTCTGTTTCTCCTACCAT  
AACTGAAGAAATTTTCGCTGGAAGTCGTTTGACTGGCTGTTTCTCTGACTTCACCTTCTTTGTCAAACCTGAGTC  
TTTTTACCTCATGCCCCCTCAGCTTCCACAGCATCTTCATCTGGATGTTTATTTTTCAAAGGGCTCACTGAGGAA  
ACTTCTGATTGAGAGGTCGAAGAGTCACTGTGATTTTTCTCCTCATTTTGTGCAAATTTGCCTCTTTGTGTC  
TGTGCTCTCAGGCAACCCATTTGTTGTGATGGGGGTGACAAAGAAACCTTTGGTCGATTAAGTGGCCTGGGTG  
TCCCAGGCCCATTTATATTAGACCTCTCAGTATAGCTTGGTGAATTTCCAGGAAACATAACACCATTTCATTCGA  
TTTAAACTATTGGAATTGGTTTT

## 11766.2.contig

GAGGGTTGGTGGTAGCGGCTTGGGGAGGTGCTCGCTCTGTGGTCTTGCTCTCTCGCACGCTTCCCCGGCTCC  
CTTCGTTTTCCCCCCCCGGTGCCTGCGTGCCGGAGTGTGTGCGAGGGAGGGGGAGGGCGTGGGGGGGTGGGG  
GGAGGCGTTCCGGTCCCCAAGAGACCCGCGGAGGGAGGCGGAGGCTGTGAGGGACTCCGGGAAGCCATGGACGT  
CGAGAGGCTCCAGGAGGCGCTGAAAGATTTTGAAGAAGGGGGAAAAAGGAAGTTGTCTGTCTGGATCAGT  
TTCTTTGTGATGTAGCCAAGACTGGAGAAACAATGATTCAGTGGTCCCAATTTAAAGGCTATTTTATTTTCAA  
CTGGAGAAAGTGATGGATGATTTCAGAACTTCAGCTCCTGAGCCAAGAGGTCTCCCAACCCTAATGTGCA

## 11773.2.contig

AAGCAGGCGGCTCCCGCGCTCGCAGGGCCGTGCCACCTGCCGCCCGCCGCTCGCTCGCTCGCCGCCGCGCC  
GCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGCTGCCCGCGCTGCCGXTGCCG

## 11775-1&amp;2

ATCTCTTGATGCCAAATATTTAATATAAATCTTTGAAACAAGTTCAGATGAAATAAAATCAAAGTTTGCAA  
AACGTGAAGATTAACTTAATTGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTATTTCTATGCAAAA  
GTATGCCTTCAAAGTCTTAAATGATATATGATATGATACACAAACAGTTTTCAAATAGTAAAGCCAGTCATC  
TTGCAATTGTAAGAAATAGGTAAAGATTATAAGACACCTTACACACACACACACACACACAGTGTGCACG  
CCAATGACAAAAACAATTTGGCCTCTCCTAAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGGGAACA  
CTGTGTCAACCCTCCCTACAATCCAGGTAGTTTCCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGT  
GATTCTGACAGCCACGTTGAAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGCCTGAAAAATGCCAA  
TAATTTTTCGCTCCCACTTCTGTGCTGTCTCTTCCACATCCTCACATAGACCCAGACCCGCTGGCCCTGGC  
TGGGCATCGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTACAGAAGCGATACACCAAATTGCC  
TGGTCGGTCATTGTGATAACAGAGA

**Fig. 1D**

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11777.1&amp;2.cons

CAGACGGGGTTTCACTATGTTGGCTAGGCTGGTCTTGAACCTCTGACTTCAGGTGATCTGCCTGCCTTGGCCTC  
CCAAAGTGCTGGGATTACAGGCATAAGCCACTGCGCCCGGCTGATCTGATGGTTTCATAAGGCTTTTCCCCCTT  
TTGCTCAGCACTTCTCCTTCTGCGCCATGTGAAGAAGGACATGTTTGCTTCCCTTCCACCACGATTGTAAG  
TTGTTTCTGAGGCCTCCCCGGCCATGCTGAACTGTGAGTCAATTAACCTCTTTCTTTATAAATTATCCAGT  
TTTGGGTATGTCTTTATTAGTAGAATGAGAACAGACTAATACAACCCTTAAAGGAGACTGACGGAGAGGATTCT  
TCCTGGATCCCAGCACTTCTCTGAATGCTACTGACATTCTTCTTGAGGACTTTAACTGGGAGATAGAAAACA  
GATTCATGGCTCAGCAGCCTGAGAGCAGGGAGGGAGCCAAGCTATAGATGACATGGGCAGCCTCCCCTGAGGC  
CAGGTGTGGCCGAACCTGGGCAGTGCTGCCACCCACCCACAGGGCCAAAGTCTGTCTTGAGAGCCAAGCC  
TCAATCACTGCTAGCCTCAAGTGTCCTCAAGCCACAGTGGCTAGGGGGACTCAGGGAACAGTTCCAGTCTGCC  
CTACTTCTTTACCTTTACCCCTCATACCTCCAAAGTAGACCATGTTTCATGAGGTCAAAGG

11779.2.contig

AAGCGAGGAAGCCACTGCGGCTCCTGGCTGAAAAGCGGCGCCAGGCTCGGGAACAGAGGGAACGCGAAGAACAG  
GAGCGGAAGCTGCAGGCTGAAAGGGACAAGCGAATGCGAGAGGAGCAGCTGGCCCGGGAGGCTGAAGCCCGGGC  
TGAACGTGAGGCCGAGGCGGAGACGGGAGGAGCAGGAGGCTCGAGAGAAGGCGCAGGCTGAGCAGGAGGAGC  
AGGAGCGACTGCAGAAGCAGAAAGAGGAAGCCGAAGCCCGGTCCCGGGAAGAAGCTGAGCGCCAGCGCCAGGAG  
CGGGAAAAGCACTTTCAGAAGGAGGAACAGGAGAGACAAGAGCGAAGAAAGCGGCTGGAGGAGATAATGAAGAG  
GACTCGGAAATCAGAAGCCGCCGAAACCAAGAAGCAGGATGCAAGGAGACCGCAGCTAACAATTCGGGCCAG  
ACCCTTGTGAAAGCTGTAGAGACTCGGCCCTCTGGGCTTCAGAAAGGATTCTATTGCAGAAAGGAAGGAGCTX  
GGCCCCCAXGGA

11781 &amp; 37.cons

CTCTGTGAAAACCTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGA  
TTACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCCTCATCACTGGGCTGGA  
TTCATACTACCCACACAGACCGGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCAGATGATG  
TTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCCAGGAACTGGATTCTTTAACTAACTGACCATGG  
ACTAGAGGAGATTTCTTCTGTGCGCCAGAAAGGATTTTCATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCT  
GCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTC  
CAAGAACAACAAAACCATATCAGTGTACTGTAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTG  
TAGATAGTAGAAAGGGGGGCATCACXTGAGAAAGAGCTGATTTTGATTTTCAGGTTTGAAAAGAAATAACTGAA  
CATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACCTCAGAAATTAAGTTACTCA  
GAAATTAAGTAGCTCAGAAATTAAGAAAGAAATGGTATAATGAACCCCATATACCTTCTCTCTGGATTACCA  
ATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTTAATTTCAATTTGTTTATATTTACCTCTG  
GGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTGATTTTCTGTGGTTTATGG  
CAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACATC  
CCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTTCAGGATATTTTCTCTACAATAAAGTA  
ACAAT

*Fig. 1E*

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11781-76-87-37

CTCTGTGGAAAAGTATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGA  
TTACTGCAACACAGAGAACGAAGAAGAACTTTTCCTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGA  
TTCATACTACCCACACAGACCGCGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCAGATGATG  
TTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCAGGAACTGGATTCTTTAACTAACTGACCATGG  
ACTAGAGGAGATTTCTTCCTGTGCGCCAGAAAGGATTTTCATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCT  
GCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTC  
CAAGAACAACAAAACCATATCAGTGTACTGTAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTG  
TAGATAGTAGAAAGGGGGGCATCACCTGAGAAAGAGCTGATTTTGATTTTCAGGTTTGAAAGAAATAACTGAA  
CATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAAGTCAAGAAATTAAGTTACTCA  
GAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCATATACCTTCCTTCTGGATTACCA  
ATTGTTAACATTTTTTTCCTCTCAGCTATCCTTCTAATTTCTCTCTAATTTCAATTTGTTTATTTTACCTCTG  
GGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTGGATTTTCTGTGGTTTATGG  
CAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACATC  
CCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTTCAGGATATTTTCTCTACAATAAAGTA  
ACAATTA

11784-1 &amp; 2

GGACGACAAGGCCATGGCGATATCGGATCCGAATTCAAGCCTTTGGAATTAATAAACCTGGAACAGGGAAGGT  
GAAAGTTGGAGTGAGATGCTTCCATATCTATACCTTTGTGCACAGTTGAATGGGAAGTGTGGGTTTAGGGC  
ATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTGGGAGGTCAAGTGGGAAGTTGGTGAATGTGGA  
ATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAGCTTTCCTGACATGCAAGGATCTACTTTAATTC  
CACACTCTCATTAAATAAATTGAATAAAAGGGAATGTTTTGGCACCTGATATAATCTGCCAGGCTATGTGACAGT  
AGGAAGGAATGGTTTCCCCTAACAAGCCCAATGCACTGGTCTGACTTTATAAATTATTTAATAAAATGAAGTAT  
TATC

11785.2.contig

GGCAGTGACATTACCATCATGGGAACACCTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCACCCA  
GTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGTGC  
CAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAACTTTCTAACT  
TCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAAGTGGTGTTACC  
CAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAACAGGATGTGCTTTCCTTTGCC  
ATTTAGGGTTTCTTCTCTTTCCTTTCTCTTTATTAACCACT

**Fig. 1F**



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11718-182 cons

TGCGCTGAAAAACAACGGCCTCCTTTACTGTTAAAATGCAGCCACAGGTGCTTAGCCGTGGGCATCTCAACCACC  
AGCCTCTGTGGGGGGCAGGTGGGCGTCCCTGTGGGCCTCTGGGCCACGTCCAGCCTCTGTCTCTGCCTTCCG  
TTCTTCGACAGTGTTCCTGGCATCCCTGGTCACTTGGTACTTGGCGTGGGCCTCCTGTGCTGCTCCAGCAGCTC  
CTCCAGGXGGTCGGCCCCGCTTCACCGCAGCCTCATGTTGTGTCCGGAGGCTGCTCACGGCCTCCTCCTTCTCG  
CGAGGGCTGTCTTACCCTCCGGXGCACCTCCTCCAGCTCCAGCTGCTGGCGGGCCTGCAGCGTGGCCAGCTCG  
GCCTTGGCCTGCCGCGTCTCCTCCTCARAGGCTGCCAGCCGGTCTCGAACTCCTGGCGGATCACCTGGGCCAG  
GTTGCTGCGCTCGCTAGAAAGCTGCTCGTTCACCGCCTGCGCATCCTCCAGCGCCGCTCCTTCTGCCGCACAA  
GGCCTTGACAGCAGATTCTCGCCCTCGGCCTCCCAAGCTGGCCCTTCAGCTCCGAGCACCCTCCTGAAGC  
TTCGCTCCGACTGCTCCAGCTCGGAGAGCTCGGCCTCGTACTTGTCCCGTAAGCGCTTGATGCGGCTCTCGGC  
AGCCTTCTCACTCTCCTCCTTGGCCAGCGCCATGTGCGCCTCCAGCCGGTGAATGACCAGCTCAATCTCCTTGT  
CCCGGCCTTTCCGATTCTTCCCTCAGCTCCTGTTCCCGGTTCCAGAGCCACGCCTCCTCCTTCTGTTGCGG  
CCGGCCTCCACGCCTGCCTCTCCAGCTCCAGCTGCTGCTTCAGGGTATTAGCTCCATCTGGCGGGCCTGCAG  
CGTGGCCA

13690.4

CAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTTCCAGGCTGTGATATATTTTCTAGTGGT  
TTGACTTTAAAAATAAATAAGGTTTAATTTTCTCCCC

13693.1

TGCAAGTCACGGGAGTTTATTTATTTAATTTTTTTTCCCAGATGGAGACTCTGTGCGCCAGGCTGGAGTGCAAT  
GGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCACAGCCTCCCGAGTAGC  
TGGGATTACAGGTGCCCGCCACCACACCCAGCTAATTTTTATATTTTATAGTAAAGACAGGGTTTCCCATGTTG  
GCCAGGCTGGTCTTGAACCTCTGACCTCAGGTGATCCACCTGCCTCGGCCTCCCAAAGTGTGGGATTACAGGC  
GTGAGCTACCCGTGCCTGGCCAGCCACTGGAGTTTAAAGGACAGTCATGTTGGCTCCAGCCTAAGCGGGCATT  
TCCCCATCAGAAAGCCCGCGGCTCCTGTACCTCAAAATAGGGCACCTGTAAAGTCAGTCAGTGAAGTCTCTGC  
TCTAACTGGCCACCCGGGGCCATTGGCNTCTGACACAGCCTTGCCAGGANGCCTGCATCTGCAAAAGAAAAGTT  
CACTTCTTTCCG

13694.1

CAGAGAATCTKAGAAAGATGTGCGTTTTCTTTAATGAATGAGAGAAGCCATTTGTATCCCTGAATCATTGA  
GAAAAGGCGGCGGTGGCGACAGCGGCGACCTAGGGATCGATCTGGAGGGACTTGGGGAGCGTGACAGACCTCT  
AGCTCGAGCGGAGGGACCTCCCGCCGGGATGCCTGGGGAGCAGATGGACCCTACTGGAAGTCAGTTGGATTCA  
GATTTCTCTCAGCAAGATACTCCTTGCTGATAATTGAAGATTCTCAGCCTGAAAGCCAGGTTCTAGAGGATGA  
TTCTGGTTCTCACTTCAGTATGCTATCTCGACACCTTCTAATCTCCAGACGCACAAAGAAAATCCTGTGTTGG  
ATGTTGNGTCCAATCCTTGAACAAACAGCTGGAGAAGAACGAGGAGACCGGTAATAGTGGGTTCAATGAACATT  
TGAAAGAAAACCAGGTTGCAGACCTG

**Fig. 1G**

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13694.2

GACTGTCCTGAACAAGGGACCTCTGACCAGAGAGCTGCAGGAGATGCAGAGTGGTGGCAGGAGTGGAAGCCAAA  
GAACACCCACCTTCCTCCCTTGAAGGAGTAGAGCAACCATCAGAAGATACTGTTTTATTGCTCTGGTCAAACAA  
GTCTTCCTGAGTTGACAAAACCTCAGGCTCTGGTGACTTCTGAATCTGCAGTCCACTTTCATAAGTTCTTGTG  
CAGACAACTGTTCTTTTGCTTCCATAGCAGCAACAGATGCTTTGGGGCTAAAAGGCATGTCCTCTGACCTTGCA  
GGTGGTGGATTTTGTCTTTTACAACATGTACATCCTTACTGGGCTGTGCTGTCACAGGGATGTCCTTGCTGGA  
CTGTTCTGCTATGGGGATATCTTCGTTGGACTGTTCTTCATGCTTAATTGCAGTATTAGCATCCACATCAGACA  
GCCTGGTATAACCAGAGTTGGTGGTACTGATTGTAGCTGCTCTTTGTCCACTTCATATGGCACAAGTATTTTC  
CTCAACATCCTGGCTCTGGGAAG

13695.1

GAAATGTATATTTAATCATTCTCTTGAACGATCAGAACTCTRAAATCAGTTTTCTATAACARCATGTAATACAG  
TCACCGTGGCTCCAAGGTCCAGGAAGGCAGTGGTTAACACATGAAGAGTGTGGGAAGGGGGCTGGAAACAAAGT  
ATCTTTTCCTTCAAAGCTTCATTCTCAAGGCCTCAATTCAAGCAGTCATTGTCCTTGCTTTCAAAGTCTGT  
GTGTGCTTCATGGAAGGTATATGTTTGTTCCTTAATTTGAATTGTGGCCAGGAAGGGTCTGGAGATCTAAATT  
CAGAGTAAGAAAACCTGAGCTAGAACTCAGGCATTTCTCTTACAGAACTTGGCTTGCAAGGTAGAATGAANGGA  
AAGAACTTAGAAGCTCAACAAGCTGAAGATAATCCCATCAGGCATTTCCCATAGGCCTTGCAACTCTGTTTAC  
TGAGAGATGTTATCCTG

13695.2

AGTCTGGAGTGAGCAACAAGAGCAAGAAACAARRAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAA  
ATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTGTGTTAAGAGTGATAA  
GTAAATGCACGTGGAGACAAGTGCATCCCGAGATCTCAGGGACCTCCCGCTGCCTGTACCTGGGGAGTGAGA  
GGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTGTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCC  
TGGAAAGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGC  
TAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATG  
CTTCCCAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCCAAGTTGAGAAAAATGATCATAATTTTAGCA  
TAAACCGAGCAATCGGCGACCCC

13697.1

TAGCTGTCTTCCTCACTCTTATGGCAATGACCCCATATCTTAATGGATTAAGATAATGAAAGTGATTTCTTAC  
ACTCTGTATCTATCACCAGAAGCTGAGGTGATAGCCCGCTTGTCTTGTATCCATATTCTGGGACTCAGGCGG  
GAACTTTCTGGAATATTGCCAGGGAGCATGGCAGAGGGGCACAGTGCATTCTGGGGGAATGCACATTGGCTCAG  
CCTGGGTAATGAGTGATATACATTACCTCTGTTCACTCACTATGCCCAGCACCAGTACAAGGCCCCACCAAA  
TACCAGAGCCCAAGAAATGTAGTCCTGTTGATATGTTTTGCTGTGTCCCAACCCAAATCTCATCTTGAATTGT  
AAGCTCCCATAAATCCCATGTGTTGTGGGAGGGACCTGGTG

*Fig. 1H*

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13697.2

ATCATGAGGATGTTACCAAAGGGATGGTACTAAACCATTGTATTGCTCTGTTTTCACTGCTTTGAAGATAC  
TACCTGAGACTGGTAATTTATAAAACAAAGAGATTTAATTGACTCACAGTTCTGCATGGCTGAAGAGGCTCA  
GGAACTTACAGTCATGGTGGAGGCAAAGGAGGAGCAAGGCATGTCTTACATGTCAGTAGGAGAGAGAGCGAG  
AGCAGGAGAACCTGCCACTTATAAACCATTCAGATCTCATAACTCCCTATCATGAGAAAAACATGGAGGAAACC  
ACCCTCATGATCCAATCACCTCCCGCCAGGTCCCTCCCTCGACACGTGGGGATTATAATTGAGGATTAGAGGGA  
CACAGAGACAAACCATATCATCATTATGAGAAATCCACCCTCATAGTCCAATCAGCTCCTACCAGGCCCCACC  
TCCAACACTGGGGATTGCAATTCAACATGAGATTTGGATGGGGACACAGATTCAAACCATATCATAC

13699.1&amp;2

CATGGCCTTTCTCCTTAGAGGCCAGAGGTGCTGCCCTGGCTGGGAGTGAAGCTCCAGGCACTACCAGCTTTCTT  
GATTTTCCGTTTGGTCCATGTGAAGAGCTACCACGAGCCCCAGCCTCACAGTGTCCACTCAAGGGCAGCTTGG  
TCCTCTTGTCTGCAGAGGCAGGCTGGTGTGACCTGGGAACCTTGACCCGGGAACAACAGGTGGCCCAGAGTGA  
GTGTGGCCTGGCCCTCAACCTAGTGTCCGTCTCCTCTCTCTGAGCCAGTCTTGAGTTTAAAGGCATTAAG  
TGTTAGATAAAGCTCCTTGTGGCTGGAAAAACACCCCTCTGCTGATAAAGCTCAGGGGGCACTGAGGAAGCAG  
AGGCCCTTGGGGGTGCCCTCCTGAAGAGAGCGTCAGGCCATCAGCTCTGTCCCTCTGGTGTCCACGTCTGT  
TCCTCACCTCCATCTCTGGGAGCAGCTGCACCTGACTGGCCACGCGGGGGCAGTGGAGGCACAGGCTCAGGGT  
GGCCGGGCTACCTGGCACCTATGGCTTACAAAGTAGAGTTGGCCAGTTTCTTCCACCTGAGGGGAGCACTC  
TGACTCCTAACAGTCTTCTTGGCCTGCCATCATCTGGGGTGGCTGGCTGTCAAGAAAGGCCGGGCATGCTTTC  
TAAACACAGCCACAGGAGGCTTGTAGGGCATCTTCCAGGTGGGGAAACAGTCTTAGATAAGTAAGGTGACTTGC  
CTAAGGCCTCCAGCACCTTGATCTTGAGTCTCACAGCAGACTGCATGTSAAACACTGGAACCGAAAACATG  
CCTCAGTATAAAA

13703.3

CCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCTCTTGGAGACACAGAGGGTTTCACCTTGGATGACCTCTA  
GAGAAATTGCCAAGAAGCCCACCTTCTGGTCCCAACCTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGC  
TGTAAGAGGTCACTTGGCTCCATTGCCTGCTTCCAACCAATGGGCAGGAGAGAAGGCCTTTATTTCTCGCCAC  
CCATTCTCCTGTACCAGCACCTCCGTTTTAGTCAGYGTGTGTCAGCAACGGTACCGTTTACACAGTCA

13705.1

TGCATGTAGTTTTATTTATGTGTTTTSGTCTGGAAAACCAAGTGTCCAGCAGCATGACTGAACATCACTCACT  
TCCCCTACTTGATCTACAAGGCCAACGCCGAGAGCCAGACCAGGATTCCAAACACACTGCACGAGAATATTGT  
GGATCCGCTGTCTAGGTAAGTGTCCGTCACTGACCCARACGCTGTTACGTGGCACATGACTGTACAGTGCCACGT  
AACAGCACTGTACTTTTCTCCCATGAACAGTTACCTGCCATGTATCTACATGATTCAGAACATTTTGAACAGTT  
AATTCTGACACTTGAATAATCCCATCAAAAACCGTAAATCACTTTGATGTTTGAACGACAACATAGCATCAC  
TTTACGACAGAATCATCTGGAAAAACAGAACCAACATACATCTTAAAAAATGCTGGGGTGGGCCAGGCA  
CAGCTTCACGCCTGTAATCCAGCACTTTGGGAGGCTTAAGCGGGTG

*Fig. 11*

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13705.2

TGGGGCGGAAAGAAGCCAAGGCCAAGGAGCTGGTGCGGCAGCTGCAGCTGGAGGCCGAGGAGCAGAGGAAGCAG  
AAGAAGCGGCAGAGTGTGTGGGCCTGCACAGATACCTTCACCTGGATGGAAATGAAAATTACCCGTGTCT  
TGTGGATGCAGACGGTGATGTGATTTCTTCCCACCAATAACCAACAGTGAGAAGACAAAGGTTAAGAAAACGA  
CTTCTGATTTGTTTTTGGAAAGTAACAAGTGCCACCAGTCTGCAGATTTGCAAGGATGTCATGGATGCCCTCATT  
CTGAAAATGGCAAGAAATGAAAAAGTACACTTTAGAAAATAAAGAGGAAGGATCACTCTCAGATACTGAAGCCG  
ATGCAGTCTCTGGACAACCTCCAGATCCACAACGAATCCAGTGCTGGAAGGACGGGCCCTTCTTCTGGTG  
GTGGAACANGTCCCGGTGGTGGATCTTGAANGGAACCTGAANGTGGTGTACCCCGTCCAAGGCCGACCTTGGC  
CAC

13707.4

TCCCGCGCTCGCAGGGCNCGTGCCACCTGCCYGTCCGCCCGCTCGCTCGCTCGCCCGCCGCGCCGCTGCCGA  
CCGYCAGCATGCTGCCGAGAGTGGGTGCCCGCGCTGCCGCTGCCGCCGCGCCGCTGCTGCCGCTGCTGCCG  
CTGCTGCTGCTGC

13708.1&amp;2

GGCGGGTAGGCATGGAAGTGAAGAAGCAAGAAGCTTTCAGACTACGTGGGGAAGAATGAAAAACCAAAATT  
ATCGCCAAGATTGAGCAAGGGGACAGGGAGCTCCAGCCGAGAGCCTATTATTAGCAGTGAGGAGCAGAAGCA  
GCTGATGCTGTACTATCACAGAAGACAAGAGGAGCTCAAGAGATTGGAAGAAAATGATGATGATGCCTATTTAA  
ACTCACCATGGGCGGATAACACTGCTTTGAAAAGACATTTTCATGGAGTGAAAGACATAAAGTGGAGACCAAGA  
TGAAGTTCACCAGCTGATGACACTTCCAAGAGATTAGCTCACCT

13709.1

TCTGAAGGTTAAATGTTTCATCTAAATAGGGATAATGRTAAACACCTATAGCATAGAGTTGTTTGAGATTAAAT  
GAGATAATACATGTAAATATGTGCCTGGCATAACAGCAAGATTGTTGTTGTTGTTGATGATGATGATGATGAT  
GATAATATTTTTCTATCCCCAGTGCACTGCTTGAACCTATTAGATAATCAATACATGTTTCTTGAAGTGAAG  
ATCAATTTCCCATGTTGTCTGACTGATGAAGCCCTACATTTTCTTCTAGAGGAGATGACATTTGAGCAAGATC  
TTAAAGAAAATCAGATGCCTTCACTGACCACTGCTTGGTGATCCCATGGCACTTTGTACATCTCTCCATTAGC  
TCTCATCTCACCAGCCCATCATTATTGTATGTGCTGCCTTCTGAAGCTTGCAGCTGGCTACCATCMGGTAGAAT  
AAAAATCATCCTTTCATAAAATAGTGACCCTCCTTTTTTATTTGCATTTCCCAAAGCCAAGCACCGTGGGANGG  
TAG

**Fig. 1J**

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13709.2

TATGAAGAAGGGAAAAGAAGATAATTTGTGAAAGAAATGGGTCCAGTTACTAGTCTTTGAAAAGGGTCAGTCTG  
TAGCTCTTCTTAATGAGAATAGGCAGCTTTCAGTTGCTCAGGGTCAGATTTCTTAGTGGTGTATCTAATCACA  
GGAAACATCTGTGGTCCCTCCAGTCTCTTCTGGGGGACTTGGGCCACTTCTCATTTCAATTAATTAGAGGA  
AATAGAACTCAAAGTACAATTTACTGTTGTTAACAATGCCACAAAGACATGGTTGGGAGCTATTTCTTGATTT  
GTGTAATGCTGTTTTGTGTGCTCATAATGGTTCCAAAAATTGGGTGCTGGCCAAAGAGAGATACTGTTACA  
GAAGCCAGCAAGAAGACCTCTGTTCAATCACACCCCGGGGATATCAGGAATTGACTCCAGTGTGTGCAAATCC  
AGTTTGGCCTATCTTCT

13712.1&amp;2

TGAGGGACTGATTGGTTTGTCTCTGCTATTCAATCCCAAGCCCACTTGTTCTGCAGCGTCTCCTTCTCA  
TTCCCTTTAGTTGTACCTCTCTTTCATCTGAGACCTTTCCTTCTTGATGTCGCTTTTCTTCTTGTCTTTT  
TCTGATGTTCTGCTCAGCATGTTCTGGGTGCTTCTCATCTGCATCATTCCTTTCAGATGCTGTAGCTTCTTCT  
CCTCTTCTGCCTCCTTTTCTTTTCTTTTTTGGGGGGCTTGCTCTGACTGCAGTTGAGGGGCCCCAGGG  
TCCTGGCCTTTGAGACGAGCCAGGAAGGCCTGCTCCTGGGCCTTAGGCGAGCAAGCTTGGCCTTCATTGTGAT  
CCCAAGACGGGCAGCCTTGTGTGCTGTTGCCCCCTCACAGGCTTGAGCAGCATCTCATCAGTCAGAACTTTG  
GGGACTTGGACCCCTGGTTGTGTCATCACTGCAGCTCTCCAAGTCTTTGTTTGGCTTCTCTCCACCTGAAGTC  
AATGTAGCCATCTTCACAACTTCTGATACAGCAAGTTGGGCTTGGGATGATTATAACGGGTGGTCTCCTTAGA  
AAGGCTCCTTATCTGTACTCCATCCTGCCAGTTTCCACTACCAAGTTGGCCGAGTCTTGTGAAGAGCTCAT  
TCCACCAAGTGGTTTGTGAACCTTGGCAGGGTCATGTCCTACCCATGAGTGTCTTGCTTCAGYGTACCCTG  
AGAGCCTGAGTGATACCATTCCTTCCG

13714.1&amp;2

GACAAATGAATAAATCCTAGAGGACAAAATTAACCTCAATAGAGTGTAGTCTAGTTAAAAACTCGAAAAATG  
AGCAAGTCTGGTGGGAGTGGAGGAAGGGCTATACTATAAATCCAAGTGGGCCTCTGATCTTAACAAGCCATGC  
TCATTATACACATCTCTGAACCTGGACATACCACCTTACGCAGGAACAGGGCTTGGAACTTCTAAGGGAAATT  
AACATGCACCACCCACATCTAACCTACCTGCCGGTAGGTACCATCCCTGCTTGGCTGAAATCAGTGCTC

13716.1&amp;2

TTGGAATTAATAAACCTGGAACAGGGAAGGTGAAAGTTGGAGTGAGATGCTTCCATATCTATACCTTTGTGC  
ACAGTTGAATGGGAAGTGTGGGTTAGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTG  
GGAGGTCAAGTGGGAAGTTGGTGAATGTGAATAACTTACCTTTGTGCTCACTTAAACCAGATGTGTTGCAG  
CTTTCCTGACATGCAAGGATCTACTTTAATTCCACACTCTCATTAATAAATTGAATAAAAGGGAATGTTTTGGC  
ACCTGATATAATCTGCCAGGCTATGTGACAGTAGGAAGGAATGGTTTCCCTAACAAGCCCAATGCACTGGTCT  
GACTTTATAAATTATTTAATAAAATGAATATTATC

**Fig. 1K**

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13718.2

AAACTGGACCTGCAACAGGGACATGAATTTACTGCARGGTCTGAGCAAGCTCAGCCCCTCTACCTCAGGGCCCC  
ACAGCCATGACTACCTCCCCAGGAGCGGGAGGGTGAAGGGGGCCTGTCTCTGCAAGTGGAGCCAGAGTGGAGG  
AATGAGCTCTGAAGACACAGCACCCAGCCTTCTCGCACCAGCCAAGCCTTAAGTGCCTGCCTGACCCTGAACCA  
GAACCCAGCTGAAGTGGCCCTCCAAGGGACAGGAAGGCTGGGGGAGGGAGTTACAACCCAAGCCATTCCACCC  
CCTCCCCTGCTGGGGAGAATGACACATCAAGCTGCTAACAATTGGGGGAAGGGGAAGGAAGAAAAGTCTGAAAA  
CAAAATCTTGT

13722.3

CATGCGTTTCACCACTGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGCAATCCACCCGCTCAGCCTCCA  
AAAGTGCTGGGATTACAGATGTGAGCCATGGCACCATGCCAAAAGGCTATATTCCTGGCTCTGTGTTCCGAGA  
CTGCTTTTAATCCCACTTCTCTACATTTAGATTAATAATATTTTATTCATGGTCAATCTGGAACATAATTAC  
TGCATCTTAAGTTTCACTGATGTATATAGAAGGCTAAAGGCACAATTTTATCAAATCTAGTAGAGTAACCAA  
ACATAAAATCATTAACTTTCACTTAATACTAATTGACATTCTCAAAGAGCTGTTTTCAATCCTGATA  
GGTCTTTATTTTTCAAATATATTTGCCATGGGATGCTAATTTGCAATAAGGCGCATAATGAGAATACCCCA  
AATGGA

13722.4

GTTGGACCCCAGGGACTGGAAAGACACTTCTTGCCCGAGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTA  
TGCTTCTGGATCCGAATTTGATGAGATGTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAG  
CAAAGGCGAATGCTCCTTGTGTTATATTTATTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCA  
ATGCATCCATATTTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCCAATGAAGGAGT  
TATCATAATAGGAGCCACAACTTCCAGAGGCATTAGATAATGCCTTAATACCGTCTGGTCTTTTGACATG  
CAAGTTACAGTTCCAAGGCCAGATGTAAAGGTGCAACAGAAATTTTGAATGGTATCTCAATAAAATAAAGTT  
TGATCAATCCCGTTGATCCAGAAATATAGCCTCGAGGTAAGTGGTGGCTTTCCGGAAGCAGAGTTGGGAGAAT  
CTT

13724-13698-13748

GCCTACAACATCCAGAAAGAGTCTACCCTGCACCTGGTGTCTCGTCTCAGAGGTGGGATGCAGATCTTCGTGAA  
GACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCGAGTGACACCATYGAGAACGTCAAAGCAAAGATCC  
ARGACAAGGAAGGCRTYCCTCCTGACCAGCAGAGGTTGATCTTTGCCGAAAGCAGCTGGAAGATGGDCGCACC  
CTGTCTGACTACAACATCCAGAAAGAGTCYACCCTGCACCTGGTGTCTCCGTCTCAGAGGTGGGATGCARATCTT  
CGTGAAGACCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCAGTGACACCATCGAGAATGTCAAGGCAA  
AGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGA  
CGCACCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTGCGCTTGAGGGGGGTGTCTA  
AGTTTCCCTTTTAAGGTTTCAACAAATTTCAATGCACTTTCCTTTCAATAAAGTTGTTGCATTCCC

*Fig. 1L*

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13730.1

GAACTGGGCCCTGAGCCCAAGTCATGCCTTGTGTCCGCATCTGCCGTGTACCTCTGTCCTGCCCTCACCCC  
TCCCTCCTGGTCTTCTGAGCCAGCACCATCTCCAAATAGCCTATTCCTTCTGCAAATCACACACATGCGGG  
CCACACATACCTGCTGCCCTGGAGATGGGGAAGTAGGAGAGATGAATAGAGGCCATACATTGTACAGAAGGAG  
GGGCAGGTGCAGATAAAAGCAGCAGACCCAGCGCAGCTGAGGTGCATGGAGCACGGTTGGGGCCGGCATTGGG  
CTGAGCACCTGATGGGCTCATCTCGTGAATCCTCGAGGCAGCGCCACAGCAGAGGAGTTAAGTGGCACCTGGG  
CCGAGCAGAGCAGGAGACTGAGGGTCAGAGTGGAGGCTAAGCTGCCCTGGAACCTCTCAATCTTGCTGCCCC  
TAGTATGAAGCCCCCTTCCTGCCCTACAATTCCTGA

13732.1

ATGGATCTTACTTTGCCACCCAGGTTGGAGTGCAGTGCTGCAATCTTGGCTCACTGCAGCCTTAACCTCCAGG  
CTCAAGCTATCCTCCTGCCAAAGCCTTCCACATAGCTGGGACTACAGGTACACNGCCACCACCCAGCTAAAA  
TTTTTGTATTTTTGTAGAGACGGGATCTCGCCAGGTTGCCAGGCTGGTCCCATCCTGACCTCAAGCAGATCT  
GCCACCTCAGCCCCCAACGTGCTAGGATTACAGGCGTGAGCCACCGCACCCAGCCTTTGTTTTGCTTTTAAT  
GGAATCACCAGTTCCCTCCGTGTCTCAGCAGCAGCTGTGAGAAATGCTTTGCATCTGTGACCTTTATGAAGGG  
GAACCTCCATGCTGAATGAGGGTAGGATTACATGCTCCTGTTTCCCGGGGGTCAAGAAAGCCTCAGACTCCAGC  
ATGATAAGCAGGGTGAG

13732.2

ATAGGGGCTTTAAGGAGGGAATTCAGGTTCAATGAGGTCGTAAGGCCAGGGCTCTTATCCAGTAAGACTGGGGT  
CCTTAGATGAGAAAGAGACACCCGAGGTCCTTCTCTGCCGTGTGAGGATGCATCAAGAAGGCGGCCGTCTGC  
AAGCGAAGGAGAGGGCCGACCAGAAACCGACACCTTCATCTTGGACTTGACAGCCTCTAGAAGTGAAGAAATAAC  
TGTCTGTTGGTTAAGCCACCCAGTTTGTAGTATTCTCTTATGGCTTCCTAAGCAGACTAACAAACAAACACCCA  
AAATTAACATGATGGCTTCGCTGTCTTCTGTAAAAATTGCTATGAGAGAACTTTTCACTCACTGTTTTGCAGTTT  
CTCCCTCAGTCCCTGGTTCTTTCTTCTCACATAATCCCAATTTCAATTTATAGTTCATGGCCAGGCAGAGTCA  
TTCATCACGGCATCTCCTGAGCTAAACCAGCACCTGCTCTGCTCACTTCTTGACTGGCTGCTCATCATCAGCCC  
TCTTGAGAGATTCATTTCTCCCGTGCCAGGTACTTCAGCACCAAGCTCA

**Fig. 1M**

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13735.1

GGATAATGAAGTTGTTTTATTTAGCTTGGACAAAAAGGCATATTCCTCTATTTTCTTATACAACAAATATCCCC  
AAAATAAAGCAAGCATATATATCTTGAATGTGTAATAATCCAGTGATAAACAAGAGCAGTACTTTAAAAGAAAA  
AAAAATATGTTTTCTGTCAGGTTAAATGAGAATCAAAACCATTTACTCTGCTAACTCATTATTTTTTGCTTT  
CTTTTTGGTTAAGAGAGGCAATGCAATACACTGAAAAAGGTTTTATCTTATCTGGCATTGGAATTAGACATAT  
TCAAACCCAGCCCCATTTCCAACTTTAAGACCACAAACAAGTAATTTACTTTTCTGAACATTGGTTTTTTC  
TGGAAATGGGAATTATAAAATAGACTTTGCAGACTCTTATGAGATTAATAAGATAATGTATGAAATTCCTTC  
TTCTTTTTTACTTCTTTTTCTTTTTGAGATGGAGTCTACCCCGTCACCCAGGCTGGAGTACAGTG

13735.2

CCACTGCACTCCAGCCTGGGTGACGGAGTGAGACTCTGTCTCAAAAAACAAACAAACAAACAAAAAACT  
GAAAAGGAAATAGAGTTCCTCTTTCCTCATATATGAATATATTATTTCAACAGATTGTTGATCACCTACCATAT  
GCTTGGTATTGTTCTAATTGCTGGGGATACAGCAAGAGGTTCTGCAGAACTTCATGGAGCATGAAAGTAAATAA  
ACAAAGTTAATTTCAAGGCCAGGCATGGTTGCTCACACCTTTAGTCCCAGCACTTTGGGAGGCTGAGGCAGGTG  
GATCACTTGGGCCAGGAGTTCAAGGCTGCAGTGAGCAAGATTGTGCCACTACTCTCCAGGCTGGGCAACAGA  
GCAAGACCCTGTCTCAGGGGGAACAAAAAGTTAATTTAGATTTTGTAAAGTGTGTAAAGGAAGTAAATAGGT  
TGATATTCAAGAGAGCACCTGAAGGCCAGGCGTGGTGGCTCAGCCTGTGGTCTAACGCTTTGGGAAGCCCGAG  
CGGGCGGATCACAAGGTCAGGAGAATTTTGGCCAGGCATGGTG

13736.1

AGAATCCATTTATTGGGTTTTAACTAGTTACACAACCTGAAATCAGTTTGGCACTACTTTATACAGGGATTACG  
CCTGTGTATGCCGACACTTAAATACTGTACCAGGACCACTGCTGTGCTTAGGTCTGTATTCAGTCATTCAGCAT  
GTAGATACTAAAAATATACTGTAGTGTTCTTTAAGGAAGACTGTACAGGGTGTGTTGCAAGATGACATTCACC  
AATTTGTGAATTATTTCAACCCAGAAGATACCTTTCACTCTATAAACTTGTATAGGCAACATGTGGTGTAG  
CATTGAGAGATGCACACAAAAATGTTACATAAAAGTTCAGACATTCTAATGATAAGTGAAGTGAACAAAAA  
AACCCACATCTCAATTTTTGTAAACAAGATAAAGAAAAATAATTTAAAAACACAAAAAATGGCATTGAGTGGGT  
CAAAGCC

13737.1&amp;2

CAAATATTTAATATAAATCTTTGAAACAAGTTCAGAKGAAATAAAAAATCAAAGTTTGCAAAAACGTGAAGATTA  
ACTTAATGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTTATTTCTATGCAAAAGTATGCCTTCAAA  
CTGCTTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCATCTTGCAATTGTAAG  
AAATAGGTAAAAGATTATAAGACACCTTACACACACACACACACACACACACAGTGTGCACCGCCAATGAC  
AAAAACAATTTGGCCTCTCCTAAAATAAGAACATGAAGACCTTAATTGCTGCCAGGAGGGAACACTGTGTCA  
CCCCTCCCTACAATCCAGGTAGTTTCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGTGATTCTGA  
CAGCCACSGTTGAAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGCCCTGAAAAAATGCCAATAATTTT  
TCGCTCCCACTTCTGCTGCTGTCTCTTCCACATCCTCACATAGACCCAGACCCGCTGGCCCCTGGCTGGGCAT  
CGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTCACAGAAGCGATACACCAAATTGCCTGGTCGG  
TCATTGTCATAACCAG

**Fig. 1N**



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13738.1

TTTGACTTTAGTAGGGGTCTGAACTATTTATTTTACTTTGCCMGTAATATTTARACCYTATATATCTTTCATTA  
TGCCATCTTATCTTCTAATGBCAAGGGAACAGWTGCTAAMCTGGCTTCTGCATTWATCACATTAATAATGGCTT  
TCTTGAAAATCTTCTTGATATGAATAAAGGATCTTTTAVAGCCATCATTTAAAGCMGNTTCTCTCCAACACG  
AGTCTGCTSASGGGGGKGAGCTGTGAACTCTGGCTGAAGGCTTTCCATACACACTGCAATGACMTGGTTTCT  
GACCAGBTGAGTTA

13738.2

AGAGAAGCCCCATAAATGCAATCAGTGTGGGAAGGCCTTCAGTCAGAGCTCAAGCCTTTTCTCCATCATCGGG  
TTCATACTGGAGAGAAACCCTATGTATGTAATGAATGCGGCAGAGCCTTTGGTTTTAACTCTCATCTTACTGAA  
CACGTAAGGATTCACACAGGAGAAAAACCCTATGTTTGAATGAGTGCGGCAAAGCCTTTCTGTCGGAGTTCCAC  
TCTTGTTCAGCATCGAAGAGTTCACACTGGGGAGAAGCCCTACCAAGTGCCTTGAATGTGGGAAAGCTTTAGCC  
AGAGCTCCAGCTCACCTACATCAGCCGAGTTCACACTGGAGAGAAGCCCTATGACTGTGGTGACTGTGGGAA  
GGCCTTCAGCCGGAGGTCAACCCTCATTAGCATCAGAAAGTTCACAGCGGAGAGACTCGTAAGTGCAGAAAAAC  
ATGGTCCAGCCTTTGTTTATGGCTCCAGCCTCACAGCAGATGGACAGATTCCCACTGGAGAGAAGCACGGCAGA  
ACCTTTAACCATGGTGCAAATCTCATTCTGCGCTGGACAGTTC

13739.1&amp;2

GAGACAGGGTCTCACTTTGTCAACCAGGCTGGAATGCAGTGGTGCGATCTTACGTAGCTCACTGCAGCCCTGAC  
CTCCTGGACTCAAACAATTCTCCTGCCTCAGCCCTGCAAGTAGCTGGGACTGTGGGTGCATGCCACCATGCCTG  
GCTAACTTTTGTAGTTTTTGTAAAGATGGGGTTTTGCCATGTTGCACATGCTGGTCTTGAACCTCTGAGCTCAA  
ACGATCTGCCCACCTCGGCCTCCAGAAATGTTGGGATTACAGGGGTAAACCACCACGCCTGGCCCCATTAGGGT  
ATTCTTAGCATCCACTTGCTCACTGAGATTAATCATAAGAGATGATAAGCACTGGAAGAAAAAAATTTTACTA  
GGCTTTGGATATTTTTTCTTTTTCAGCTTTATACAGAGGATTGGATCTTTAGTTTTCTTTAACTGATAATA  
AAACATTGAAAGGAAATAAGTTTACCTGAGATTACAGAGATAACCGGCATCACTCCCTTGCTCAATTCCAGTC  
TTTACCACATCAATTATTTTTCAGAGGTGCAGGATAAAGGCCTTTAGTCTGCTTTTCGCACTTTTCTTCCACTTT  
TTTGTAAACCTGTTGCCTGACAAATGGAATTGACAGCGTATGCCATGACTATTCCATTGTGAGGCATACGCTG  
TCAATTTTTCCACCAATCCCTTGTCTCTTTGGAGAGATCTTCTTATCAGCTAGTCTTTGGCAAAAGTAATT  
GCAACTTCTTCTAGGTATTCTATTGTCCGTTCCACTGGTGGAAACCCTGGGACCAGGACTAAACCTCCAG

13741.1

ATCTCATATATATATTTCTTCTGACTTTATTTGCTTGCTTCTGNACGCATTTAAAAATATCACAGAGACCAAA  
ATAGAGCGGCTTTCTGGTGGAACGCATGGCAGTCACAGGACAAAATACAAAACCTAGGGGGCTCTGTCTTCTCAT  
ACATCATACAATTTTCAAGTATTTTTTTATGTACAAAGAGCTACTCTATCTGAAAAAAATTAATAATAAAT  
GAGACAAGATAGTTTATGCATCCTAGGAAGAAAGAATGGGAAGAAAGAACGGGGCAGTTGGGTACAGATTCTTG  
TCCCCTGTTCCAGGGACCACTACCTTCTGCACTGAGTTCACACAGCCTCACCCATCATGTACAGGGCA  
AGTGCCAGGGTAGGTGGGAGCAGTGGAGACAGGAACAGCAACATACTTTGGCCTGGAAGATAAGGAGAAAGT  
CTCAGAAAACACTGGTGGGAAGCAATCCACNCGCCGTGCCCCANGAGCTTCCACCTGCTGCTGGCTCCCTG  
GGTGGCTTTGGGAACAGCTTGGGCAGGCCCTTTTGGGTGGGGNCCAACCTGGGCTTTGGGCCCGTGTGGAAG

*Fig. 10*

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13742.1

AAACATTGAGATGGAATGATAGGGTTTCCAGAATCAGGTCCATATTTTAACTAAATGAAAATTATGATTTATA  
GCCTTCTCAAATACCTGCCATACTTGATATCTCAACCAGAGCTAATTTTACCTCTTTACAAATTAATAAGCAA  
GTAACCTGGATCCACAATTTATAATACCTGTCAATTTTTCTGTATTAAACCTCTATCATAGTTTAAAGCCTATTA  
GGGTACTTAATCCTTACAAATAAACAGGTTTAAATCACCTCAATAGGCAACTGCCCTTCTGGTTTTCTTCTTT  
GACTAAACAATCTGAATGCTTAAGATTTTCCACTTTGGGTGCTAGCAGTACACAGTGTTACACTCTGTATTCCA  
GACTTCTTAAATTATAGAAAAAGGAATGTACACTTTTTGTATTCTTCTGAGCAGGGCCGGGAGGCAACATCAT  
CTACCATGGTAGGGACTTGTATGCATGGACTACTTTA

14351.1

ACTCTGTCGCCCAGGCTGGAGCCCBTGGMGCGATCTCGACTCCCTGCAAGCTMCGCCTCACAGGWTATGCCA  
TTCTCCTGCCTCAGCATCTGGAGTAGCTGGGACTACAGGCGCCAGCCACCATGCCAGCTAATTTTT

14351.2

ACCTTAAAGACATAGGAGAATTTATACTGGGAGAGAAAGCTTACAAATGTAAGGTTTCTGACAAGACTTGGGAG  
TGATTCACACCTGGAACAACATACTGGACTTCACACTGGABAGAAACCTTACAAGTGTAATGAGTGTGGCAAAG  
CCTTTGGCAAGCAGTCAACACTTATTCACCATCAGGCAATTCA

14354.2

AGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAAG  
AACGTAATAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGGAGGTACATAACAGGTGATCAAGCCCGT  
ACTTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAATATGGGCCTTATCAGATCTGAACAAGGA  
TGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAACTCATCAAGTTAAAGTTGCAGGGCCAACAGCTGC  
CTGTAGTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGA  
AGCATGCCAATCTGTCCATTCATCAGCCATTGCCTCCAGTTGCACCTATAGCAACACCCTTGCTTCTGCTAC  
TTCAGGGACCAGTATTCCTCCCTAATGATGCCTGCT

14354.1

CTTTCGATTTCTTCAATTTGTACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTATTATAGCT  
TTCTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTTTCAAGAG  
CATCTAATTGTTCTTTAAGTCTTTGGCATAATTCTTCTTTCTGATGACTTTCTATGAAGTAACTGATCCCT  
GAATCAGGTGTGTTACTGAGCTGCATGTTTTTAATCTTTCTGTTTAATAGCTGCTTCTCAGGGACCAGATAGAT  
AAGCTTATTTTGATATTCCTTAAGCTCTTGGTGAAGTTGTTGATTTCCATAATTTCCAGGTCACACTGGTTAT  
CCCAAACCTTCT

***Fig. 1P***

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16431.1.2

GTGGAGGTGAAACGGAGGCAAGAAAGGGGGCTACCTCAGGAGCGAGGGACAAAGGGGGCGTGAGGCACCTAGGC  
CGGGGACACCCGGCGACAGGAAGCCGTCTGAACCGGGCTACCGGGTAGGGGAAGGGCCCGCGTAGTCCTCGCA  
GGGCCCCAGAGCTGGAGTCGGCTCCACAGCCCCGGGCGTCGGCTTCTCACTTCTGACCTCCCCGGCGCCCG  
GGCCTGAGGACTGGCTCGGCGGAGGGAGAAGAGGAAACAGACTTGAGCAGCTCCCCGTTGTCTCGCAACTCCAC  
TGCCGAGGAACCTCTATTCTTCCCTCGCTCCTTACCCCCACCTCATGTAGAAAGGTGCTGAAGCGTCCGGA  
GGGAAGAAGAACCTGGGCTACCGTCTGGCCTTCCMCCCCCTTCCCGGGGCGCTTTGGTGGGCGTGAGGTTGG  
GGTTGGGGGGTGGGTGGGGGTTCTTTTTGGAGTGCTGGGGAACTTTTTCCCTTCTTCAAGTCAAGGGAAAG  
GGAATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAACTTTGACGCCGTC  
ATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCGAAGCACAAGCGGCATAAGTCCAAAC  
ACTCCAAAGACATGGGGTTGGTGACCCCCGAAGCAGCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTAT  
GATGATATCAGCTCTGATTCCGACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGA  
ACGTCGTGGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGGGACTTAC  
TAAAAGCTAAACAGACCG

16432-1

GACATGTTTGCCTGCAGGGGACCAGAGACAATGGGATTAGCCAGTGCTCACTGTTCTTTATGCTTCCAGAGAGG  
ATGGGGACAGCTCTCAGGTGAGAATCCAGGCTGAGAAGGCCATGCTGGTTGGGGGCCCCGGAAGCACGGTCCG  
GATCCTCCCTGGCATCAGCGTAGACCCGCTGCTCAGGCTTGGGGTACCAAACCTCATGCTCTGTACTGTTTTGGC  
CCCATGCGGTGAGAGGAAAACCTAGAAAAAGATTGGTCGTGCTAAGGAATCAGCTGCCCCCTCATCTCCGCAT  
CCAATGCTGGTGACAACATATTCCTCTCCAGGACACAGACTCGGTGACTCCACACTGGGCTGAGTGGCCTCT  
GGAGGCTCGTGGCTAAGGCAGGGCTCCGTAAGGCTGATCGGCTGAACTGGGTGGGGTGAGGGTTTCTGACCCT  
TCGCTTCCCATCCCATAAACCGCTGTCAATGAGTCCACTGTGGTCA

16432-2

GATGGCATGGTCGTTGCTAATGTGCCTGCTGGGATGGAGCACTTCCTCCTGTGAGCCAGGGGACCCGCCTGTC  
CCTGGAGCTTGGGGCAAGGAGGGAAGAGTGATACCAGGAAGGTGGGGCTGCAGCCAGGGGCCAGAGTCAGTTCA  
GGGAGTGGTCCTCGGCCCTCAAAGCTCCTCCGGGACTGCTCAGGAGTGATGGTGCCCTGGAGTTTGCCCCAAC  
TTCCCTGGCCACCCTGGAAGGTGCCTGGCTGCTCAGGCCTCTAGGCTGGGCTGATGGGTTTCTCCAGGACACA  
AGTATCATTAAAGCCACCCTCTCCTCAGCTTGTGAGGCCGCACATGTGGGACAGGCTGTGCTCACAACCCCTC  
GCCTGCCCTGCCCTCCATCAGGAGGAGCCAGTGGAACCTTCGGAAGCTCCAGCATCTCAGCAGCCCTCAAAA  
GTCGTCCTGGGGCAAGCTCTGGTTCTCCTGACTGGAGGTGATCTGGGCTTGGCCTGCTCTCTCTCGC

17184.3

TAAAAAGTGTAACAAAGGTTTATTTAGACTTTCTTCATGCCCCAGATCCAGGATGTCTATGTAAACCGTTAT  
CTTACAAAGAAAGCACAATATTTGGTATAAACTAAGTCAGTGACTTGCTTAAGTAACTGAAATAGCGTCCATCAAAA  
GTGGGTTTAAAGTAAACTACCTGACGATATTGGCGGGGATCCTGCAGTTTGGACTGCTTGCCGGGTTTGTCCA  
GGGTTCCGGGTCTGTTCTTGGCACTCATGGGGACAGGCATCCTGCTCGTCTGTGGGGCCCCGCTGGAGCCCTTA  
CGTGAAGCTGAAGGTATCGACCSTAGGGGGCTCTAGGGCAGTGGGACCTTCATCCGGAACCTAACAAGGGTCGGG  
GAGAGGCCTCTTGGGCTATGTGGG

*Fig. 1Q*

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17184.4

CAAGCGTTCCTTTATGGATGTAAATTCAAACAGTCATGCTGAGCCATCCCGGGCTGACAGTCACGTTWAAGACA  
CTAGGTCGGGCGCCACAGTGCCACCCAAGGAGAAGAAGAATTTGGAATTTTTCATGAAGATGTACGGAAATCT  
GATGTTGAATATGAAAATGGCCCCAAATGGAATTCAAAAGGTTACCACAGGGGCTGTAAGACCTAGTGACCC  
TCCTAAGTGGGAAAGAGGAATGGAGAATAGTATTTCTGATGCATCAAGAACATCAGAATATAAACTGAGATCA  
TAATGAAGGAAAATTCATATCCAATATGAGTTTACTCAGAGACAGTAGAACTATTCCCAGG

17185.1

TAGGAATAACAAATGTTTATTCAGAAATGGATAAGTAATACATAATCACCTTCATCTCTTAATGCCCTTCCT  
CTCCTTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGGAGGAGGACACAGGACTAGCCAC  
CACCTTCTCTTCCCGGTCTCCAAGATGACTGCTTATAGAGTGGAGGAGGCAAACAGGTCCCCTCAATGTACCA  
GATGGTCACCTATAGCACCAGCTCCAGATGGCCACGTGGTTGCAGCTGGACTCAATGAACTCTGTGACAAACCA  
GAAGATACCTGCTTTGGGATGAGAGGGAGGATAAAGCCATGCAGGGAGGATATTTACCATCCCTACCCTAAGCA  
CAGTGCAAGCAGTGAGCCCCGGCTCCAGTACCTGAAAAACCAAGGCCTACTGNCTTTTGATGCTCTCTTGG  
GCCACG

17188.2

AAGCCTCCTGCCCTGGAAATCTGGAGCCCCTTGAGCTGAGCTGGACGGGGCAGGGAGGGGCTGAGAGGCAAGA  
CCGTCTCCCTCCTGCTGCAGCTGCTTCCCAGCAGCCACTGCTGGGCACAGCAGAAACGCCAGCAGAGAAAATG  
GGAGCCGAGAGTCTTAGCCCTGGAGCTGAGGCTGCCTCTGGGCTGACCCGCTGGCTGTACGTGGCCAGAACTG  
GGGTTGGCATCTGGCATCCATTGAGGCCAGGGTGGAGGAAAGGGAGGCCAACAGAGGAAAACCTATTCTGCT  
GTGACAACACAGCCCTTGTCACGCAGCCTAAGTGCAGGGAGCGTGATGAAGTCAGGCAGCCAGTCGGGGAGG  
ACGAGGTAAGTCAGCAGCAATGTCACCTTGAGCCTATGCGCTCAATGGCCCGAGGGGCAGCAACCCCCGCA  
CACGTCAGCCAACAGCAGTGCTCTGCAGGCACCAAGAGAGCGATGATGGACTTGAGCGCCGTGTTT

17190.1

GTTTGGCAGAAGACATGTTTAATAACATTTTCATATTTAAAAAATACAGCAACAATTCTCTATCTGTCCACCAT  
CTTGCCCTTGCCCTTCTGGGGCTGAGGCAGACAAAGGAAAGGTAATGAGGTTAGGGCCCCCAGGCGGGCTAAGT  
GCTATTGGCCTGCTCCTGCTCAAAGAGAGCCATAGCCAGCTGGGCACGGCCCCCTAGCCCCCTCAGGTTGCTGA  
GGCGGCAGCGGTGGTAGAGTTCTTCACTGAGCCGTGGGCTGCAGTCTCGCAGGGAGAACTTCTGCACCAGCCCT  
GGCTCTACGGCCCCGAAAGAGGTGGAGCCCTGAGAACCGGAGGAAAACATCCATCACCTCCAGCCCCCTCAGGGC  
TTCCTCCTCTTCTGGCCTGCCAGTTCACCTGCCAGCCGGGCTCGGGCCGCCAGGTAGTCAGCGTTGTAGAAGC  
AGCCCTCCGAGAAGCCTGCCGGTCAAATCTCCCCGCTATAGGAGCCCCCGGGAGGGGTACGACC

**Fig. 1R**

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17190.2

CAAGTTGAACGT CAGGCTTGGCAGAGGTGGAGTGTAGATGAAAACAAAGGTGTGATTATGAAGAGGATGTGAGT  
CCTTTGGGTGTAGGAGAGAAAGGCTGTTGAGCTTCTATTTCAAGATACTTTTACCTGTGCAAAAAGCACATTTT  
CCACCTCCTTCTCATGGCATTGTGTAAAGGTGAGTATGATTCTATTCCATCTGCATTTTAGAGGTGAAGAATA  
ACGTACAAGGGATT CAGTGATTAGCAAGGGACCCCTCACTAAGTGTTGATGGAGTTAGGACAGAGCTCAGCTGT  
TTGAATCTCAGAGCCAGGCAGCTGGAGCTGGGTAGGATCCTGGAGCTGGCACTAATGTGAGGTGCATTCCCTC  
CAACCCAGGCTCAGATCCGGAACCTGACCGTGCTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGG  
CTCCCTGCTCCTTTCACACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGC

17191.2&amp;89.2

TGGCCTGGGCAGGATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTATGACC  
CCATCATTTCCCAGAGGTCTCGGCCTCCTTTGGTGTT CAGCAGCTGCCCTGGAGGAGATCTGGCCTCTCTGT  
GATTTCACTACTGTGCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCCAGTG  
CAAGAAGGGGGTGCGTGTGGTGAACGTGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGCCCTGC  
AGTCTGGCCAGTGTGCCGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCACGGGACCGGGCCTTGTTGGAC  
CATGAGAATGTCATCAGCTGTCCCACTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAAT  
TGCTGTT CAGTTCGTGGACATGGTGAAGGGGAAATCTCTCACGGGGGTTGTGAATGCCCAGGCCCTT

***Fig. 1S***

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AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGG  
CCAAATATGTGGGCTATTACATCTGAAGAACGTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGG  
AGGTTACATAACAGGTGATCAAGCCCGTACTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAA  
TATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAACTCATC  
AAGTTAAAGTTGCAGGGCCAACAGCTGCCTGTAGTCCTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCC  
ACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCAATCTGTCCATTTCATCAGCCATTGCCTCCAGTTGCAC  
CTATAGCAACACCCTTGCTTCTGCTACTTCAGGGACCAGTATTCCTCCCTAATGATGCCTGCTCCCTAGTG  
CCTTCTGTAGTACATCCTCATTACCAAATGGAAGTGCAGTCTCATTAGCCTTTATCCATTCTTATTCTTC  
TTCAACATTGCCTCATGCATCATCTTACAGCCTGATGATGGGAGGATTTGGTGGTGCTAGTATCCAGAAGGCCC  
AGTCTCTGATTGATTTAGGATCTAGTAGCTCAACTTCCTCAACTGCTTCCCTCTCAGGGAACTCACCTAAGACA  
GGGACCTCAGAGTGGGCAGTTCTCAGCCTTCAAGATTAAAGTATCGGCAAAAATTTAATAGTCTAGACAAAGG  
CATGAGCGGATACCTCTCAGGTTTTCAAGCTAGAAATGCCCTTCTTCAGTCAAATCTCTCTCAAACCTCAGCTAG  
CTACTATTTGGACTCTGGCTGACATCGATGGTGACGGACAGTTGAAAGCTGAAGAATTTATTCTGGCGATGCAC  
CTACTGACATGGCCAAAGCTGGACAGCCACTACCACTGACGTTGCCTCCCGAGCTTGTCCCTCCATCTTTCAG  
AGGGGGAAAGCAAGTTGATTCTGTTAATGGAAGTCTGCCTTCATATCAGAAAACACAAGAAGAAGAGCCTCAGA  
AGAACTGCCAGTTACTTTTTGAGGACAAACGGAAAGCCAATATGAACGAGGAAACATGGAGCTGGAGAAGCGA  
CGCCAAGTGTTGATGGAGCAGCAGCAGAGGGAGGCTGAACGCAAGCCAGAAAGAGAAGGAAGAGTGGGAGCG  
GAAACAGAGAGAACTGCAAGAGCAAGAATGGAAGAAGCAGCTGGAGTTGGAGAAACGCTTGGAGAAACAGAGAG  
AGCTGGAGAGACAGCGGGAGGAAGAGAGGAGAAAGGAGATAGAAAGACGAGAGGCAGCAAAACAGGAGCTTGAG  
AGACAACGCCGTTTAGAATGGGAAAGACTCCGTCGGCAGGAGCTGCTCAGTCAGAAGACCAGGGAACAAGAAGA  
CATTGTCAGGCTGAGCTCCAGAAAGAAAAGTCTCCACCTGGAAGTGAAGCAGTGAATGGAAAACATCAGCAGA  
TCTCAGGCAGACTACAAGATGTCAAATCAGAAAGCAAACACAAAAGACTGAGCTAGAAGTTTTGGATAAACAG  
TGTGACCTGGAAATTTATGGAAATCAAACAACCTTCAACAAGAGCTTAAGGAATATCAAATAAGCTTATCTATCT  
GGTCCCTGAGAAGCAGCTATTAAACGAAAGAATTAATAACATGCAGCTCAGTAACACACCTGATTAGGGATCA  
GTTTACTTCATAAAAAGTCATCAGAAAAGGAAGAATTATGCCAAAGACTTAAAGAACAATTAGATGCTCTTGAA  
AAAGAACTGCATCTAAGCTCTCAGAAATGGATTCAATTAACAATCAGCTGAAGGAACTCAGAGAAAGCTATAA  
TACACAGCAGTTAGCCCTTGAACAACCTCATAAAATCAAACGTGACAAATTGAAGGAAATCGAAAGAAAAGAT  
TAGAGCAAAAAAAAAAAAA

*Fig. 2A*

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ATGGCAGTGACATTCACCATCATGGGAACACCTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCACC  
CAGTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGT  
GCCAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAACTTTCTAA  
CTTCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAACCTGGTGTTA  
CCCAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAAACAGGATGTGCTTTCCTTTGC  
CCATTTAGGGTTTCTTCTCTTTCCTTCTCTTTATTAACCACTA

***Fig. 2B***

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ATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGA  
ACAAGATAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAA  
GAGTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGG  
GGAGTGAGAGGACAGGATAGTGCA TGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGA  
GGAAGCCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTAGTATGTACCCTA  
AGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTT  
TTTATGATGCTTCAAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATA  
ATTTTAGCATAAACAGAGCAGTCGGCGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAACAA  
ATGCGGGTTTATTTCTCAGATGATGTTTCATCCGTGAATGGTCCAGGGAAGGACCTTTCACCTTGACTATATGGC  
ATTATGTCATCACAAGCTCTGAGGCTTCTCCTTTCCATCCTGCGTGGACAGCTAAGACCTCAGTTTTCAATAGC  
ATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGCGCCCCCATCTCGGGGGAATGCTGTAAGACAATTTTGT  
ACCTCAATGAGGGAGTGGAGGAGGATACAGTGCTACTACCAACTAGTGGATAAAGGCCAGGGATGCTGCTCAAC  
CTCCTACCATGTACAGGACGTCTCCCCATTACAACACCAATCCGAAGTGTCAACTGTGTCAGGACTAAGAAA  
CCCTGGTTTTGAGTAGAAAAGGGCCTGGAAAGAGGGGAGCCAACAAATCTGTCTGCTTCTCACATTAGTCATT  
GGCAATAAGCATTCTGTCTCTTTGGCTGCTGCCTCAGCACAGAGAGCCAGAACTCTATCGGGCACCAGGATAA  
CATCTCTCAGTGAACAGAGTTGACAAGGCCTATGGGAAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTC  
TAAGTTTCTTTCCCTTCATTCTACCTGCAAGCCAAGTTCTGTAAGAGAAATGCCTGAGTTCTAGCTCAGGTTT  
TCTTACTCTGAATTTAGATCTCCAGACCCTTCTGGCCACAATTCAAATTAAGGCAACAAACATATACCTTCCA  
TGAAGCACACACAGACTTTTGAAGCAAGGACAATGACTGCTTGAATTGAGGCCTTGAGGAATGAAGCTTTGAA  
GGAAAAGAATACTTTGTTTCCAGCCCCCTTCCCACTCTTCATGTGTTAACCACTGCCTTCTGGACCTTGGA  
GCCACGGTGACTGTATTACATGTTGTTATAGAAAAGTATTTAGAGTTCTGATCGTTCAAGAGAATGATTAAA  
TATACATTTCTA

*Fig. 2C*



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[illegible]

Fig. 3

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TCGAGCGGCCGCCGGGCAGGTCCTTCAGACTTGGACTGTGTCACTGCCAGGCTTCAGGGCTCCAATTGC  
AGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACACCATGGTT  
TTATCCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATATTTCTAC  
CTCGGCCGCGACCACGCT

*Fig. 4*

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TAGCGYGGTCGCGGCCGAGGYCTGCTTYTCTGTCCAGCCCAGGGCCTGTGGGGTCAGGGCGGTGGGTGCAGATG  
GCATCCACTCCGGTGGCTTCCCATCTTTCTCTGGCCTGAGCAAGGTCAGCCTGCAGCCAGAGTACAGAGGGCC  
AACACTGGTGTTCTTGAACAAGGGCCTTAGCAGGCCCTGAAGGRCCCTCTCTGTAGTGTTGAACCTCCTGGAGC  
CAGGCCACATGTTCTCCTCATACCGCAGGYTAGYGATGGTGAAGTTGAGGGTGAAATAGTATTMANGRAGATGG  
CTGGCARACCTGCCCGGGCGGCCGCTCSAAATCC

*Fig. 5*

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AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTGAGCTCTCTG  
TACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCAC  
CCATCGTCCTGACCCAAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACG  
GCATCACTGAGCTGGGCCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCT  
GTACCCACCACCAGCACCAGGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

*Fig. 6*

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TTGGGGNTTTMGAGCGGCCGCCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACTTCACCA  
TCAACAACCTGCGGTATGAGGAGAACATGCAGCACCCCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTT  
CAGGGCCTGCTCAGGTCCCTGTTCAAGAGCACCAGTGTGGCCCTCTGTACTCTGGCTGCAGACTGACTTTGCT  
CAGACTTGAGAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCTTGATCCCACTGGTCCTG  
GACTGGACAGAGAGCGGCTATACTGGGAGCTGAGCCAGTCTCTGGCGGNGACNCCNCTT

***Fig. 7A***

AGCGTGGTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCACTGGCACAGTGAGGAAGATCTCTG  
CTGTCACTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAAGTGCATTTAATACACCTAACGTATCGAACAT  
CATAGCTTGGCCAGGTTATCTCATATGTGCTCAGAACTTACAATAGCCTGCAGACCTGCCCGGGCGGCCGC  
TCGA

***Fig. 7B***

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TGTGGTGTGAACTTCCTGGAGNCAGGGTGACCCATGTCCTCCCATACTGCAGGTTGGTGATGGTGAAGTTGA  
GGGTGAATGGTACCAGGAGAGGGCCAGCAGCCATAATTGTSGRGCKGSMGMSSGAGGMWGGWGTYYCWGAGGTT  
CYRARRTCCACTGTGGAGGTCCCAGGAGTGCTGGTGGTGGGCACAGAGSTCYGATGGGTGAAACCATTGACATA  
GAGACTGTTCCCTGTCCAGGGTGTAGGGGCCCAGCTCTTYRATGYCATTGGYCAGTTKGCTYAGCTCCCAGTACA  
GCCRCTCTCKGYYGWCCAGSGCTTTTGGGGTCAAGATGATGGATGCAGATGGCATCCACTCCAGTGGCTGCT  
CCATCCTTCTCGGACCTGAGAGAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTTCCTTTGAATA

*Fig. 8*

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TCGAGCGGCCGCCGGGCAGGTCAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCACCTGTGCTG  
CGGACATCTCCAGGGAGTGCAGAAGGGAAGCAGGTCAAAGTCTCAGATCAGTCAGACTGGCTGTTCTCAGTTC  
TCACCTGAGCAAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTGAACAAGGGCTTGAGCA  
GACCCTGCAGAACCTCTTCCGTGGTGTGAACCTCCTGGAAACCAGGGTGTTCATGTTTTCTCATAATGC  
AAGGTTGGTGATGG

*Fig. 9*

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| Gene Name     | Ref. Probe 1<br>Exp. Name | Probe 2<br>Name      | Gene<br>ID | Probe1<br>Value | Probe2<br>Value | Probe1<br>R/S | Probe2<br>R/S | Probe1<br>AK | Probe2<br>AK |
|---------------|---------------------------|----------------------|------------|-----------------|-----------------|---------------|---------------|--------------|--------------|
| 42100188 (D3) | +7.0 205A Ovary T         | 230A Liver N         | 42200606   | 8620            | 1240            | 57.7          | 63            | 63           | 63           |
| 42100188 (D3) | +5.9 323 Ovary T          | 536 Spinal Cord N    | 42200628   | 5894            | 1002            | 35.3          | 89            | 89           | 89           |
| 42100188 (D3) | +5.7 385A Ovary T         | 591 Fetal testis     | 42200607   | 12151           | 2121            | 54.3          | 73            | 73           | 73           |
| 42100188 (D3) | +5.1 426A Ovary T (man)   | 415A Adip N          | 42200611   | 7487            | 1480            | 57.0          | 73            | 73           | 73           |
| 42100188 (D3) | +5.5 269A Ovary T         | 573 Breast N         | 42200623   | 7302            | 2116            | 39.2          | 84            | 84           | 84           |
| 42100188 (D3) | +5.3 283A Ovary T (man)   | 11 Colon N           | 42200609   | 3714            | 1113            | 20.4          | 83            | 83           | 83           |
| 42100188 (D3) | +9.0 939A Ovary T (SCID)  | 12 Skin N            | 42200601   | 2435            | 814             | 12.1          | 75            | 75           | 75           |
| 42100188 (D3) | +2.6 382A Ovary T (man)   | 322A Dendritic cell  | 42200608   | 4578            | 1754            | 25.0          | 69            | 69           | 69           |
| 42100188 (D3) | +2.2 264A Ovary T         | 52 Pancreas N        | 42200629   | 7904            | 5595            | 38.5          | 81            | 81           | 81           |
| 42100188 (D3) | +2.0 386A Ovary T         | 540 PBMC testis      | 42200605   | 2191            | 1081            | 14.0          | 90            | 90           | 90           |
| 42100188 (D3) | +2.0 511A Ovary T (man)   | CT10 Small intestine | 42200604   | 1978            | 971             | 10.4          | 80            | 80           | 80           |
| 42100188 (D3) | +2.0 265A Ovary T         | CT5 Heart N          | 42200604   | 1811            | 953             | 13.3          | 93            | 93           | 93           |
| 42100188 (D3) | +2.0 395A Ovary T         | 57 Ovary N           | 42200606   | 1666            | 819             | 9.8           | 100           | 100          | 100          |
| 42100188 (D3) | +1.9 428A Ovary T (man)   | 243A Esophagus N     | 42200612   | 1887            | 1430            | 13.4          | 97            | 97           | 97           |
| 42100188 (D3) | +1.5 261A Ovary T         | 518 Spleen muscle    | 42200601   | 5914            | 1653            | 30.4          | 86            | 86           | 86           |
| 42100188 (D3) | +1.5 265A Ovary T         | 521 Ovary N          | 42200603   | 2039            | 1274            | 11.9          | 50            | 50           | 50           |
| 42100188 (D3) | +1.5 822 Ovary T          | CT9 Kidney N         | 42200607   | 1756            | 1072            | 11.0          | 92            | 92           | 92           |
| 42100188 (D3) | +1.4 948A OT 1-P (SCID)   | 545 GT 5-P (SCID)    | 42200602   | 4204            | 3034            | 23.0          | 93            | 93           | 93           |
| 42100188 (D3) | +1.4 262A Ovary T         | 534A Large Intestine | 42200622   | 3002            | 2101            | 16.6          | 89            | 89           | 89           |
| 42100188 (D3) | +1.3 525 Ovary T          | CT4 Bone Marrow      | 42200619   | 1853            | 1297            | 9.6           | 90            | 90           | 90           |
| 42100188 (D3) | +1.2 429A Ovary T (man)   | 364A Ovary N         | 42200614   | 2521            | 2084            | 22.0          | 85            | 85           | 85           |
| 42100188 (D3) | +1.2 982A Ovary T         | CT19 Brain N         | 42200610   | 2072            | 1663            | 10.9          | 88            | 88           | 88           |
| 42100188 (D3) | +1.2 285A Ovary T         | CT12 Lung N          | 42200625   | 1840            | 1473            | 10.7          | 87            | 87           | 87           |
| 42100188 (D3) | +1.1 201A Ovary T         | 56 Spleen N          | 42200620   | 1329            | 1204            | 9.1           | 90            | 90           | 90           |

Fig. 10



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| Gene Name     | Exp Name                  | Probe 1 | P1 | P2 | Probe 2               | Probe 2 Name | Gene ID  | Probe1 Value | Probe2 Value | Probe1 S/B | Probe2 S/B |
|---------------|---------------------------|---------|----|----|-----------------------|--------------|----------|--------------|--------------|------------|------------|
| 421B0181 (C3) | +18.8 385A Ovary T        |         |    |    | S91 Fetal tissue      |              | 422X0607 | 26711        | 1424         | 103.3      | 54         |
| 421B0181 (C3) | +11.5 523 Ovary T         |         |    |    | S26 Spinal Cord N     |              | 422G0628 | 13559        | 1779         | 65.3       | 68         |
| 421B0181 (C3) | +11.1 426A Ovary T (meas) |         |    |    | 415A Adip N           |              | 422X0611 | 14125        | 1273         | 67.3       | 61         |
| 421B0181 (C3) | +10.8 205A Ovary T        |         |    |    | 270A Liver N          |              | 422Q0606 | 16121        | 1488         | 93.1       | 43         |
| 421B0181 (C3) | +5.1 263A Ovary T         |         |    |    | S73 Breast N          |              | 422H0623 | 11326        | 2235         | 58.2       | 68         |
| 421B0181 (C3) | +4.6 389A Ovary T (meas)  |         |    |    | 272A Dendrocytes      |              | 422H0608 | 6583         | 1424         | 24.5       | 40         |
| 421B0181 (C3) | +4.4 254A Ovary T         |         |    |    | S27 Puncta N          |              | 422N0629 | 9865         | 2245         | 40.9       | 64         |
| 421B0181 (C3) | +4.2 429A Ovary T (meas)  |         |    |    | 364A Ovary N          |              | 422J0614 | 2803         | 658          | 22.6       | 60         |
| 421B0181 (C3) | +4.2 251A Ovary T         |         |    |    | S10 Skeletal muscle N |              | 422X0621 | 8271         | 1949         | 39.3       | 68         |
| 421B0181 (C3) | +3.8 8115 Ovary T (meas)  |         |    |    | 2510 Small intestine  |              | 422C0604 | 3281         | 607          | 11.6       | 60         |
| 421B0181 (C3) | +2.5 265A Ovary T         |         |    |    | CT5 Heart N           |              | 422O0624 | 3192         | 1293         | 19.2       | 68         |
| 421B0181 (C3) | +2.3 822 Ovary T          |         |    |    | CT9 Kidney N          |              | 42290627 | 565          | 1276         | 3.8        | 70         |
| 421B0181 (C3) | +2.2 266A Ovary T         |         |    |    | S27 Ovary N           |              | 422S0603 | 2774         | 1260         | 14.3       | 46         |
| 421B0181 (C3) | +2.1 9334 Ovary T (SCID)  |         |    |    | 12 Skin N             |              | 422R0601 | 1724         | 887          | 8.4        | 56         |
| 421B0181 (C3) | +1.9 9483 OT 1-P (SCID)   |         |    |    | 9483 OT 1-P (SCID)    |              | 422Y0602 | 6967         | 3726         | 41.3       | 70         |
| 421B0181 (C3) | +1.6 382A Ovary T         |         |    |    | CT19 Brain N          |              | 422Q0610 | 2313         | 1471         | 6.2        | 50         |
| 421B0181 (C3) | +1.5 288A Ovary T         |         |    |    | CT12 Lung N           |              | 422V0625 | 1657         | 1054         | 9.7        | 69         |
| 421B0181 (C3) | +1.5 825 Ovary T          |         |    |    | CT4 Bone Marrow N     |              | 422H0619 | 848          | 1283         | 4.5        | 65         |
| 421B0181 (C3) | +1.4 262A Ovary T         |         |    |    | 334A Large Intestine  |              | 422A0622 | 3171         | 2214         | 16.8       | 69         |
| 421B0181 (C3) | +1.2 386A Ovary T         |         |    |    | 340 BMCM (activated)  |              | 422J0605 | 630          | 544          | 4.2        | 53         |
| 421B0181 (C3) | +1.2 335A Ovary T         |         |    |    | S7 Ovary N            |              | 42220626 | 592          | 730          | 3.7        | 75         |
| 421B0181 (C3) | +1.0 201A Ovary T         |         |    |    | S6 Stomach N          |              | 422V0620 | 1197         | 1237         | 7.8        | 65         |
| 421B0181 (C3) | +1.0 428A Ovary T (meas)  |         |    |    | 243A Esophagus N      |              | 422A0612 | 783          | 797          | 4.5        | 95         |
| 421B0181 (C3) | +383A Ovary T (meas)      |         |    |    | 11 Colon N            |              | 422B0609 | 2470         | 882          | 8.9        | 24         |

Fig. 11

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| Gene Name    | Ref. Probe 1             | Probe 1               | Probe 2  | Probe 1 Value | Probe 2 Value | Probab1 | Probab2 | Probe 1 | Probe 2 |
|--------------|--------------------------|-----------------------|----------|---------------|---------------|---------|---------|---------|---------|
| Gene Name    | Ref. Probe 1             | Probe 1               | Probe 2  | Probe 1 Value | Probe 2 Value | Probab1 | Probab2 | Probe 1 | Probe 2 |
| 4210182 (H7) | +16.7 469A Ovary T (neu) | 415A Adip N           | 422X0611 | 7705          | 962           | 46.3    | 75      | 3.5     | 75      |
| 4210182 (H7) | +10.7 305A Ovary T       | 270A Liver N          | 422Q0606 | 10171         | 950           | 61.2    | 41      | 1.8     | 41      |
| 4210182 (H7) | +9.9 385A Ovary T        | S91 Fetal tissue      | 422X0607 | 14415         | 1439          | 62.1    | 48      | 2.2     | 48      |
| 4210182 (H7) | +8.8 523 Ovary T         | S55 Spinal Cord N     | 422Q0628 | 7781          | 880           | 47.3    | 73      | 3.4     | 73      |
| 4210182 (H7) | +6.4 383A Ovary T (neu)  | H Colon N             | 422B0609 | 4807          | 748           | 27.6    | 47      | 2.2     | 47      |
| 4210182 (H7) | +5.1 263A Ovary T        | S73 Breast N          | 422H0623 | 9815          | 1909          | 57.1    | 74      | 4.2     | 74      |
| 4210182 (H7) | +4.9 429A Ovary T (neu)  | M4A Ovary N           | 422D0614 | 2661          | 543           | 26.3    | 61      | 6.7     | 61      |
| 4210182 (H7) | +3.5 264A Ovary T        | S2 Puncture N         | 422N0629 | 7934          | 2274          | 38.8    | 71      | 3.9     | 71      |
| 4210182 (H7) | -2.9 525 Ovary T         | C74 Bone Marrow       | 422H0619 | 480           | 1975          | 3.5     | 80      | 3.0     | 80      |
| 4210182 (H7) | +2.8 261A Ovary T        | S10 Skeletal muscle   | 42230621 | 8993          | 3245          | 34.6    | 69      | 5.1     | 69      |
| 4210182 (H7) | +2.5 5115 Ovary T (neu)  | C71.0 Small intestine | 422C0604 | 1864          | 738           | 8.1     | 67      | 2.2     | 67      |
| 4210182 (H7) | +2.3 933A Ovary T (SCII) | T2 Skin N             | 422R0601 | 2532          | 1113          | 12.7    | 41      | 2.6     | 41      |
| 4210182 (H7) | -2.3 522 Ovary T         | C19 Kidney N          | 42290627 | 386           | 889           | 3.2     | 69      | 3.4     | 69      |
| 4210182 (H7) | +2.2 384A Ovary T (neu)  | C72A Dendritic cells  | 42240608 | 3516          | 1567          | 18.7    | 55      | 2.2     | 55      |
| 4210182 (H7) | -2.2 382A Ovary T        | C75 Brain N           | 422Q0610 | 608           | 1520          | 4.2     | 60      | 2.3     | 60      |
| 4210182 (H7) | +1.9 265A Ovary T        | C75 Brain N           | 422Q0604 | 2063          | 1080          | 13.6    | 87      | 3.5     | 87      |
| 4210182 (H7) | +1.8 265A Ovary T        | S27 Ovary N           | 42250608 | 1550          | 847           | 7.0     | 58      | 2.1     | 58      |
| 4210182 (H7) | +1.5 262A Ovary T        | S34A Large Intestine  | 422A0622 | 2559          | 1631          | 14.2    | 73      | 3.2     | 73      |
| 4210182 (H7) | -1.4 386A Ovary T        | S40 HBMC (advent)     | 422J0605 | 334           | 738           | 3.9     | 62      | 2.2     | 62      |
| 4210182 (H7) | -1.3 288A Ovary T        | C712 Lung N           | 422V0625 | 893           | 1120          | 5.3     | 69      | 3.1     | 66      |
| 4210182 (H7) | +1.2 335A Ovary T        | S7 Ovary N            | 42220626 | 440           | 567           | 3.3     | 60      | 2.2     | 60      |
| 4210182 (H7) | +1.2 3485 OT 1-P (SCID)  | S485 OT 1-P (SCID)    | 42230602 | 4188          | 3520          | 21.6    | 66      | 9.5     | 66      |
| 4210182 (H7) | +1.1 428A Ovary T (neu)  | 243A Esophagus N      | 42240612 | 725           | 689           | 6.2     | 65      | 2.8     | 65      |
| 4210182 (H7) | -1.0 201A Ovary T        | S6 Stomach N          | 42280620 | 1008          | 1018          | 7.4     | 62      | 3.2     | 62      |

Fig. 12

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| Gene<br>Name  | Rel. Probe 1<br>Exp. Value | Probe 2<br>Name      | Probe 2<br>ID | Probe 1<br>Value | Probe 2<br>Value | Probe 1<br>S/B | Probe 2<br>S/B |
|---------------|----------------------------|----------------------|---------------|------------------|------------------|----------------|----------------|
| 421V0189 (D1) | +33.2 426A Ovary T (mes)   | 415A Aorta N         | 422X0611      | 3072             | 243              | 55.2           | 2.4            |
| 421V0189 (D1) | +13.7 323 Ovary T          | 836 Spinal Cord N    | 422G0628      | 7367             | 537              | 42.6           | 2.5            |
| 421V0189 (D1) | +12.6 429A Ovary T (mes)   | 344A Ovary N         | 422J0614      | 2850             | 227              | 21.7           | 3.5            |
| 421V0189 (D1) | +8.0 385A Ovary T          | 897 Fetal tissue     | 422X0607      | 11791            | 1469             | 54.0           | 2.2            |
| 421V0189 (D1) | +7.3 269A Ovary T          | 873 Breast N         | 422H0623      | 6949             | 952              | 37.8           | 2.6            |
| 421V0189 (D1) | +58.5 335 Ovary T          | CT14 Bone Marrow     | 422H0619      | 308              | 1210             | 2.1            | 2.9            |
| 421V0189 (D1) | +5.0 205A Ovary T          | 370A Liver N         | 422Q0605      | 3676             | 1737             | 52.3           | 2.6            |
| 421V0189 (D1) | +4.5 384A Ovary T (mes)    | 11 Colon N           | 422B0609      | 3149             | 707              | 17.4           | 2.0            |
| 421V0189 (D1) | +4.4 261A Ovary T          | 819 Skeletal muscle  | 422J0621      | 6332             | 1443             | 29.1           | 2.9            |
| 421V0189 (D1) | +4.2 264A Ovary T          | 32 Pancreas N        | 422N0629      | 7612             | 1809             | 38.1           | 3.3            |
| 421V0189 (D1) | +3.3 382A Ovary T          | CT19 Brain N         | 422Q0610      | 468              | 1508             | 3.4            | 2.3            |
| 421V0189 (D1) | +2.9 933A Ovary T (SCII)   | 22 Skin N            | 422R0601      | 2300             | 860              | 12.3           | 2.1            |
| 421V0189 (D1) | +2.5 3115 Ovary T (mes)    | CT16 Small Intestine | 422C0604      | 1824             | 559              | 6.7            | 2.1            |
| 421V0189 (D1) | +2.4 265A Ovary T          | CT5 Esort N          | 422Q0624      | 1742             | 723              | 11.8           | 2.8            |
| 421V0189 (D1) | +2.3 385A Ovary T (mes)    | 272A Dendritic cell  | 422A0608      | 3083             | 1342             | 17.0           | 2.0            |
| 421V0189 (D1) | +1.9 266A Ovary T          | 827 Ovary N          | 422S0603      | 1370             | 732              | 8.0            | 2.0            |
| 421V0189 (D1) | +1.7 243A Ovary T          | 849 PBMC (activated) | 422J0605      | 207              | 580              | 2.6            | 2.0            |
| 421V0189 (D1) | +1.3 385A Ovary T          | 334A Large Intestine | 422A0622      | 2097             | 1202             | 11.2           | 2.7            |
| 421V0189 (D1) | +1.1 288A Ovary T          | 57 Ovary N           | 422V0625      | 989              | 1094             | 2.9            | 2.0            |
| 421V0189 (D1) | +1.1 201A Ovary T          | CT12 Lung N          | 422V0625      | 989              | 1094             | 2.9            | 2.0            |
| 421V0189 (D1) | +1.1 408A Ovary T (mes)    | 56 Stomach N         | 422W0620      | 750              | 672              | 5.6            | 2.4            |
| 421V0189 (D1) | +1.0 9485 Ovary T (mes)    | 243A Esophagus N     | 422A0612      | 498              | 448              | 4.2            | 2.1            |
| 421V0189 (D1) | -1.0 9485 Ovary T (mes)    | 9485 OT 5-P (SCID)   | 422Y0602      | 3117             | 3174             | 16.7           | 8.2            |
| 421V0189 (D1) | -1.0 9485 Ovary T          | CT9 Kidney N         | 422S0627      | 294              | 403              | 2.3            | 2.3            |

Fig. 13

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| Gene Name      | Seq. Probe 1             | Seq. Probe 2         | Gene ID  | Probe 1 Value | Probe 2 Value | Probe 1 S/E | Probe 2 S/E | Probe 1 AS | Probe 2 AS |
|----------------|--------------------------|----------------------|----------|---------------|---------------|-------------|-------------|------------|------------|
| 421H0187 (B11) | +20.2 425A Ovary T (met) | 415A Adip N          | 422X0611 | 5441          | 270           | 36.3        | 50          | 2.3        | 50         |
| 421H0187 (B11) | +10.0 523 Ovary T        | 556 Spinal Cord N    | 422C0628 | 5318          | 333           | 27.1        | 56          | 2.3        | 56         |
| 421H0187 (B11) | +8.3 425A Ovary T (met)  | 344A Ovary N         | 422U0614 | 1252          | 150           | 10.1        | 58          | 2.5        | 58         |
| 421H0187 (B11) | +5.7 385A Ovary T        | 591 Fetal tissue     | 422X0607 | 9307          | 1668          | 33.8        | 45          | 2.1        | 45         |
| 421H0187 (B11) | +4.4 205A Ovary T        | 370A Liver N         | 422Q0606 | 5456          | 1295          | 31.1        | 50          | 2.0        | 50         |
| 421H0187 (B11) | +4.2 265A Ovary T        | CT5 Heart N          | 422O0624 | 1834          | 438           | 11.9        | 48          | 2.0        | 48         |
| 421H0187 (B11) | -4.1 382A Ovary T        | CT19 Brain N         | 422Q0610 | 399           | 1259          | 2.6         | 48          | 2.0        | 48         |
| 421H0187 (B11) | +3.6 261A Ovary T        | 510 Skeletal muscle  | 422B0621 | 9733          | 1036          | 17.7        | 55          | 2.3        | 55         |
| 421H0187 (B11) | +3.4 263A Ovary T        | 573 Breast N         | 422H0623 | 4163          | 1239          | 23.0        | 62          | 3.0        | 62         |
| 421H0187 (B11) | +2.5 5115 Ovary T (met)  | CT10 Small intestine | 422C0604 | 1563          | 627           | 8.8         | 47          | 2.1        | 47         |
| 421H0187 (B11) | +2.1 264A Ovary T        | 32 Pancreas N        | 422N0629 | 3435          | 1690          | 14.9        | 60          | 3.0        | 60         |
| 421H0187 (B11) | +2.1 394A Ovary T (met)  | 272A Dendritic cell  | 422A0608 | 2667          | 1370          | 13.4        | 44          | 1.9        | 44         |
| 421H0187 (B11) | +2.1 593A Ovary T        | CT9 Kidney N         | 422Q0627 | 291           | 605           | 2.4         | 51          | 2.5        | 51         |
| 421H0187 (B11) | -1.7 966A Ovary T        | 840 PBMC (unphased)  | 422J0605 | 410           | 687           | 3.2         | 47          | 2.0        | 47         |
| 421H0187 (B11) | +1.6 933A Ovary T (SCT)  | 21 Skin N            | 422R0601 | 1622          | 984           | 7.9         | 44          | 2.2        | 44         |
| 421H0187 (B11) | +1.5 262A Ovary T        | 334A Large Intestine | 422A0622 | 1892          | 1245          | 10.1        | 50          | 2.6        | 50         |
| 421H0187 (B11) | -1.5 288A Ovary T        | CT12 Lung N          | 422V0625 | 604           | 908           | 4.1         | 62          | 2.6        | 62         |
| 421H0187 (B11) | -1.4 428A Ovary T (met)  | 243A Esophagus N     | 422A0612 | 236           | 325           | 2.7         | 78          | 1.9        | 78         |
| 421H0187 (B11) | -1.3 335A Ovary T        | 57 Ovary N           | 422D0626 | 382           | 501           | 2.9         | 58          | 2.0        | 58         |
| 421H0187 (B11) | -1.2 201A Ovary T        | 56 Spleen N          | 422W0620 | 538           | 677           | 4.8         | 58          | 2.3        | 58         |
| 421H0187 (B11) | +1.0 9085 OT 1-P (SCT)   | 9485 OT 5-P (SCT)    | 422Y0602 | 2582          | 2493          | 15.1        | 57          | 6.3        | 57         |
| 421H0187 (B11) | 483A Ovary T (met)       | 41 Colon N           | 422H0608 | 2251          | 562           | 12.5        | 38          | 1.7        | 38         |
| 421H0187 (B11) | 266A Ovary T             | 537 Ovary N          | 422B0603 | 1739          | 963           | 9.7         | 36          | 2.2        | 36         |
| 421H0187 (B11) | 525 Ovary T              | CT4 Bone Marrow      | 422H0619 | 283           | 843           | 2.2         | 44          | 2.2        | 44         |

Fig. 14

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11721-1

ACGGTTTCAATGGACACTTTTATTGTTTACTTAATGGATCATCAATTTTGTCTCACTACCTACAAATGGAATTT  
CATCTTGTTTCCATGCTGAGTAGTGAAACAGTGACAAAGCTAATCATAATAACCTACATCAAAAGAGAACTAAG  
CTAACTGCTCACTTTTCTTTTAAACAGGCAAAATATAAATATATGCACTCTAXAATGCACAATGGTTTAGTCA  
CTAAAAAATTCAAATGGGATCTTGAAGAATGTATGCAAATCCAGGGTGCAGTGAAGATGAGCTGAGATGCTGTG  
CAACTGTTTAAAGGTTCCCTGGCACTGCATCTCTTGGCCACTAGCTGAATCTTGACATGGAAGGTTTTAGCTAAT  
GCCAAGTGGAGATGCAGAAAATGCTAAGTTGACTTAGGGGCTGTGCACAGGAACTAAAAGGCAGGAAAGTACTA  
AATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAGCTCCAACTGGCACCACCCCAAGTGC  
TCACATGGCTGACTTTATCCTCCGTGTTCCATTTGGCACAGCAAGTGGCAGTG

11721-2

AAGGCTGGTGGGTTTTGATCCTGCTGGAGAACCTCCGCTTTCATGTGGAGGAAGAAGGGAAGGGAAAAGATGC  
TTCTGGGAACAAGTTAAAGCCGAGCCAGCCAAAATAGAAGCTTCCGAGCTTCACTTTCCAAGTAGGGGATG  
TCTATGTCAATGATGCTTTTGGCACTGCTCACAGAGCCACAGCTCCATGGTAGGAGTCAATCTGCCACAGAAG  
GCTGGTGGGTTTTGATGAAGAAGGAGCTGAACTACTTTGCAAAGGCCTTGAGAGCCAGAGCGACCCCTTCT  
GGCCATCCTGGGCGGAGCTAAAGTTGCAGACAAGATCCAGCTCATCAATAATATGCTGGACAAAGTCAATGAGA  
TGATTATTGGTGGTGAATGGCTTTTACCTTCCCTAAGGTGCTCAACAACATGGAGATTGGCACTTCTCTGTTT  
GATGAAGAGGGAGCCAAGATTGTCAAAGACCTAATGTCCAAAGCTGAGAAGAATGGTGTGAAGATTACCTTGCC  
TGTTGACTTTGTCACTGCTGACAAGTTTGATGA

11724-1

TTTGTTCCTTACATTTTTCTAAAGAGTTACTTAAATCAGTCAACTGGTCTTTGAGACTCTTAAGTTCTGATTCC  
AACTTAGCTAATTCATTCTGAGAACTGTGGTATAGGTGGCGTGTCTTCTAGCTGGGACAAAAGTTCTTTGTT  
TTCCCCCTGTAGAGTATCACAGACCTTCTGCTGAAGCTGGACCTCTGTCTGGGCCTTGACTCCCAAATCTGCT  
TGTCATGTTCAAGCCTGGAAATGTTAATCTTTAATTCTTCCATATGGATGGACATCTGTCTAAGTTGATCCTTT  
AGAACTGCAATTATCTTCTTTGAGTCTAATTTCTTCTTCTTTGCTTTGAATCGCATCACTAAACTTCTCTC  
CCATTTCTTAGCTTCATCTATCACCTGTACGATCATCTGGAGGGAAGACATGCTCTTAGTAAAGGCTGCAA  
GCTGGGTACAGTACTGTCCAAGTTTTCTGAAGTTGCTGAACCTTCTTGTCTTTCTTGTTCAAAGTAACCTGA  
ATCTCTCCAATTGTCTCTTCCAAGTGGACTTTTTCTCTGCGCAAAGCATCCAG

11724-2

TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTCAATCAATCAAAGGATTCA  
GCATGTGGTGAAGCTGTGAGGCAAGAGAAACAAGAACTGTATGGCAAGTTAAGAAGCACAGAGGCAACAAGA  
AGGAGACAGAAAAGCAGTTGCAGGAAGCTGAGCAAGAAATGGAGGAAATGAAAGAAAAGATGAGAAAGTTTGCT  
AAATCTAAACAGCAGAAAATCCTAGAGCTGGAAGAAGAGAATGACCGGCTTAGGGCAGAGGTGCACCCTGCAGG  
AGATACAGCTAAAGAGTGTATGGAAACACTTCTTTCTTCCAATGCCAGCATGAAGGAAGAAGTTGAAAGGGTCA  
AAATGGAGTATGAAACCTTTCTAAGAAGTTTCAGTCTTTAATGTCTGAGAAAGACTCTCTAAGTGAAGAGGTT  
CAAGATTTAAAGCATCAGATAGAAGGTAATGTATCTAAACAAGCTAACCTAGAGGCCACCGAGAAACATGATAA  
CCAAACGAATGTCACTGAAGAGGGAACACAGTCTATACCAGGT

**Fig. 15A**

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11725-32-1.2

AAGCCAATAATCACCATTATTACTTAATATATGCCAACCACTGTACTTGGCAGTTCACAAATTCTCACCGTTA  
CAACAACCCCATGAGGTATTTATTCCTTCTATAGATAGGGAAACCACAGCTCAAGTAAGTTAGGAACTGAG  
CCAAGTATACACAGAATACGAAGTGGCAAACTAGAAGGAAAGACTGACACTGCTATCTGCTGGCTCCAGTGT  
CCTGGCTCTTTTACACGGGTCAATGTCTCCAGCGTCTGCTGCTGCTGCATTACCATGCCCTCATTGTTTT  
TCTTCCTCTGGTGTCAACTGCATCCTTCAAAGAATCTAACTCATTCCAGAGACCACTATTTCTTTCTCTCTT  
TCTGAAATTACTTTTAATAATTCTTCATGAGGGGGAAAGAAGATGCCTGTTGGTAGTTTTGTTGTTAAAGCTG  
CTCAATTTGGGACTTAAACAATTTGTTTTCATCTTGTACATCCTGTAACAGCTGTGTTTTGCTAGAAAGATCAC  
TCTCCCTCTCTTTAGCATGGCTTCTAACCTCTTCAATTCATTTTCTTTTCTTTCAACACAATCTCAAGTTCT  
TCAAAGTGTGATGCAGAAGAGGCTCTTTCAAGTTATGTTGTGCTACTTCTGAACATGTGCTTTTAAAGATTC  
ATTTTCTTCTGAAGATCCTGTAACCACTTCCCTGTATTGGCTAGGTCTTTCTTTCTTCTTCCAAACAGCCT  
TCATGGTATTCATCTGTTCTCTTTCTTTTAAATAAGTTCAGGAGCTTCAGAAC

11726-1&amp;2

CAAGCTTTTTTTTTTTTTTAAAAAGTGTTAGCATTAAATGTTTTATTGTCACGCAGATGGCAACTGGGTTTATG  
TCTTCATATTTTATATTTTGTAAATTAAAAAATTACAAGTTTTAAATAGCCAATGGCTGGTTATATTTTTCAG  
AAACATGATTAGACTAATTCATTAATGGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCT  
TTTGTCCCTTCTTAAAAAAGTGAATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCA  
TCCACATCTACTTCAAGGAATATCACGTTGGAATACTTTTCAAGAGAGGAATGAAAGAAAGGCTTGATCATTTT  
GCAAGGCCACACACAGTGGCTGAGAAGTCACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAA  
AAGCAGTCTTGCTCTCGATCTGCTTACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGA  
AATGGATCCAAAGCACCAACAGAGCTTCAAGACTCGCTGCTTGGCTTGAATTCGGATCCGATATCGCCATGGC  
CT

11727-1&amp;2

AAGTGTTAGCATTAAATGTTTTATTGTCACGCAGATGGCAACTGGGTTTATGTTCTTCATATTTTATATTTTGT  
AATTAAAAAATMCAAGTTTTAAATAGCCAATGGCTGGTTATATTTTTCAGAAAACATGATTAGACTAATTCAT  
TAATGGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCTTTTGTCCCTTCTTAAAAAAGTGG  
AATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCATCCACATCTACTTCAAGGAATAT  
CACGTTGGAATACTTTTCAAGAGAGGAATGAAAGAAAGGCTTGATCATTTTGAAGGCCACACACAGTGGCTG  
AGAAGTCACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAAAAGCAGTCTTGCTCTCGATCTGC  
TTCACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGAATGGATCCAAAGCACCAACAG  
AGCTTCAAGACTCGCTGCTTGGCATGAATTCGGATCCGA

**Fig. 15B**

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11728.1.40.19.19

TACAAACTTTATTGAAACGCACACGCGCACACACACAAACACCCCTGTGGATAGGGAAAAGCACCTGGCCACAG  
 GGTCCACTGAAACGGGGAGGGGATGGCAGCTTGTAAATGTGGCTTTTGCCACAACCCCTTCTGACAGGGAAGGC  
 CTTAGATTGAGGCCACCTCCCATGGTGATGGGGAGCTCAGAATGGGGTCCAGGGAGAATTTGGTTAGGGGA  
 GGTGCTAGGGAGGCATGAGCAGAGGGCACCTCCGAGTGGGGTCCGAGGGCTGCAGAGTCTTCAGTACTGTCC  
 CTCACAGCAGCTGTCTCAAGGCTGGGTCCCTCAAAGGGCGTCCAGCGCGGGGCTCCCTGCGCAAACACTTG  
 GTACCCCTGGCTGCGCAGCGAAGCCAGCAGGACAGCAGTGGCGCCGATCAGCACAAACAGACGCCCTGGCGGTA  
 GGGACAGCAGGCCAGCCCTGTGGTTGTCTCGGCAGCAGGTCTGGTTATCATGGCAGAAGTGTCTTCCCACA  
 CTTACGTCCTTACACCCACGTGAXGGCTACXGGCCAGGAAG

11728.2.40.19.19

CCCGTGGGTGCCATCCACGGAGTTGTTACCTGATCTTTGGAAGCAGGATCGCCCGTCTGCACTGCAGTGGAAGC  
 CCCGTGGGCAGCAGTGATGGCCATCCCCGCATGCCACGGCCTCTGGGAAGGGGCAGCAACTGGAAGTCCCTGAG  
 ACGGTAAAGATGCAGGAGTGGCCGGCAGAGCAGTGGGCATCAACCTGGCAGGGGCCACCCAGATGCCGTGCTCAG  
 TGTGTGGGCCATTTGTCCAGAAGGGGACGGCAGCAGCTGTAGCTGGCTCCTCCGGGGTCCAGGCAGCAGGCCA  
 CAGGGCAGAACTGACCATCTGGGCACCGGTTCCAGCCACCAGCCCTGCTGTTAAGGCCACCCAGCTCACCAGG  
 GTCCACATGGTCTGCCTGCGTCCGACTCCGCGGTCTTGGGCCCTGATGGTTCTACCTGCTGTGAGCTGCCAG  
 TGGGAAGTATGGCTGCTGCCAATGCCAACGCCACCTGCTGCTCCGATCACCTGCACTGCTGCCCCAAGACACT  
 GTGTGTGACCTGATCCAGAGTAAGTGCCTCTCCAAGGAGAAGC

11730-1

GAATCACCTTTCTGGTTTAGCTAGTACTTTGTACAGAACAATGAGGTTTCCACAGCGGAGTCTCCCTGGGCTC  
 TGTTTGGCTCTCGGTAAGGCAGGCCTACACCTTTTCTCTCTATGGAGAGGGGAATATGCATTAAGGTGAA  
 AAGTCACCTTCCAAAAGTGAGAAAGGGATTGATTGCTGCTTCAGGACTGTGGAATTATTTGGAATGTTTTACA  
 AATGGTTGCTACAAAACAACAAAAAGGTAATTACAAAATGTGTACATCACAACATGCTTTTTAAGACATTAT  
 GCATTGTGCTCACATTCCCTTAAATGTTGTTTCCAAAGGTGCTCAGCCTCTAGCCAGCTGGATTCTCCGGGAA  
 GAGGCAGAGACAGTTTGGCGAAAAAGACACAGGGAAGGAGGGGGTGGTGAAAGGAGAAAGCAGCCTTCCAGTTA  
 AAGATCAGCCCTCAGTTAAAGGTGAGCTTCCCGCAXGCTGGCCTCAXGCGGAGTCTGGGTGAGAGGGAGGAGCA  
 GCAGCAGGGTGGGACTGGGGCGT

11730-2

AACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGAT  
 CCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGAGAAA  
 GGCGGGCCCGGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTG  
 GACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAAGCTGAAAAAGCTGCTGATGAGAGTGA  
 GAGAGGTATGAAGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAAGATGGAAGTCCAGGAAATCCAACCTCA  
 AAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAA  
 GGAGACTTGGAAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGATTAG  
 ACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

**Fig. 15C**

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11732.1contig

GAGAACTTGGCCTTTATTGTGGGCCCAGGAGGGCACAAAGGTCAGGAGGCCCAAGGGAGGGATCTGGTTTTCTG  
GATAGCCAGGTCATAGCATGGGTATCAGTAGGAATCCGCTGTAGCTGCACAGGCCTCACTTGCTGCAGTCCGG  
GGAGAACACCTGCACTGCATGGCGTTGATGACCTCGTGGTACACGACAGAGCCATTGGTGCAGTGAAGGGCAC  
GCGCATGGGCTCCGCTCTCGAGGGCAGGCAGCAGGAGCATTGCTCCTGCACATCCTCGATGTCAATGGAGTACA  
CAGCTTTGCTGGCACACTTTCCCTGGCAGTAATGAATGTCCACTTCCTCTTGGGACTTACAATCTCCCACTTTG  
ATGTACTGCACCTTGGCTGTGATGTCTTTGCAATCAGGCTCCTCACATGTGTCACAGCAGGTGCCTGGAATTTT  
CACGATTTTGCCTCCTTCAGCCAGACACTTGTGTTTCATCAAATGGTGGGCAGCCCGTGACCCTCTTCTCCAGA  
TGACTCTCCTCT

11732.2contig

GCCTGGACCTTGCCGGATCAGTGCCACACAGTGACTTGCTTGGCAAATGGCCAGACCTTGCTGCAGAGTCATCG  
TGTCAATTGTGACCATGGACCCCGCCTTCATGTGCCAACAGCCAGTCTCCTGTTCCGGTGGAGGAGACGTGTG  
GCTGCCGCTGGACCTGCCCTTGTGTGTGCACGGGCAGTTCACCTCGGCACATCGTCACCTTCGATGGGCAGAAT  
TTCAAGCTTACTGGTAGCTGCTCCTATGTCATCTTTCAAAACAAGGAGCAGGACCTGGAAGTGCTCCTCCACAA  
TGGGGCCTGCAGCCCCGGGGCAAAACAAGCCTGCATGAAGTCCATTGAGATTAAGCATGCTGGCGTCTCTGCTG  
AGCTGCACAGTAACATGGAGATGGCAGTGGATGGGAGACTGGTCTTGCCCCGTACGTTGGTGAAACATGGAA  
GTCAGCATCTACGGCGCTATCATGTATGAAGTCAGGTTTACCCATCTTGGCCACATCCTCACATACACCGCCXC  
AAAACAACGAGTT

11735-1-2

AGATCAACCTCTGCTGGTCAGGAGGAATGCCTTCCTTGTCTTGGATCTTTGCTTTGACGTTCTCGATAGTRWCA  
aCTKKRYTSRAMSKMAAGKGYRATGRWMTTKSYWGNRASYKTMWWMRSGRARAYTTaGaCAYCCCMCTCWgAG  
aCGSAGKACCARGTGCAgAgGTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGTCCATCTTCCAGCTGT  
TTCCAGCAAAGATCAACCTCTGCTGATCAGGAGGGATGCCTTCCTTATCTTGGATCTTTGCCTTGACATTCTC  
GATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATYGCATCCAC  
CTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGYCCATCTTCC  
AGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCCTTGTCTGGATCTTTGCTTTGA  
CRTTCTCRATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATCTGC  
ATCCACCTCTAA

11740.2.contig

AAGTCACAAACAGACAAAGATTATTACCAGCTGCAAGCTATATTAGAAGCTGAACGAAGAGACAGAGGTCATGA  
TTCTGAGATGATTGGAGACCTTCAAGCTCGAATTACATCTTTACAAGAGGAGGTGAAGCATCTCAAACATAATC  
TCGAAAAAGTGGAAGGAGAAAGAAAGAGGCTCAAGACATGCTTAATCACTCAGAAAAGGAAAAGAATAATTTA  
GAGATAGATTTAACTACAACTTAAATCATTACAACAACGGTTAGAACAAGAGGTAAATGAACACAAAGTAAC  
CAAAGCTCGTTAACTGACAAACATCAATCTATTGAAGAGGCAAAGTCTGTGGCAATGTGTGAGATGGAAAAA  
AGCTGAAAGAAGAAAGAGAAGCTCGAGAGAAGGCTGAAAATCGGGTTGTTGAGATTGAGAAACAGTGTTCCATG  
CTAGACGTTGATCTGAAGCAATCTCAGCAGAACTAGAACATTTGACTGGAAATAAAGAAAGGATGGAGGATGA  
AGTTAAGAATCTA

**Fig. 15D**



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11765.2&amp;64.2.contig

CGCCTCCACCATGTCCATCAGGGTGACCCAGAAGTCCTACAAGGTGTCCACCTCTGGCCCCGGGCCTTCAGCA  
GCCGCTCCTACACGAGTGGGCCCCGGTTCCCGCATCAGCTCCTCGAGCTTCTCCCGAGTGGGCAGCAGCAACTTT  
CGCGGTGGCCTGGGCGGCGGCTATGGTGGGGCCAGCGGCATGGGAGGCATCACCAGTACGGTCAACCAGAG  
CCTGCTGAGCCCCCTTGTCTGGAGGTGGACCCCAACATCCAGGCCGTGCGCACCCAGGAGAAGGAGCAGATCA  
AGACCCTCAACAACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCTGGAGCAGCAGAACAAGATGCTGGAG  
ACCAAGTGGAGCCTCCTGCAGCAGCAGAAGACGGCTCGAAGCAACATGGACAACATGTTTCGAGAGCTACATCAA  
CARCCTTAGGCGGCAGCTGGAGACTCTGGGCCAGGAGAAGCTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGG  
GGCTGGTGGAGGACTTCAAGAACAAGTATGAGGATGAGATCAATAAGCGTACAGAGATGGAGAACGAATTTGTC  
CTCATCAAGAAGGATGTGGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACCGA  
CGAGATCAACTTCTCAGGCAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCAGATCTCGGACACATCTG  
TGGTGTGTCCATGGACAACAGCCGCTCCCTGGACATGGACAGCATCATTGCTGAGGTCAAGGCACGTACGAG  
GATATTGCCAACCGCAGCCGGGCTGAGGCTGAGAGCATGTACCAGGTCAAGTATGAGGAGCTGCAGAGCCTGGC  
TGGGAAGCACGGGGATGACCTGCGGCGCACAAAGACTGAGATCTCTGAGATGAACCCGGAACATCAGCCCGGCT  
XCAGGCTGAGATTGAGGGCCTCAAAGGCCAGAXGGCTTXCCTGGAXGXCCGCCAT

11767.2.contig

CCCGGAGCCAGCCAACGAGCGGAAAATGGCAGACAATTTTTGCTCCATGATGCGTTATCTGGGTCTGGAAACC  
CAAACCTCAAGGATGGCCTGGCGCATGGGGGAACCAAGCCTGCTGGGGCAGGGGGCTACCCAGGGGCTTCCTAT  
CCTGGGGCTACCCCGGGCAGGCACCCCCAGGGGCTTATCCTGGACAGGCACCTCCAGGCGCCTACCCTGGAGC  
ACCTGGAGCTTATCCCGGAGCACCTGCACCTGGAGTCTACCCAGGGCCACCCAGCGGCCCTGGGGCTACCCAT  
CTTCTGGACAGCCAAGTGCCACCGGAGCCTACCCTGCCACTGGCCCCTATGGCGCCCCTGCTGGGCCACTGATT  
GTGCCTTATAACCTGCCTTTGCCTGGGGGAGTGGTGCCTCGCATGCTGATAACAATTCTGGGCACGGTGAAGCC  
CAATGCAACAGAATTGCTTTAGATTTCAAAGAGGGAATGATGTTGCCTTCCACTTTAACCACGCTTCAATG  
AGAACAACAGGAGAGTCATTGGTTGCAATACAAAGCTGGATAA

11768-1&amp;2

GGGAATGCAACAACCTTTATTGAAAGGAAAGTGCAATGAAATTTGTTGAAACCTTAAAGGGGAACTTAGACAC  
CCCCCTCRAgCGMAGKACCARGTGCAAgGTGGACTCTTCTGGATGTTGTAGTCAGACAGGGTRCGNCCATC  
TTCAGCTGTTTTYCCRGCAAAGATCAACCTCTGCTGATCAGGAGGRATGCCTTCCTTATCTTGGATCTTTGCCT  
TGACATTCTCGATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATY  
TGCATCCACCTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTCTGGATGTTGTAGTCAGACAGGGTGCG  
YCCATCTTCAGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCCTTGTCYTGGATC  
TTTGCTTGACRTTCTCAATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCAC  
GAAGATCTGCATCCACCTCTAAGACGGAGCACCAGGTGCAGGGTGGACTCTTCTGGATGgTTGTAGTCAGAC  
AGGGTGCGTCCATCTTCAGCTGTTTCCAGCAAAGATCAACCT

**Fig. 15E**

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11768-1&2-11735-1&2

AGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACcCATCCAGAAAGAGTCCA  
CCCTGCACCTGGTGCTCCGTCTTAGAGGTGGGATGCAGATCTTCGTGAAGACCCTGACTGGTAAGACCATCACT  
CTCGAAGTGGAGCCGAGTGACACCATTGAGAAYGTCAARGCAAAGATCCARGACAAGGAAGGCATYCCTCCTGA  
CCAGCAGAGGTTGATCTTTGctSGGAAAgCAGCTGGAAGATGGRCGCACCCTGTCTGACTACAACATCCAGAAA  
GAGTCYACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGATGCARATCTTCGTGAAGACCCTGACTGGTAAGAC  
CATCACCTCGAGGTGGAGCCAGTGACACCATCGAGAATGTCAAGGCAAAGATCCAAGATAAGGAAGGCATCC  
CTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATC  
CAGAAAGAGTCCACcTYTGCACTGGTMCtBCGtCTYAGAGGKGGRTGcaaaTCTWMGTKWagaCaCtCaCTK  
KYAAGRYYaTcAMCMwtgAKKTCgAKYSCASTKWCaCTWTCRAKAAMGTYRWWGCAWagaTCCMAGACAAGGAA  
GGCATTCTCCTGACCAGCAGAGGTTGATCT

## 11769.1.contig

ATGGAGTCTCACTCTGTGACCAAGGCTGGAGCGCTGTGGTGCGATATCGGCTCACTGCAGTCTCCACTTCTGG  
GTTCAAGCGATCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCAGGCGTACCATAATTTTGTATT  
TTTAGTAGAGACATGGTTTCGCCATGTTGGCTGGGCTGGTCTCGAACTCTGACCTCAAGTGATCTGTCTCTGGC  
CTCCCAAAGTGTTGGGATTACAGGCGAAAGCCAACGCTCCCGCCAGGGAACAACTTTAGAATGAAGGAAATAT  
GCAAAAGAACATCACATCAAGGATCAATTAATTACCATCTATTAATTACTATATGTGGGTAATTATGACTATTT  
CCCAAGCATTCTACGTTGACTGCTTGAGAAGATGTTTGTCTGCATGGTGGAGAGTGGAGAAGGGCCAGGATTC  
TTAGGTT

## 11769.2.contig

AGCGCGGTCTTCCGGCGCGAGAAAGCTGAAGGTGATGTGGCCGCCCTCAACCGACGCATCCAGCTCGTTGAGGA  
GGAGTTGGACAGGGCTCAGGAACGACTGGCCACGGCCCTGCAGAACTGGAGGAGGCAGAAAAAGCTGCAGATG  
AGAGTGAGAGAGGAATGAAGGTGATAGAAAACCGGGCCATGAAGGATGAGGAGAAGATGGAGATTGAGGAGATG  
CAGCTCAAAGAGGCCAAGCACATTGCGGAAGAGGCTGACCGCAAATACGAGGAGGTAGCTCGTAAGCTGGTCAT  
CCTGGAGGGTGAGCTGGAGAGGGCAGAGGAGCGTGCGGAGGTGTCTGAACTAAAATGTGGTGACCTGGAAGAAG  
AACTCAAGAATGTTACTAACAATCTGAAATCTCTGGAGGCTGCATCTGAAAAGTATTCTGAAAAGGAGGACAAA  
TATGAAGAAGAAATTAACCTTCTGTCTGACAACTGAAAGAGGCTGAGACCCGTGCTGAATTTGCAGAGAGAAC  
GGTTGCAAACTGGAAGAGACAATTGATGACCTGGAAGAGAACTTGCCACAGC

## 11770.1.contig

GTGCACAGGTCCCATTTATTGTAGAAAATAATAATAATTACAGTGATGAATAGCTCTTCTTAAATTACAAAACA  
GAAACCACAAAGAAGGAAGAGGAAAAACCCAGGACTTCCAAGGGTGAAGCTGTCCCCTCCTCCCTGCCACCT  
CCCAGGCTCATTAGTGTCTTGGAAGGGGCAGAGGACTCAGAGGGGATCAGTCTCCAGGGGCCCTGGGCTGAAG  
CGGGTGAGGCAGAGAGTCTTGAGGCCACAGAGCTGGGCAACCTGAGCCGCCCTCTCTGGCCCCCTCCCCACCAC  
TGCCCAAACCTGTTTACAGCACCTTCGCCCTCCCTCTAAACCCGTCCATCCACTCTGCACTTCCAGGCAGG  
TGGGTGGGCCAGGCCTCAGCCATACTCTGGGCGCGGGTTTGGTGAGCAAGGCACAGTCCAGAGGTGATATC  
AAGGCCT

**Fig. 15F**

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11770.2.contig

GCAAGGAAGTGGTCTGCTCACACTTGCTGGCTTGCGCATCAGGACTGGCTTTATCTCCTGACTCACGGTGCAAA  
GGTGCACTCTGCGAACGTTAAGTCCGTCCCAGCGCTTGAATCCTACGGCCCCACAGCCGGATCCCCTCAGC  
CTTCCAGGTCTCAACTCCCGTGGACGCTGAACAATGGCCTCCATGGGGCTACAGGTAATGGGCATCGCGCTGG  
CCGTCTGGGCTGGCTGGCCGTATGCTGTGCTGCGCGCTGCCATGTGGCGCGTGACGGCCTTCATCGGCAGC  
AACATTGTACCTCGCAGACCATCTGGGAGGGCCTATGGATGAACTGCGTGGTGCAGAGCACCGGCCAGATGCA  
GTGCAAGGTGTACGACTCGCTGCTGGCACTGCCGAGGACCTGCAGGCGGCCCGCGCCCTCGTCATCATCA

11773.1.contig

TGCAAAAGGGACACAGGGGTTCAAAAATAAAAAATTTCTCTTCCCCCTCCCCAACCTGTACCCAGCTCCCCGA  
CCACAACCCCTTCTCCCCCGGGGAAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAGGCC  
GGGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCAAATATAAATACXTGTGTGAGAACTGGAAAATCCTCCAGC  
ACCCACCACCAAGCACTCTCCGTTTTCTGCCGTTGTTGGAGAGGGGCGGGGGCAGGGGCGCCAGGCACCGG  
CTGGCTGCGGTCTACTGCATCCGCTGGGTGTGACCCCGGAGCCTCCTGCTGCTCATTGTAGAAGAGATGACA  
CTCGGGTCCCCCGGATGGTGGGGCTCCCTGGATCAGCTTCCCGGTGTTGGGGTTCACACACCAGCACTCCC  
CACGCTGCCCGTTCAGAGACATCTTGCACTGTTTGAGGTTGTACAGGCCATGCTTGTCACAGTTG

11778.1.contig

GGGTTGGAGGGAAGTGGTCTTTATTTCAAAAAGACACTTGTCATATTCAAGTATCAAAACAGTTGCACTATTGA  
TTTCTCTTTCTCCAATCGGCCCCAAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGA  
TGACACCTAACAGACCTCCTAGAAACCTTACCAGAAAATGGGGAAGTGGGTAGGGAAGGAACTTAAAGATCA  
ACAACTGCCAGCCACGGAAGTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAGC  
AAAGTTTCAAAATAATATAAAATTTAAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGAT  
ACAAAGCACAATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAGTTTCA  
CATGGCTAAATCAGTGGCAAAAACACAGTCTTCTTTCTTTCTTTCTTTCAAGGAGGCAGGAAAGCAATTAAGTG  
GTCACCTCAACATAAGGGGGACATGATCCATTCTGTAAGCAGTTGTGAAGGGG

11778-2830-2

CAGGAACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCA  
AGATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGA  
GAAAGGCGGGCCCGGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGA  
GCTGGACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGA  
GTGAGAGAGGTATGAAGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAAGATGGAAGTCCAGGAAATCCAA  
CTCAAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCAT  
TGAAGGAGACTTGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGA  
TTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

**Fig. 15G**

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## 11782.1.contig

ATCTACGTCATCAATCAGGCTGGAGACACCATGTTCAATCGAGCTAAGCTGCTCAATATTGGCTTTCAAGAGGC  
CTTGAAGGACTATGATTACAACGCTTTGTGTTCAAGTGATGTGGACCTCATTCCGATGGACGACCGTAATGCCT  
ACAGGTGTTTTTCGACGCCACGGCACATTTCTGTTGCAATGGACAAGTTCGGGTTTAGCCTGCCATATGTTTCA  
TATTTTGGAGGTGTCTCTGCTCTCAGTAAACAACAGTTTCTTGCCATCAATGGATTCCCTAATAATTATTGGGG  
TTGGGGAGGAGAAGATGACGACATTTTAAACAGATTAGTTTCATAAAGGCATGTCTATATCACGTCCAAATGCTG  
TAGTAGGGAGGTGTGAATGATCCGGCATTCAAGAGACAAGAAAAATGAGCCCAATCCTCAGAGGTTTGACCGG  
ATCGCACATACAAAGGAAACGATGCGCTTCGATGGTTTGAACCTCACTTACCTACAAGGTGTTGGATGTCAGAGA  
TACCGTTATATACCCAAATCAC

## 11782.2.contig

CTAGACCTCTAATTTAAAGGCACAATCATGCTGGAGAATGAACAGTCTGACCCCGAGGGCCACAGCGAATTTTA  
GGGAAGGAGGCAAAGAGGTGAGAAGGGAAAGGAAGGAAGGAGAACAATAAGAACTGGAGACGTTGG  
GTGGGTGAGGAGTGTGGTGGAGGCTCGGAGAGATGGTAAACAAACCTGACTGCTATGAGTTTTCAACCCATA  
GTCTAGGGCCATGAGGGCGTCAGTTCTTGGTGGCTGAGGGTCTTCCACCCAGCCACCTGGGGGAGTGGAGTG  
GGGAGTTCTGCCAGGTAAGCAGATGTTGTCTCCCAAGTTCCTGACCCAGATGTCTGGCAGGATAACGCTGACCT  
GTTCCCTCAACAAGGGACCTGAAAGTAATTTTGCTCTTAC

## 11783-1 &amp; 2

CCGAATTCAGCGTCAACGATCCYTCCCTTACCATCAAATCAATTGGCCACCAATGGTACTGAACCTACGAGTA  
CACCGACTACGGGGGACTAATCTTCAACTCCTACATACTTCCCCATTATTCCTAGAACCAGGCGACCTGCGA  
CTCCTTGACGTTGACAATCGAGTAGTACTCCCGATTGAAGCCCCCATTCTGTATAATAATTACATCACAAGACGT  
CTTGCACTCATGAGCTGTCCACATTAGGCTTAAAAACAGATGCAATTCGGGACGTCTAAGCCAAACCACTT  
TCACCGCTACACGACCGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAACCACAGTTTCATGCCC  
ATCGTCTAGAATTAATTCCTTAAAAATCTTTGAAATAGGGCCCGTATTTACCCTATAGCACCCCTCTACCC  
CCTCTAG

## 11786.1.contig

GCTCTTCACACTTTTATTGTTAATTCTCTTCACATGGCAGATACAGAGCTGTGCTCTTGAAGACCACCACTGAC  
CAGGAAATGCCACTTTTACAAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAGCGT  
TGAAGGGTGACCAGCACATTTGCACATGCAAAAAAGGAGTGACCCCAAGGCCTCAACCACACTTCCAGAGCTC  
ACCATGGGCTGCAGGTGACTTGCCAGGTTTGGGGTTCGTGAGCTTTCCTTGCTGCTGCGGTGGGGAGGCCCTCA  
AGAACTGAGAGGCCGGGGTATGCTTCATGAGTGTTAACATTTACGGGACAAAAGCGCATCATTAGGATAAGGAA  
CAGCCACAGCACTTCATGCTTGTGAGGGTAGCTGTAGGAGCGGGTGAAGGATTCCAGTTTATGAAAATTTAA  
AGCAAAACAACGGTTTTTATGCTGGGTGGGAAACAGGAAACTGTGATGTGCGCCAATGACCACCATTTTTCTGCC  
CATGTGAAGGTCCCATGAAACC

**Fig. 15H**

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11786.2.contig

CAAGCGCTTGGCGTTTGGACCCAGTTCAGTGAGGTTCTTGGGTTTTGTGCCTTTGGGGATTTTGGTTTGACCCA  
GGGGTCAGCCTTAGGAAGGTCTTCAGGAGGAGGCCGAGTCCCTTCAGTACCACCCCTCTCTCCCACTTTCC  
CTCTCCCGCAACATCTCTGGGAATCAACAGCATATTGACACGTTGGAGCCGAGCCTGAACATGCCCTCGGCC  
CCAGCACATGGAAAACCCCTTCCCTTGCCTAAGGTGTCTGAGTTTCTGGCTCTTGAGGCATTTCCAGACTTGAA  
ATTCTCATCAGTCCATTGCTCTTGAGTCTTTGCAGAGAACCTCAGATCAGGTGCACCTGGGAGAAAGACTTTGT  
CCCCACTTACAGATCTATCTCCTCCCTTGGGAAGGGCAGGGAATGGGACGGTGTATGGAGGGGAAGGGATCTC  
CTGCGCCCTTCATTGCCACACTTGGTGGGACCATGAACATCTTATGTGTCTGAGCTTCTCAAATTACTGCAATA  
GGA

13691.1&amp;2

AGCGTCAAATCAGAATGGAAAAGACTCAAAACCATCATCAACACCAAGATCAAAAGGACAAGRATCCTTCAAGA  
AACAGGAAAAAACTCCTAAAACACCAAAAGGACCTAGTTCTGTAGAAGACATTAAGCAAAAATGCAAGCAAGT  
ATAGAAAAAGGTGGTTCTTCCCAAAGTGGAAAGCCAAATTCATCAATTATGTGAAGAATTGCTTCCGGATGAC  
TGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTTAAGAAAATAGTTTAAACAATTTGTTAA  
AAAATTTTCCGTCTTATTTTCATTTCTGTAACAGTTGATATCTGGCTGTCTTTTTATAATGCAGAGTGAGAACT  
TTCCCTACCGTGTTTGATAAATGTTGTCCAGGTTCTATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTAGTT  
TTTAAAGATGGAACTCCACCCTTTGCTTGGTTTTAAGTATGTATGGAATGTTATGATAGGACATAGTAGTAGCG  
GTGGTCAGACATGGAAATGGTGGGSMGACAAAAATATACATGTGAAATAA

13692.1&amp;2

TCCGAATTCGAAGCAATTATGGACAAACGATTCCTTTTAGAGGATTACTTTTTCAATTTCCGTTTTAGTAAT  
CTAGGCTTTGCCTGTAAGAATAACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATTC  
TAGAACCTTTGTATATTTGATAGTATTTCTAACTTTCATTTCTTTACTGTTTGCAGTTAATGTTTCATGTTCTGC  
TATGCAATCGTTTATATGCAGTTTCTTTAATTTTTTTAGATTTTCTGGATGTATAGTTTAAACAACAAAAAG  
TCTATTTAAACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAACTTTGTATTTCT  
TTCTTATAGAGGCTTCTAAAAAGGTATTTTATATGTTCTTTTAACAAATATTGTGTACAACCTTTAAACAT  
CAATGTTTGGATCAAAACAAGACCCAGCTTATTTTCTGC

13693.2

TGTGGTGGCGCGGGCTGAGGTGGAGGCCAGGACTCTGACCCTGCCCTGCCTTCAGCAAGGCCCCCGGCAGCG  
CCGGCCACTACGAAGTCCCGTGGGTTGAAAAATATAGGCCAGTAAAGCTGAATGAAATTGTGGGAATGAAGAC  
ACCGTGAGCAGGCTAGAGGTCTTTGCAAGGGAAGGAAATGTGCCAACATCATCATTGCGGGCCCTCCAGGAAC  
CGGCAAGACCACAAGCATTCTGTGCTTGGCCCGGGCCCTGCTGGGCCCAGCACTCAAAGATGCCATGTTGGAAC  
TCAATGCTTCAAATGACAGGGGCATTGACGTTGTGAGGAATAAAATTTAAATGTTTGTCTAACAAAAAGTCACT  
CTTCCCAAAGGCCGACATAAGATCATCATTCTGGATGAAGCAGACAGCATGACCGACGGAGCCCAGCAAGCCTT  
GAGGAGAACCATGGAAATCTACTCTAAACCACTCGTTGCCCTTGCTTGAATGCTTCGGATAAGATCATCGA  
GCC

*Fig. 15I*

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13696.1-13744.1

CTTTGCAAAGCTTTTATTTTCATGTCTGCGGCATGGAATCCACCTGCACATGGCATCTTAGCTGTGAAGGAGAAA  
GCAGTGCACGAGAAGGAATGAGTGGGCGGAACCAACGGCCTCCACAAGCTGCCTTCCAGCAGCCTGCCAAGGCC  
ATGGCAGAGAGAGACTGCAAACAAACACAAGCAAACAGAGTCTCTTCACAGCTGGAGTCTGAAAGCTCATAGTG  
GCATGTGTGAATCTGACAAAATTTAAAGTGTGCATAGTCCATTACATGCATAAAACACTAATAATAATCCTGTT  
TACACGTGACTGCAGCAGGCAGGTCCAGCTCCACCACTGCCCTCCTGCCACATCACATCAAGTGCCATGGTTTA  
GAGGGTTTTTCATATGTAATTCCTTTATTCTGTAAAAGGTAACAAAATATACAGAACAAAACCTTCCCTTTTAA  
AACTAATGTTACAAATCTGTATTATCACTTGGATATAAATAGTATATAAGCTGATC

13700.1

CAAGGGATATATGTTGAGGGTACRGRGTGACACTGAACAGATCACAAAGCACGAGAAACATTAGTTCTCTCCCT  
CCCCAGCGTCTCCTTCGTCTCCCTGGTTTTCCGATGTCCACAGAGTGAGATTGTCCCTAAGTAACTGCATGATC  
AGAGTGCTGKCTTTATAAGACTCTTCATTACAGCGTATCCAATTCAGCAATTGCTTCATCAAATGCCGTTTTTG  
CAGGCTACAGGCCTTTTCAGGAGAGTTTAGAATCTCATAGTAAAAGACTGAGAAATTTAGTGCCAGACCAAGAC  
GAATTGGGTGTGTAGGCTGCATTNCTTTCTTACTAATTTCAAATGCTTCCTGGTAAGCCTGCTGGGAGTTGAC  
ACAAGTGGTTTTGTTTGTGCTCCAGATGCCACTTCAGAAAGATACCTAAAATAATCTCCTTTCATTTCAAAGT  
AGAACAC

13700.2

TCCGGAGCCGGGGTAGTCGCCGCCGCCGCCGCCGGTGCAGCCACTGCAGGCACCGCTGCCGCCGCCCTGAGTAGT  
GGGCTTAGGAAGGAAGAGGTATCTCGCTCGGAGCTTCGCTCGGAAGGGTCTTTGTTCCCTGCAGCCCTCCAC  
GGGAATGACAATGGATAAAAAGTGAGCTGGTACAGAAAGCCAAACTCGCTGAGCAGGCTGAGCGATATGATGATA  
TGGCTGCAGCCATGAAGGCAGTCACAGAACAGGGGCATGAACTCTCAACGAAGAGAGAAATCTGCTCTCTGTT  
GCCTACAAGAATGTGGTAAGGCCGCCGCCGCTCTTCCTGGCGTGTATCTCCAGCATTGAGCAGAAAAACAGAG  
AGGAATGAGAAGAAGCAGCAGATGGGCAAAGAGTACCGTGAGAAGATAGAGGCAGAACTGCAGGACATCTGCAA  
TGATGTTCTGGAGCTTGTGGACAAATATCTTATTCCAATGCTACACAACCCAGAAA

13701.1

AAAAAGCAGCARGTTCAACACAAAATAGAAATCTCAAATGTAGGATAGAACAAAACCAAGTGTGTGAGGGGGGA  
AGCAACAGCAAAAGGAAGAAATGAGATGTTGCAAAAAAGATGGAGGAGGGTTCCCTCTCCTCTGGGGACTGAC  
TCAAACTGATGTGGCAGTATACACCATTCAGAGTCAGGGGTGTTCAATCTTTTTTGGGAGTAAGAAAAGGT  
GGGGATTAAGAAGACGTTTTCTGGAGGCTTAGGGACCAAGGCTGGTCTCTTTCCCCCTCCCAACCCCTTGATC  
CCTTTCTCTGATCAGGGGAAAGGAGCTCGAATGAGGGAGGTAGAGTTGGAAAGGGAAAGGATTCCACTTGACAG  
AATGGGACAGACTCCTTCCCA

*Fig. 15J*

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13701.2

TGGCAATAGCACAGCCATCCAGGAGCTCTTCARGCGCATCTCGGAGCAGTTCCTGCCATGTTCCGCCGGAAGG  
CCTTCCTCCACTGGTACACAGGCGAGGGCATGGACGAGATGGAGTTCACCGAGGCTGAGAGCAACATGAACGAC  
CTCGTCTCTGAGTATCAAGCAGTACCAGGATGCCACCGCAGAAGAGGAGGAGGATTTCCGGTGAAGGAGGCCGAAG  
AGGAGGCCTAAGGCAGAGCCCCATCACCTCAGGCTTCTCAGTTCCTTAGCCGTCTTACTCAACTGCCCTTT  
CCTCTCCCTCAGAATTTGTGTTTGCTGCCTCTATCTGTTTTTGTCTTCTGGGGGGTCTAGAACAGT  
GCCTGGCACATAGTAGGCGCTCAATAAATACTTGGTTGNTGAATGTCTCCT

13702.2

AGCTGGCGCTAGGGCTCGGTTGTGAAATACAGCGTRGTGAGCCCTTGGCGCTCAGTGTAGAAACCCACGCCTGTA  
AGGTCCGTCTTCGTCCATCTGCTTTTTCTGAAATACACTAAGAGCAGCCACAAAACCTGTAACCTCAAGGAAAC  
CATAAAGCTTGGAGTGCCTTAATTTTAACCAAGTTTCAATAAAACGGTTTACTACCT

13704.2-13740.2

GGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCARGCGGGCAGCTGAAGATGATGAGGATGACGATGTCGA  
TACCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAAGGAAAAGTTAAA

13706.1

GATGAAAATTAATACTTAAATTAATCAAAAGGCACTACGATACCACCTAAACCTACTGCCTCAGTGGCAGTA  
KGCTAAKGAAGATCAAGCTACAGSACATYATCTAATATGAATGTTAGCAATTACATAKCARGAAGCATGTTTGC  
TTCCAGAAGACTATGGNACAATGGTCATTWGGGCCAAGAGGATATTTGGCCNGGAAAGGATCAAGATAGATN  
AANGTAAAG

13706.2

GAGTAGCAACGCAAAGCGCTTGGTATTGAGTCTGTGGGSGACTTCGGTTCGGTCTCTGCAGCAGCCGTGATCG  
CTTAGTGGAGTGCTTAGGGTAGTTGGCCAGGATGCCGAATATCAAAATCTTCAGCAGGCAGCTCCACCAGGAC  
TTATCTCASAAAATTGCTGACCGCCTGGGCCTGGAGCTAGGCAAGGTGGTGACTAAGAAATTCAGCAACCAGGA  
GACCTGTGTGGAATTTGGTGAAAGTGTAACCGTGGAGAGGATGTCTACATTGTTTCAAGTGGNTGTGGCGAAATC  
AATGACAATTTAATGGAGCTTTTGATCATGATTAATGCCTGCAAGATTGCTTCAGCCAGCCGGGTTACTGCAGT  
CATCCCATGCTTCCCTTATGCCCCGGCAGGATAAGAAAGATNAGAGCCGGGCCCAATCTCAGCCAAGCTTGG  
TGCAAATATGCTATCTGTAGCAGTGCAGATCATATTATCACCATGGACCTACATGCTTCTCAAATTCANGGCTT  
TTT

**Fig. 15K**

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13707.3

ATGCAAAAGGGGACACAGGGGGTTCAAAAATAAAATTTCTCTTCCCCCTCCCCAAACCTGTACCCAGCTCCC  
CGACCACAACCCCTTCCTCCCCGGGGAAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAG  
GCCGGGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCCAAATATAAATACGTGTGTCAGAACTGGAAATCCTCC  
AGCACCCACCACCAAGCACTCTCCGTTTTCTGCCGGTGTGTTGGAGAGGGGCGNGGGCAGGGGCGCCAGGCAC  
CGGCTGGCTGCGGTCTACTGCATCCGCTGGGTGTGCACCCCGCA

13710.2

AGGTTGGAGAAGGTCATGCAGGTGCAGATTGTCCAGGSKCAGCCACAGGGTCAAGCCCAACAGGCCCAGAGTGG  
CACTGGACAGACCATGCAGGTGATGCAGCAGATCATCTAACACAGGAGAGATCCAGCAGATCCCGGTGCAGC  
TGAATGCCGGCCAGCTGCAGTATATCCGCTTAGCCCAGCCTGTATCAGGCACTCAAGTTGTGCAGGGACAGATC  
CAGACACTTGCCACCAATGCTCAACAGATTACACAGACAGAGGTCCAGCAAGGACAGCAGCAGTTCAAGCCAGT  
TCACAAGATGGACAGCAGCTCTACCAGATCCAGCAAGTCAACATGCCTGCGGGCCANGACCTCGCCAGCCCATG  
TTCATCCAGTCAAGCCAACAGCCCTTCNACGGGCAGGCCCCCAGGTGACCGGCGACTGAAGGGCCTGAGCTG  
GCAAGGCCAANGACACCCAACACAATTTTTGCCATACAGCCCCAGGCAATGGGCACAGCCTTTCTTCCAGAG  
GAC

13710-1

TGAGATTTATTGCATTTTCATGCAGCTTGAAGTCCATGCAAAGGRGACTAGCACAGTTTTTAATGCATTTAAAAA  
ATAAAAGGGAGGTGGGCAGCAAACACACAAAGTCTAGTTTCTGGGTCCCTGGGAGAAAAGAGTGTGGCAATG  
AATCCACCCACTCTCCACAGGGAATAAATCTGTCTCTTAAATGCAAAGAATGTTTCCATGGCCTCTGGATGCAA  
ATACACAGAGCTCTGGGGTCAGAGCAAGGGATGGGGAGAGGACCACGAGTGAAAAAGCAGCTACACACATTAC  
CTAATTCATCTGAGGGCAAGAACAACGTGGCAAGTCTTGGGGTAGCAGCTGTT

13711.1

TCCAGACATGCTCCTGTCTAGGCGGGGAGCAGGAACCAGACCTGCTATGGGAAGCAGAAAGAGTTAAGGGAAG  
GTTTCCTTTTCATTCTGTTCTTTCTTTTGCTTTTGAACAGTTTTTAAATATACTAATAGCTAAGTCATTTGC  
CAGCCAGGTCCCGGTGAACAGTAGAGAACAAGGAGCTTGCTAAGAATTAATTTTGCTGTTTTTACCCCATTTCA  
AACAGAGCTGCCCTGTTCCCTGATGGAGTTCATTCTGCCAGGGCACGGCTGAGTAACACGAAGCCATTCAAG  
AAAGGCGGGTGTGAAATCACTGCCACCCCATGGACAGACCCCTCACTCTTCTTCTTAGCCGAGCGCTACTTA  
ATAAATATATTTATACTTTGAAATTATGATAACCGATTTTTCCCATGCGGCATCCTAAGGGCACTTGCCAGCTC  
TTATCCGGACAGTCAAGCACTGTTGTTGGACAACAGATAAAGGAAAAGAAAAAGAAGAAAACAACCGCAACTTC  
TGT

*Fig. 15L*



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13711.2

TGAGACGGACCACTGGCCTGGTCCCCCTCATKTGCTGTCGTAGGACCTGACATGAAACGCAGATCTAGTGGCA  
GAGAGGAAGATGATGAGGAACTTCTGAGACGTCGGCAGCTTCAAGAAGAGCAATTAATGAAGCTTAACTCAGGC  
CTGGGACAGTTGATCTTGAAAGAAGAGATGGAGAAAGAGAGCCGGGAAAGGTCATCTCTGTTAGCCAGTCGCTA  
CGATTCTCCCATCAACTCAGCTTCACATATTCCATCATCTAAACTGCATCTCTCCCTGGCTATGGAAGAAATG  
GGCTTCACCGGCCTGTTTCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCAGCGGGGAGTGCGAGAT  
TACCAGACACTTCAGATGGCCACATGCCTGCAATGAGAATGGACCGAGGAGTGCTATGCCCAACATGTTGGA  
ACCAAAGATATTTCCATATGAAATGCTCATGGTGACCAACAGAGGGCCGAAACCAAATCTCAGAGAGGTGGACA  
GAA

13713.1&amp;2

TCACTTTATTTTCTTGTATAAAAACCTATGTTGTAGCCACAGCTGGAGCCTGAGTCCGCTGCACGGAGACTC  
TGGTGTGGGTCTTGACGAGGTGGTCAGTGAACCTCTGATAGGGAGACTTGGTGAATACAGTCTCCTTCAGAGG  
TCGGGGGTGAGGTAGCTGTAGGTCTTAGAAATGGCATCAAAGGTGGCCTTGGCGAAGTTGCCAGGGTGGCAGT  
GCAGCCCCGGGCTGAGGTGTAGCAGTCATCGATACCAGCCATCATGAG

13715.4

CTGGAATATAGACCCGTGATCGACAAAACCTTGAACGAGGCTGACTGTGCCACCGTCCCGCCAGCCATTCGCTC  
CTACTGATGAGACAAGATGTGGTGATGACAGAAATCAGCTTTTGTAAATTATGTATAATAGCTCATGCATGTGTCC  
ATGTCATAACTGTCTTCATACGCTTCTGCACTCTGGGGAAGAAGGAGTACATTGAAGGGAGATTGGCACCTAGT  
GGCTGGGAGCTTGCCAGGAACCCAGTGGCCAGGGAGCGTGGCACTTACCTTTGTCCCTTGCTTCATTCTTGTGA  
GATGATAAACTGGGCACAGCTCTTAAATAAAATATAAATGAACA

13717.1&amp;2

TGAATGGGAGGAGCTGACCCAGGAAATGGAGCTTGNGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAG  
TGGGCATCTGTGGTGGTGCCTCTTGGGAAGGAGCAGAAGTACACATGCCATGTGGAACATGAGGGGCTGCCTGA  
GCCCCACCCCTGAGATGGGGCAAGGAGGAGCCTCTTCATCCACCAAGACTAACACAGTAATCATTGCTGTTC  
CGTTGTCTTGGAGCTGTGGTCATCCTTGGAGCTGTGATGGCTTTTGTGATGAAGAGGAGGAGAAACACAGGT  
GGAAAAGGAGGGGACTATGCTCTGGCTCCAGGCTCCAGAGCTCTGATATGTCTCTCCAGATTGTAAAGTGTG  
AAGACAGCTGCCTGGTGTGGACTTGGTGACAGACAATGTCTTCACACATCTCCTGTGACATCCAGAGACCTCAG  
TTCTCTTTAGTCAAGTGTCTGATGTTCCCTGTGAGTCTGCGGGCTCAAAGTGAAGAAGTGTGGAGCCCAGTCCA  
CCCCTGCACACCAGGACCCTATCCCTGCACTGCCCTGTGTTCCCTTCCACAGCCAACCTTGCTGCTCCAGCCAA  
ACATTGGTGGACATCTGCAGCCTGTGAGTCCATGCTACCCTGACCTTCAACTCCTCACTTCCCACTGAGAAT  
AATAATTTGAATGTGGGTGGCTGGAGAGATGGCTCAGCGTGACTGCTCTTCAAAGGTCTGAGTTCAAATCC  
CAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATCTAATACCCTCTTCTGCAGTGTCTGAAGACASCT  
ACAGTGTACTTACATATAATAATAAATAAG

**Fig. 15M**

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13719.1&amp;2

GGCCGGGCGCGCGCGCCCCGCCACGCACGCCGGGCGTGCCAGTTTATAAAGGGAGAGAGCAAGCAGCGAGT  
CTTGAAGCTCTGTTTGGTGCTTTGGATCCATTTCCATCGGTCCTTACAGCCGCTCGTCAGACTCCAGCAGCCAA  
GATGGTGAAGCAGATCGAGAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAAGTTGTAGTAG  
TTGACTTCTCAGCCACGTGGTGTGGGCCCTTGCAAAATGATCAAGCCTTTCTTTCATTCCCTCTCTGAAAAGTAT  
TCCAACGTGATATTCCTTGAAGTAGATGTGGATGACTGTCAGGATGTTGCTTCAGAGTGTGAAGTCAAATGCAT  
GCCAACATTCCAGTTTTTAAAGAAGGGACAAAAGGTGGGTGAATTTTCTGGAGCCAATAAGGAAAAGCTTGAAG  
CCACCATTAATGAATTAGTCTAATCATGTTTTCTGAAAATATAACCAGCCATTGGCTATTTAAAAGTTGTAATT  
TTTTTAATTTACAAAAATATAAAATATGAAGACATAAACCCMGTTGCCATCTGCGTGACAATAAACATTAATG  
CTAACACTT

13721.1

TCACATAAGAAATTTAAGCAAGTTACRCTATCTTAAAAACACAACGAATGCATTTTAATAGAGAAACCCCTTCC  
CTCCCTCCACCTCCCTCCCCACCCCTCCTCATGAATTAAGAATCTAAGAGAAGAAGTAACCATAAAACCAAGTT  
TTGTGGAATCCATCATCCAGAGTGCTTACATGGTGATTAGGTAAATATTGCCTTCTTACAAAATTTCTATTTTA  
AAAAAAATTATAACCTTGATTGCTTATTACAAAAAATTCAGTACAAAAGTTCAATATATTGAAAAATGCTTTT  
CCCCTCCCTCACAGCACCGTTTTATATATAGCAGAGAATAATGAAGAGATTGCTAGTCTAGATGGGGCAATCTT  
CAAATTACACCAAGACGCACAGTGGTTTATTTACCCTCCCCTTCTCATAAG

13721.2

GGAAAGGATTCAAGAATTAGAGGACTTGCTTGCTRRAGAAAAAGACAACTCTCGTCGCATGCTGACAGACAAAG  
AGAGAGAGATGGCGGAAATAAGGGATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAG  
TTAGCCCTGGACATGGAAATCAGTGCTTACAGGAACTCTTAGAAGGCGAAGAAGAGAGGTTGAAGCTGTCTCC  
AAGCCCTTCTTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACCGTACAAGTACAGGAAAGCGG  
AAGAGGGTTGATGTGGAAGAATCAGAGGCGAAGTAGTAGTGTAGCATCTCTCATTCCGCCTCAACCACTGGAA  
ATGTTTGCATCGAAGAAATTGATGTTGATGGGAAATTTATCCGCTTGAAGAACACTTCTGAACAGGATCAACC  
AATGGGAAGGCTTGGGAGATGATCAGAAAAATTGGAGACACATCAGTCAGTTATAAATATACCTCAA

13723.1

CATGGGTTTACCAGGTTGGCCAGGCTGCTCTTGAAGTCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCA  
AAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCAAAGCTGTTTCTTTGTCTTTAGCGTAAAGCT  
CTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGCTCAGTCACTCCGTGGTCTTTTCTCTTT  
CCAGTTCTTCTCTCTCTTCAAGTTCTGCCCTCAGTGAAAGCTGCAGGTCCCAGTTAAGTGATCAGGTGAGGG  
TTCTTTGAACCTGGTTCTATCAGTCGAATTAATCCTTCATGATGG

**Fig. 15N**

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13723.2

GATGTGTTGGACCTCTGTGTCAAAAAAACCTCACAAAGAATCCCCTGCTCATTACAGAAGAAGATGCATTTA  
AAATATGGGTATTTTTCAACTTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTCAGAAGAGATTGAATAC  
CTGCTTAAGAAAGCTTACAGAAGCTATGGGAGGAGGTGGCAGCAAGAACAATTTGAACATTATAAAATCAACTT  
TGATGACAGTAAAAATGGCCTTTCTGCATGGGAACCTATTGAGCTTATTGGAAATGGACAGTTTAGCAAAGGCA  
TGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTTAATGAACCTATATTAGATGTGTTAAAGCAGGGT  
TACATGATGAAAAAGGGCCACAGACGGAAAACTGGACTGAAAGATGGTTTGTACTAAAACCCAACATAATTTCT  
TACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTGGATGAAAATTGCTGTGTAGAAGTCC  
TTGCCTGACAAAAGATGGAAAGAAATGCCTTTT

13725.1

GACTGGTTCCTTTATTTCAAAAAGACACTTGTCAATATTCAGTRTCAAAACAGTTGCACTATTGATTTCTCTTTC  
TCCCAATCGGCCCCAAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGATGTACACCTA  
ACAGACCTCCTAGAAACCTTACCAGAAAATGGGGACTGGGTAGGGAAGGAACTTAAAAGATCAACAACTGCC  
AGCCACGGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAGCAAAGTTTCAA  
AATAATATAAAATTTAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGATACAAAGCACA  
ATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAAGTTTACATGGCTAA  
ATCAGTGGCAAAAACACAGTCTTCTTCTTCTTCTTCAAGGANGCAGGAAAGCAATTAAGTGGTCACCTTA  
ACATAAGGGGGAC

13725.2

TGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGATCCAGGTTCTGCAGCAGCAGGC  
AGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGAGAAAGCGGGCCCGGGAACAGGCTG  
AGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTGGACCGTGCTCAGGAGCGCCTG  
GCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGAGAGAGGTATGAAGGTTATTGA  
AAACCGGGCCTTAAAAGATGAAGAAAAGATGGAACCTCCAGGAAATCCAACCTCAAAGAAGCTAAGCACATTGCAG  
AAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAAGGAGACTTGGAAACGCACAGA  
AGGAACGAGCTTGAGCTTGGCAAAAGTCCCGTTGCCAGAGATGGGATGAACCAGATTAGACTGATGGACCANA  
ACC

13726.1&amp;2

AGGGGCGNGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCG  
AGAGTGACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTGTGCG  
CTGCATTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGTAA  
CCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGACCTCGGGCACTC  
AAGAGATTGCGAAATTTGCCATGAAGGAGATGGGAACCTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGC  
TGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGGTGTGCGGCTGTCCAGAAAACGTAATGAGGAT  
GAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGT  
CAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAAT

**Fig. 150**

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13727.1

TCCGGGAGCCACACTTGGCCCTCTTCTCTCCAAAGSGCCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCTC  
TTGGAGACACAGAGGGTTTACCTTGGATGACCTCTAGAGAAATTGCCAAGAAGCCCACCTTCTGGTCCCAAC  
CTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGCTGTAGAAGGTCACCTGGCTCCATTGCCTGCTTCCAAC  
CAATGGGCAGGAGAGAAGGCCCTTTATTTCTCGCCACCCATTCTCCTGTACCAGCACCTCCGTTTTTCAGTCAG  
TGTTGTCCAGCAACGGTACCGTTTACACAGTCACCTCAGACACACCATTTACCTCCCTTGCCAAGCTGTTAGC  
CTTAGAGTGATTGCAGTGAACACTGTTTACACACCGTGAATCCATTCCCATCAGTCCATTCCAGTTGGCACCAG  
CCTGAACCATTTGGTACCTGGTGTTAACTGGAGTCCTGTTTACAAGGTGGAGTCGGGGCTTGCTGACTTCTCTT  
CATTTGAGGGCAC

13727.2

ACCTAGACAGAAGGTGGGTGAGGGAGGACTGGTAGGAGGCTGAGGCAATTCCTTGGTAGTTTGTCTGAAACCC  
TACTGGAGAAGTCAGCATGAGGCACCTACTGAGAGAAGTGCCCAGAACTGCTGACTGCATCTGTTAAGAGTTA  
ACAGTAAAGAGGTAGAAGTGTGTTCTGAATCAGAGTGGAAGCGTCTCAAGGGTCCACAGTGGAGGTCCCTGA  
GCTACCTCCCTTCCGTGAGTGGGAAGAGTGAAGCCCATGAAGAAGTGAAGCAAGGATGGGGTTCTGGG  
CTCCAGGCAAGGGCTGTGCTCTCTGCAGCAGGGAGCCCCACGAGTCAGAAGAAAAGAACTAATCATTGTTGCA  
AGAAACCTTGCCCGGATACTAGCGGAAAAGTGGAGGCGNGGTGGGGGCACAGGAAAGTGAAGTGATTGATG  
GAGAGCAGAGAAGCCTATGCACAGTGGCGGAGTCCACTTGTAAGTG

13728.1&amp;2

TTCAAGCAATTGTAACAAGTATATGTAGATTAGAGTGAGCAAAATCATATACAATTTTCATTTCCAGTTGCTAT  
TTTCCAAATTGTTCTGTAATGTGTTAAATTACTTAAAAATTAACAAAGCCAAAAATTATTTATGACAAGA  
AAGCCATCCCTACATTAATCTTACTTTTCCACTCACCGGCCCATCTCCTTCTCTTTTCTTAATATGCCATT  
AAAAGTGTCTACTGGGCCGGGCGTGTGGCTCATGCCTGTAATCCAGCATTTTGGGAGGCCAAGGCAGGCGGA  
TCATGAGGTCAAGAGATTGAGACCATCTGGCCAACATGGTGAACCCCGCCTCGACTAAGAATACAAAAATTA  
GCTGGGCATGGTGGCGCATGCCTGTAGTCTCAGCTACTCGGGAGGCTGAGGCAGAAGATCGCTTGAACCCGGG  
AGGCAGAGGATGCAGTGAGCCCCGATCGCGCACTGCACTCTAGCCTGGGCGACAGACTGAGACTCTGCTC

13731.1&amp;2

TGTGCCAGTCTACAGGCCTATCAGCAGCGACTCCTTCAGCAACAGATGGGGTCCCTGTTGAGCCCAACCCCAT  
GAGCCCCCAGCAGCATATGCTCCCAAATCAGGCCAGTCCCCACACCTACAAGGCCAGCAGATCCCTAATTCTC  
TCTCCAATCAAGTGCGCTCTCCCCAGCCTGTCCCTTCTCCACGGCCACAGTCCCAGCCCCCCCCACTCCAGTCCT  
TCCCCAAGGATGCAGCCTCAGCCTTCTCCACACCACGTTTCCCCACAGACAAGTTCCCCACATCETGGACTGGT  
AGTTGCCCAGGCCAACCCCATGGAACAAGGGCATTGTCAGCC

**Fig. 15P**

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13734.1&amp;2

TGTA AAAACTTGT TTTTAATTTTGTATAAAATAAAGGTGGTCCATGCCACGGGGGCTGTAGGAAATCCAAGCA  
GACCAGCTGGGGTGGGGGATGTAGCCTACCTCGGGGACTGTCTGTCTCAAACGGGCTGAGAAGGCCCGTC  
AGGGGCCAGGTCCACAGAGAGGCCTGGGATACTCCCCAACCCGAGGGGCAGACTGGGCAGTGGGGAGCCCC  
CATCGTGCCCCAGAGGTGGCCACAGGCTGAAGGAGGGGCTGAGGCACCGCAGCCTGCAACCCCCAGGGCTGCA  
GTCCACTAACTTTTACAGAATAAAAGGAACATGGGGATGGGGA AAAAGCACCAGGTGAGGCAGGGCCCGAGG  
GCCCCAGATCCAGGAGGGCCAGGACTCAGGATGCCAGCACCACCCTAGCAGCTCCACAGCTCCTGGCACAGG  
AGGCCGCCACGGATTGGCACAGCCGCTGCTGGCCATCAGGCCACATTTGGAGAACTTGTCCCGACAGAGGTCA  
GCTCGGAGGAGCTCCTCGTGGGCACACACTGTACGAACACAGATCTCCTTGTTAATGACGTACACACGGCGGAG  
GCTGCGGGGACAGGGCACGGGAGGTCTCAGCCCCACTT

13736.2

ATGGCTGCTGGATTTAGGTGGTAATAGGGGCTGTGGGCCATAAATCTGAAGCCTTGAGAACCTTGGGTCTGGAG  
AGCCATGAAGAGGGAAGGAAAAGAGGGCAAGTCTGAACCTAACCAATGACCTGATGGATTGCTCGACCAAGAC  
ACAGAAGTGAAGTCTGTGTCTGTGCACCTCCACAGACTGGAGTTTTTGGTGCTGAATAGAGCCAGTTGCTAAA  
AAATTGGGGGTTTGGTGAAGAAATCTGATTGTTGTGTGTATTCAATGTGTGATTTTAAAAATAACAGCAACAA  
CAATAAAACCCCTGACTGGCTGTTTTTCCCTGTATCTTTACAACATTTTTTGACCCCTTGAAAATTATTAT  
ACTTCACCTAAATGGAAGACTGCTGTGTTGTGGAATTTTGTAAATTTTAAATTTATTCTCTCTCCTT  
TTTATTTTGCTGCAGAAATCCGTTGAGAGACTAATAAGGCTTAATATTTAATTGATTTGTTTAATATGTATATA  
AAT

13744.2-13696.2

GGCATGCGAGCGCACTCGGCGGACGCAAGGGCGGCGGGAGCACGAGCACTGCAGGCGCCGGGTGGGACA  
GCGTCTTCGCTGCTGCTGGATAGTCGTGTTTTCGGGGATCGAGGATACTCACCAGAAACGAAAATGCCGAAAC  
CAATCAATGTCCGAGTTACCACCATGGATGCAGAGCTGGAGTTTGCAATCCAGCCAAATACAACCTGGAAAACAG  
CTTTTGTATCAGGTGGTAAAGACTATCGGCCTCCGGGAAGTGTGGTACTTTGGCCTCCACTATGTGGATAATAA  
AGGATTTCTACCTGGCTGAAGCTGGATAAGAAGGTGTCTGCCAGGAGGTGAGGAAGGAGAATCCCTCCAGT  
TCAAGTTCGGGGCAAAGTTCTACCTGAAGATGTGGCTGAGGAGCTCATCCAGGACATCACCAGAAACTTTT  
CTTCCTTCAAGTGAAGGAAGGAATCCTTAGCGATGAGATCTACTGCCCCCTTGARACTGCCGTGCTCTTGGGG  
TCCTACGCTTGTGCATGCCAAGTTTGGGACTACCACCAAGAAG

13746.1&amp;2-13720.1&amp;2

GAAGGAGTCGGGATACTCAGCATTGATGCACCCCAATTTCAAAGCGGCATTCTTCGGCAGGTCTCTGGGACAAT  
CTCTAGGGTCACTACCTGGAAACTCGTTAGGGTACAACCTGAATGCTGAAAGGAAAGAACACCTGCAGAACCGGA  
CAGAAATTCACCCGGCGATCAGCTGATTGATCTCGGTGACCAGAAGTCATGGCTAAAGATGACGAGGACGTT  
GTCAATTCCTGGGCTTTTGAAGTGAGTCCAGCAGCAGTCTGAGGTATTCGGGCCGGTTATGCACCTGGACCA  
CCAGCACCAGCTCCCGGGGGGCCAGGTGCCAGCCTTATCTACATTCCTCAGGGTCTGATCAAAGTTCAGCTGG  
TACACCAGGGACCGGTACCGCAGCGTCAGGTTGTCCGCTCGGGCTGGGGGACCGCCGGGACCAGGGAAGCCGCC  
GACACGTTGGAGACCCTGCGGATGCCACAGCCACAGAGGGGTGGTCCCCACCGCGCGCCGGCCACCCCGCGC  
GGGTTCCGGCTCCAGCAACGGTGGGGCGAGGGCCTCGTTCCTTTGTGCCCCATTGCTGCTCCAGAGGACGA  
AGCCGCAGGCGGCCACCAGAGCGTCAGGATTAGCACCTTCGTTTGTAGATGCGGAACCTCATGGTCTCCAGG  
GCCGGGAGCGCAGCTACAGCTCGAGCGTCGGCGCCGCCGCTAGGAGCCGCGGCTCGGCTTCGTCTCCGTCTCT  
CCATTCAGCACCACGGGTCCCGGAAAAGCTCAGCCSCGGTCCCAACCGCACCTAGCTTCGTTACCTGCGCCT  
CGCTTG

*Fig. 15Q*

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14347.1

CAGATTTTATTTGCAGTCGTCAGTGGGGCCGTTTCTTGCTGCTTATTTGTCTGCTAGCCTGCTCTTCCAGCTG  
CATGGCCAGGCGCAAGGCCTTGATGACATCTCGCAGGGCTGAGAAATGCTTGGCTTGCTGGGCCAGAGCAGATT  
CCGCTTTGTTCAAAAGGTCTCCAGGTCATAGTCTGGCTGCTCGGTTCATCTCAGAGAGCTCAAGCCAGTCTGGT  
CCTTGCTGTATGATCTCCTTGAGCTCTTCCATAGCCTTCTCCTCCAGCTCCCTGATCTGAGTCATGGCTTCGTT  
AAAGCTGGACATCTGGGAAGACAGTTCCTCCTCTTCTTGGATAAATTGCCTGGAATCAGCGCCCCGTTAGAGC  
AGGCTTCCATCTCTTCTGTTTCCATTTGAATCAACTGCTCTCCACTGGGCCCCACTGTGGGGGCTCAGCTCCTTG  
ACCCTGCTGCATATCTTAAGGGTGTTTAAAGGATATTCACAGGAGCTTATGCCTGGT

14347.2

CTCCTCTTGGTACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGA  
CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTACAGCAAGGCCACTGGTACAGACAATCT  
TTGAAGGTGGAAAAGCAACTTGTTTTGCATATGGCCAGACAGGAAGTGGCAAGACACATACTATGGGCGGAGAC  
CTCTCTGGGAAAGCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTTCCGGGACGTCTTCTTCTGAAGAAT  
CAACCCTGCTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGA  
CCTGCTCAACAAGAAGGCCAAGCTTGCGCGTGCTGGAAGACGGCAAGCAACAGGTGCAAGTGGTGGGGGCTTGC  
AGGAACATCTGGNTAACTCTGCTTGATGATGGCANTCAAGATGATCGACATGGGCAGCGCCTGCAGA

14348.2&amp;14350.1&amp;2

TCCCGAATTCAGCGACAAATTTGGAWAGTGAAATGGAAGATGCCTATCATGAACATCAGGCAAATCTTTTGGCG  
CAAGATCTGATGAGACGACAGGAAGAATTAAGACGCATGGAAGAACTTCACAATCAAGAAATGCAGAAACGTAA  
AGAAATGCAATTGAGGCAAGAGGAGGAACGACGTAGAAGAGAGGAAGAGATGATGATTCGTCAACGTGAGATGG  
AAGAACAAATGAGGCGCCAAAGAGAGGAAAGTTACAGCCGAATGGGCTACATGGATCCACGGGAAAGAGACATG  
CGAATGGGTGGCGGAGGAGCAATGAACATGGGAGATCCCTATGGTTTCAGGAGGCCAGAAATTTCCACCTCTAGG  
AGGTGGTGGTGGCATAGGTTATGAAGCTAATCCTGGCGTTCCACCAGCAACCATGAGTGGTTCATGATGGGAA  
GTGACATGCGTACTGAGCGCTTTGGGCAGGGAGGTGCGGGGCCCTGTGGGTGGACAGGGTCTAGAGGAATGGGG  
CCTGGAACCTCAGCAGGATATGGTAGAGGGAGAGAAGAGTACGAAGGC

14349.1&amp;2

TTCGTGAAGACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCCGAGTGACACCATTGAGAATGTCAAGG  
CAAAGATCCAAGACAAGGAAGGCATCCCTCCTGACCAGCAKAGGTTGATCTTTGCTGGGAAACAGCTGGAAGAT  
GGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGAT  
GCAATCTTCGTGAAGACCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCAGTGACACCATCGAGAATG  
TCAAGGCAAAGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTG  
GAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTGCGCTTGAGGGG  
GGGTGTCTAAGTTTCCCTTTTAAGGTTTCAACAAATTTATTGCACTTTCCTTTCAATAAAGTTGTTGCATTC

**Fig. 15R**

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14352.1&amp;2

GCGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCGAGAGT  
GACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAAACTCTGCTCTGAGCCTCCTTGTCGCTGCA  
TTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGTAACCCGA  
GAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGACCTCGGGCACTCAAAGA  
GATTCGGAAATTTGCCATGAAGGAGATGGGAACCTCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCT  
GGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGAT  
TCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAATGT  
GGATGAGAACTAATCGCTGATCGT

14353.1

AATTCTTTATTTAAATCAACAACTCATCTTCTCAAGCCCCAGACCATGGTAGGCAGCCCTCCCTCTCCATCC  
CCTCACCCACCCCTTAGCCACAGTGAAGGGAATGGAAAATGAGAAGCCACGAGGGCCCTGCCAGGGAAGGCT  
GCCCCAGATGTGTGGTGAGCACAGTCAGTGCAGCTGTGGCTGGGGCAGCAGCTGCCACAGGCTCCTCCCTATAA  
ATTAAGTTCCTGCAGCCACAGCTGTGGGAGAAGCATACTTGTAGAAGCAAGGCCAGTCCAGCATCAGAAGGCAG  
AGGCAGCATCAGTGACTCCAGCCATGGAATGAACGGAGGACACAGAGCTCAGAGACAGAACAGGCCAGGGGGA  
AGAAGGAGAGACAGAATAGGCCAGGGCATGGCGGTGAGGGA

14353.2

TGATGAATCTGGGTGGGCTGGCAGTAGCCCGAGATGATGGGCTCTTCTCTGGGGATCCCAACTGGTTCCCTAAG  
AAATCCAAGGAGAATCCTCGGAACCTCTCGGATAACCAAGCTGCAAGAGGGCAAGAACGTGATCGGGTTACAGAT  
GGGCACCAACCGCGGGGGCGTCTCANGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATCCCACC  
CCAGGCCCTTGCCCTGCCCTCCCACGAATGGTTAATATATATGTAGATATATATTTTAGCAGTGACATTCACAG  
AGAGCCCCAGAGCTCTCAAGCTCCTTTCTGTGAGGGTGGGGGGTTCAAGCCTGTCTGTACCTCTGAAGTGCC  
TGCTGGCATCCTCTCCCCATGCTTACTAATACATTCCCTTCCCATAGCC

17182.1&amp;2

AGCGGAGCTCCCTCCCCTGGTGGCTACAACCCACACAGCCAGGCTCAGGCATCGAGCAGAACTCCAGCGACTG  
GGTAACCACTGACATTAGGTGAAGGTGCGGGACACCTACCTGGATACACAGGTGGTGGGACAGACAGGTGTCA  
TCCGCAGTGTACGGGGGGCATGTGCTCTGTGTACCTGAAGGACAGTGAGAAGGTTGTGAGCATTTCAGTGAG  
CACCTGGAGCCTATACCCCCACCAAGAACAACAAGGTGAAAGTGATCCTGGGCGAGGATCGGGAAGCCACGGG  
CGTCTACTGAGCATTGATGGTGAGGATGGCATTGTCCGTATGGACCTTGATGAGCAGCTCAAGATCCTCAACC  
TCCGCTTCCCTGGGGAAGCTCCTGGAAGCCTGAAGCAGGCAGGGCCGGTGGACTTCGTGGATGAAGAGTGATCC  
TCCTTCCCTTCCCTGGCCCTTGCTGTGACACAAGATCCTCCTGCAGGGCTAGGCGGATTGTTCTGGATTTCCTT  
TTGTTTTTCTTTTAGGTTTCCATCTTTTCCCTCCCTGGTGCTCATTGGAATCTGAGTAGAGTCTGGGGGAGGG  
TCCCCACCTTCCGTACCTCCTCCCCACAGCTTGCTTTTGTGTACCGTCTTCAATAAAAAGAAGCTGTTTGG  
TCTA

**Fig. 15S**

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17183.2

GGTTCACAGCACTGCTGCTTGTGTGTTGCCGGCCAGGAATTCAGGCTCACAAGGCTATCTTAGCAGCTCGTTC  
TCCGGTTTTTAGTGCCATGTTTGAACATGAAATGGAGGAGAGCAAAAAGAATCGAGTTGAAATCAATGATGTGG  
AGCCTGAAGTTTTTAAGGAAATGATGTGCTTCATTACACGGGGAAGGCTCCAAACCTCGACAAAATGGCTGAT  
GATTTGCTGGCAGCTGCTGACAAGTATGCCCTGGAGCGCTTAAAGGTCATGTGTGAGGATGCCCTCTGCAGTAA  
CCTGTCCGTGGAGAACGCTGCAGAAATTCTCATCCTGGCCGACCTCCACAGTGCAGATCAGTTGAAAACCTCAGG  
CAGTGGATTTTCATCAACTATCATGCTTCGGATGTCTTGAGACCTCTTGGG

17186.1&amp;2

TCGTAGCCATTTTTCTGCTTCTTTGGAGAATGACGCCACACTGACTGCTCATTGTGCTTGGTTCCATGCCAATT  
GGTGAATAGAACCTCATCCGTTAGTGAGCCGGAGGGACATCTTGTATCAACGGTGATGGTGCGATTTGGAG  
CATACCAGAGCTTGGTGTCTCGCCATACAGGGCAAAGAGGTTGTGACAAAGAGGAGAGATACGGCATGCCTGT  
GCAGCCCTGATGCACAGTTCTCTGTGTACTCTCCACTGCCAGCCGGAGGGGCTCCCTGTCCGACAGATA  
GAAGTCACTTCCACCCCTGGCTTG

17187.1&amp;2

TGGCACACTGCTCTTAAGAACTATGAWGATCTGAGATTTTTTGTGTATGTTTTGACTCTTTGAGTGGTAA  
TCATATGTGTCTTTATAGATGTACATACCTCCTTGACAAATGGAGGGGAATTCATTTTCATCACTGGGAGTGT  
CCTTAGTGTATAAAAACCATGCTGGTATATGGCTTCAAGTTGTAAAAATGAAAGTGACTTTAAAGAAAATAGG  
GGATGGTCCAGGATCTCCACTGATAAGACTGTTTTAAGTAACTTAAGGACCTTTGGGTCTACAAGTATATGTG  
AAAAAATGAGACTTACTGGGTGAGGAAATTCATTGTTTAAAGATGGTCGTGTGTGTGTGTGTGTGTGTGTG  
TTGTGTTGTGTTTTGTTTTTAAGGGAGGGAATTTATTATTTACCGTTGCTTGAAATTACTGKGTAAATATATG  
TYTGATAATGATTTGCTYTTTGVMACATAAAATTAGGVCTGTATAAGTWCTARATGCMTCCTGGGKGTGATY  
TTCCMAGATATTGATGATAMCCCTTAAAATTGTAACCYGCCTTTTTCCCTTTGCTYTCMATTAAAGTCTATTCM  
AAAG

17191.1&amp;89.1

GGGGGTAGGCTCTTTATTAGACGGTTATTGCTGTACTACAGGGTCAGAGTGCAGTGTAAAGCAGTGTGAGGGCC  
CGCGTTCAGCCCAAGAATGTGGATTTCTCTCCCTATTGATCACAGTGGGTGGGTTTCTTCAGAAAAGCCCCAG  
AGGCAGGGACCACTGAGCTCCAAGGTTAGAAGTGGAAGTGGAGGCTTCAGTCACATGCTGCTTCACGCTTCC  
AGGCTGGGCAGCAAGGAGGAGATGCCCATGACGTGCCAGGTCTCCCCATCTGACACCAGTGAAGTCTGGTAGGA  
CAGCAGCCGCACGCCTGCCTCTGCCAGGAGGCCAATCATGGTAGGCAGCATTGCAGGGTCAGAGGTCTGAGTCC  
GGAATAGGAGCAGGGGCAGGTCCCTGCGGAGAGGCACTTCTGGCCTGAAGACAGCTCCATTGAGCCCCCTGCAGT  
ACAGGYGTAGTGCTTGGACCAAGCCACAGCTGGTAAGGGGCGCTGCCAGGGCCACGGCCAGGAGGCA

**Fig. 15T**



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17192.1&amp;2

TAATTTCTTAGTCGTTTGAATCCTTAAGCATGCAAAAGCTTTGAACAGAAGGGTTACAAAGGAACCAGGGTT  
GTCTTATGGCATCCAGTTAAGCCAGAGCTGGGAATGCCTCTGGGTCATCCACATCAGGAGCAGAAGCACTTGAC  
TTGTCGGTCCTGCTGCCACGGTTTGGGCGCCACCACGCCACGTCCACCTCGTCTCCCTGCCGCCACGTCC  
TGGGCGGCCAAGGTCTCCAAAATTGATCTCCAGCTGAGACGTTATATCATTGCTGGCTTCGGAAATGATGGT  
CCATAACCGAATCTTCAGCATGAGCCTCTTCACTCTTTGATTTATGAAGAACAAATCCCTTCTTCACTGCCCA  
TCAGCACCTTCATTTGGTTTTCGGATATTAAATTCTACTTTTGGCCGGTCCTTATTTGAATAGCCTTCCACTC  
ATCCAAAGTCATCTCTTTGGACCCTCCTCTTTACCTCTTCAACTTCATTCTCCTTATTTTCAGTGTCTGCCA  
CTGGATGATGTTCTTCACCTTCAGGTGTTTCCTCAGTCACATTTGATTGATCCAAGTCAGTTAATTCGTCTTTG  
ACAGTTCCCCAGTTGTGAGATCCGCTACCTCCACGTTTGTCTCGTGCTTCAGGCCAGATCTATCACTTCCACT  
ATGCTATCAAATTCAGTTTGGCAGGAGAATCAAATCCATCTCCTCGGCCATTCCACGTCCACGGCCCCCTC  
GACCTCTTCCAAGACCACGACCTCGAATAGGTGGTCAATAATCGGTCTATCAACTGAAAATTCGCCTCCT  
TCACCCTTTTCTTCAAGTGGCTTTTGAATCTTCGTTACGAGGTGGTCGCCTTTCTGGTCTTCTATCAATTAT  
TTCCCTTCACCCTGAAGTTGTTGATCAGGTCTTCTTCAACTCGTGC

17193

AAGCGGATGGACCTGAGTCAGCCGAATCCTAGCCCCTTCCCTTGGGCCTGCTGTGGTGCTCGACATCAGTGACA  
GACGGAAGCAGCAGACCATCAAGGCTACGGGAGGCCCGGGGCGCTTGCGAAGATGAAGTTTGGCTGCCTCTCCT  
TCCGGCAGCCTTATGCTGGCTTTGTCTTAAATGGAATCAAGACTGTGGAGACGCGCTGGCGTCCTCTGCTGAGC  
AGCCAGCGGAACGTACCATCGCCGTCCACATTGCTCACAGGACTGGGAAGGCGATGCCTGTCCGGAGCTGCT  
GGTGGAGAGACTCGGGATGACTCCTGCTCAGATTACAGGCCTTGCTCAGGAAAGGGGAAAAGTTTGGTCGAGGAG  
TGATAGCGGGACTCGTTGACATTGGGGAACTTTGCAATGCCCCGAAGACTTAACTCCCGATGAGGTTGTGGAA  
CTAGAAAATCAAGCTGCACTGACCAACCTGAAGCAGAAGTACCTGACTGTGATTTCAAACCCAGGTGGTTACT  
GGAGCCCATACCTAGGAAAGGAGGCAAGGATGTATTCCAGGTAGACATCCAGAGCACCTGATCCCTTTGGGGC  
ATGAAGTGTGACAAGTGTGGGCTCCTGAAAGGAATGTTCCRGAGAAACCAGCTAAATCATGGCACCTTCAATTT  
GCCATCGTGACGCAGACCTGTATAAATTAGGTTAAAGATGAATTTCACTGCTTTGGAGAGTCCACCCACTAA  
GCACTGTGCATGTAACAGGTTCTTTGCTCAGATGAAGGAAGTAGGGGTGGGGCTTTCTTGTGTGATGCCT  
CCTTAGGCACACAGGCAATGTCTCAAGTACTTTGACCTTAGGGTAGAAGGCAAAGCTGCCAGTAAATGTCTCAG  
CATTGCTGCTAATTTTGGTCCTGCTAGTTTCTGGATTGTACAAATAAATGTGTTGTAGATGA

**Fig. 15U**

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16443.1.edit

TCGAGCGGCCCGCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA  
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTCAGGCTGACCTGGTTCTT  
GGTCATCTCCTCCCGGGATGGGGGCAGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTGGCTTTGGAGATGG  
TTTTCTCGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGACTCCTTGCCATTCAACCAGTCCTGG  
TGCANGACGGTGAGGACGCTNACCACACGGTACGNGCTGGTGTACTGCTCCTCCCGCGGCTTTGTCTTGGCATT  
ATGCACCTCCACGCCGTCCACGTACCAATTGAACCTTGACCTCAGGGTCTTCGTGGCTCACGTCCACCACCACGC  
ATGTAACCTCAAANCTCGGNCGCCANACGC

16443.2.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT  
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG  
TACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTC  
CAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT  
ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTAT  
CCCAGCGACATCGCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAACAAGACCACGCCTCCCGTGC  
TGGACTCCGACACCTGCCGGGCGGCCGCTCGA

16444.2.edit

AGCGTGGTTNCGGCCGAGGTCCCAACCAAGGCTGCANCCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACT  
GGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCAGAAGAAGTGGTACATCAGCAAGAACCCCAAGGA  
CAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACC  
CTGCCGATGTGGACCTGCCCGGGCGGNCGCTCGA

16445.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAA  
GAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGA  
CTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCAGAAGAAGTGGTACATCAGCAAGAACCCCAAG  
GACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGA  
CCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

*Fig. 15V*

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16445.2.edit

TCGAGCGGTCGCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC  
GGNCATGCTCTCGCCGAACCAGACATGCCTCTTGNCCTTGGGGTTCTTGCTGATGTACCAGNTCTTCTGGGCCA  
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCANTCTCCATGTTGCANAAGACTTTGATGGCATCCAGGTTG  
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCAGACAGAGTGGCACATCTTGAGGTCACGGCAGGT  
GCGGGCGGGGTTCTTGACCTCGGTCGCGACACGCT

16446.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTCCTCAGAGCGGTAGCTGTTCTTATTGCCCCGGCAGCCTCCATAGATNAA  
GTTATTGCANGAGTTCCTCTCCACGTCAAAGTACCAGCGTGGGAAGGATGCACGGCAAGGCCAGTGACTGCGT  
TGGCGGTGCAGTATTCTTCATAGTTGAACATATCGCTGGAGTGGACTTCAGAATCCTGCCTCTGGGAGCACTT  
GGGACAGAGGAATCCGCTGCATTCTGCTGGTGGACCTCGGCCGCGACACGCT

16446.2.edit

AGCGTGGTCGCGGCCGAGGTCCACCAGCAGGAATGCAGCGGATTCTCTGTCCCAAGTGCTCCCAGAAGGCAGG  
ATTCTGAAGACCACTCCAGCGATATGTTCAACTATGAAGAATACTGCACCGCCAACGCAGTCACTGGGCCTTGC  
CGTGATCCTTCCCACGCTGGTACTTTGACGTGGAGAGGAACCTCTGCAATAACTTCATCTATGGAGGCTGCCG  
GGGCAATAAGAACAGCTACCGCTCTGAGGAGGACCTGCCCGGGCGGCCGCTCGA

16447.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC  
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA  
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG  
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCAGCCAGAATGGCACATCTTGAGGTCACGGCANGT  
GCGGGCGGGGTTCTTGACCTCGGCCGCGACACGCT

***Fig. 15W***

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16447.2.edit

AGCGTGGTCGCGGCCGAGGTCAAGAAACCCGCGCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGGCTGGA  
AGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAG  
ACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAGAAGTGGTACATCAGCAAGAACCCCAA  
GGACAAGAGGCATGTCTGGCTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCG  
ACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

16449.1.edit

AGCGTGGTCGCGGCCGAGGTCTGTGTCAGAGTGGCACTGGTAGAAGNTCCAGGAACCTGAACTGTAAGGGTTCT  
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGNAATGGGGCCCATGANATGGTTGN  
CTGAGAGAGAGCTTCTTGTCTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGNGG  
GCGGTGNGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGTGCTGACCANAAGTG  
CCAGGAAGCTGAATACCATTTCCAGTGTATACCCAGGGTGGGTGACGAAAGGGGTCTTTGAACTGTGGAAGG  
AACATCCAAGATCTCTGNTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGCTGTCTTTTT  
CCTTCCAATCANGGGCTCGCTCTTCTGAATATTCTTCAGGGCAATGACATAAATTGTATATTCGGTTCCTGGT  
CCAGGCCAG

16450.1.edit

TCGAGCGGCCGCGCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT  
TACCGGTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG  
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT  
CAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCCAA  
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTACCCACCCTGGGTATG  
AACTGGAATGGTATTAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAAGAAATGATCTTTGAN  
GAACATGNNTTAGGCGGACCACACCGGCCACAACGGGCACCCCATAGGCATAGGCCAAGAACATACCCGNC  
GAATGTAGGACAAGAAGCTCTNTCTCANACAANCATCTCATGGGCCCATTCANGACACTTCTGAGTACATCA  
NTTCATGGCATCTGGTGGCACTGATAAAAACCTTACAGTTA

16450.2.edit

AGCGTGGTCGCGGGCGAGGTCTGTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCTGAACTGTAAGGGTTCT  
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT  
CTGAGAGAGAGCTTCTTGTCTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGTGG  
GCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGTGCTGACCAGAAGTG  
CCAGGAAGCTGAATACCATTTCCAGTGTATACCCAGGGTGGGTGACGAAAGGGGTCTTTGAACTGTGGAAGG  
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGTCTGTCTTTT  
TCCTTCCAATCANGGGCTCGCTCTTCTGAATTATTCTTCAGGGCAATGACATAAATTGTATATTCGGNTCCCGGG  
TNCAGCCAATAATAATAACCTCTGTGACACCANGGCGGGGCCGAAGGANCACT

**Fig. 15X**

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16451.1.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTACCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA  
GAGGCATAAGGTTGCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG  
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC  
TTTAAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTAGATGTGATTCATCTAGATGGTGCCATGA  
CAATGGTGTGAACACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTC  
GA

16451.2.edit

TCGAGCGGCCGCGGCCGAGGTCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT  
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACAGTTTA  
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA  
GTCATCCGTAGGTTGGTTCAAGCCTTCGNTGACAGAGTTGCCACGGTAACAACCTCTTCCGAACCTTATGCC  
TCTGCTGGTCTTTCAGTGCCCTCACTATGATGTTGTAGGTGGTACCTCTGGTGAGGACCTCGGCCGCGACCAG  
CT

16452.1.edit

AGCGTGGCCGCGGCCGAGGTCATTGGCTGGAACGGCATCAACTTGAAGCCAGTGATCGTCTCAGCCTTGTT  
CTCCAGCTAATGGTGATGGNGGTCTCAGTAGCATCTGTACACGAGCCCTTCTTGGTGGGCTGACATTCTCCAG  
AGTGGTGACAACACCCTGAGCTGGTCTGCTTGTCAAAGTGTCTTAAGAGCATAGACACTCACTTCATATTTGG  
CGNCCACCATAAGTCCTGATACAACCACGGAATGACCTGTCAGGAAC

16452.2.edit

TCGAGCGGCCGCGGCCGAGGTCCTCAGACCGGGTCTGAGTACACAGTCAGTGTGGTTGCCTTGACGATGAT  
ATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCTGCACCAACTGACCTGAAGTTCACTCAGGT  
CACACCCACAAGCCTGAGCGCCAGTGGACACCACCAATGTTAGCTCACTGGATATCGAGTGCGGGTGACCC  
CCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCGTGGTTGTATCAGGACTT  
ATGGCGGCCACCAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT  
TGTCACCACTCTGGAGAATGTGAGCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCA  
TTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGACCTCGGCCG  
CGACCAGCTT

**Fig. 15Y**

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16453.1.edit

AGCGTGGTGC GCGCCGAGGTCTGGCCGAAGTCCAGTGTACAGGGAAGATGTACATGTTATAGNTCTTCTCGAA  
GTCCCGGGCCAGCAGCTCCACGGGGTGGTCTCCTGCCCTCCAGGCGCTTCTCATTCTCATGGATCTTCTTCACCC  
GCAGTTTCTGCTTCTCAGTCAGAAGGTTGTTGTCTCATCCCTCTCATACAGGGTGACCAGGACGTTCTTGAGC  
CAGTCCCGCATGCGCAGGGGGAATTGCGTCAGTCCAGGCAAGGGGGGATGTATTTGCAAGGCCCGAT  
GTAGTCCAAGTGGAGCTTGTGGCCCTTCTTGGTGGCCCTCAAGGTGCACTTTGTGGCAAAGAAGTGGCAGGAAG  
AGTCGAAGGTCTTGTGTCATTGCTGCACACCTTCTCAAAGTCCCAATGGGGGCTGGGCAGACCTGCCCGGGC  
GGCCGCTCGA

16453.2.edit

TCGAGCGGCCGCGCCGGGCAGGTCTGCCAGCCCCATTGGCGAGTTTGAGAAGGNGTGCAGCAATGACAACAAG  
ACCTTCGACTCTTCTGCCACTTCTTTGCCACAAAGTGACCCCTGGAGGGCACCAGAAGGGCCACAAGCTCCA  
CCTGGACTACATCGGGCCTTGCAAATACATCCCCCTTGCTGGACTCTGAGCTGACCGAATTCCCCCTGCGCA  
TGCGGGACTGGCTCAAGAACGTCCTGGTCACCCTGTATGAGAGGGATGAGGACAACAACCTTCTGACTGAGAAG  
CANAAGCTGCGGGTGAAGAAATCCATGAGAATGANAAGCGCTGNAGGCANGAGACCACCCGTTGGAGCTGCT  
GGCCCGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTGCGCCAGACCTCGGCCG  
CGACCACGCT

16454.1.edit

AGCGTGGNTGCGGACGACGCCCACAAAGCCATTGTATGTAGTTTTANTTCAGCTGCAAANAATACCNCCAGCAT  
CCACCTTACTAACCAGCATATGCAGACA

16454.2.edit

TCGAGCGGTGCGCCGGGCAGGTCTGGGCGGATAGCACCGGGCATATTTTGGGAATGGATGAGGTCTGGCACCCCTG  
AGCAGCCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGGTTCTGAGTCT  
GTGGGATAGCTGCCATGAAGNAACCTGAAGGAGGCGCTGGCTGGTANGGGTTGATTACAGGGCTGGGAACAGCT  
CGTACACTTGCCATTCTCTGCATATACTGGNTAGTGAGGCGAGCCTGGCGCTCTTCTTTGCGCTGAGCTAAAGC  
TACATACAATGGCTTTGNGGACCTCGGCCGCGACCAAGCTT

**Fig. 15Z**

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16455.1.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAAGTTCACACCAT  
TGTCATGACACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACAGTTTA  
AAGCCTGATTAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA  
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGC  
CTCTGCTGGTCTTTCAAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCA  
CGCT

16455.2.edit

AGCGTGGTTTGCGGCCGAGGTCTCACCANAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGC  
AGAGGCATAAGGTTGCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGAT  
GACTCGTGCTTTGACCCCTACACAGNTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGG  
CTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTGAGATGTGATTATCTANATGGTGTGATG  
ACAATGGTGNGAACTACAAGATTGGAGAGAAGTGGNACCGTCAGGGGANAAAATGGACCTGCCCGGGCGGCNCG  
CTCGA

16456.1.edit

AGCGTGGTGC GGCCGAGGTCTGGCTTNCTGCTCANGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGG  
CTATGCCCTGNATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATC

16456.2.edit

TCGAGCGGCCGCCGGGCAGGTCCAATTGAAACAAACAGTTCTGAGACCGTTCTTCCACCACTGATTAAGAGTG  
GGGNGCGGGTATTAGGGATAATATTCATTTAGCCTTCTGAGCTTTCTGGGCAGACTTGGTGACCTTGCCAGCT  
CCAGCAGCCTTCTGGTCCACTGCTTTGATGACACCCACCGCAACTGTCTGTCTCATATCAGGAACAGCAAAGCG  
ACCCAAAGGTGGATAGTCTGAGAAGCTCTCAACACACATGGGCTTGCCAGGAACCATATCAACAATGGGCAGCA  
TCACCAGACTTCAAGAATTTAAGGGCCATCTTCCAGCTTTTACCAGAACGGCGATCAATCTTTCTTCAGCT  
CAGCAAACCTTGCATGCAATGTGAGCCG

**Fig. 15AA**

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16459.1.edit

TCGAGCGGCCGCGCGGGCAGGTCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCT  
GGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTTGNTAC  
TGACCCAGGGCTGACCACAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACA  
CAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACTCAGNCGGGTTTGAT  
GTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAACACCCATGGGANGNCATGC  
CTGATCTGGACTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAACAGGCTGNTTGCTGANAAAGCAAGTGA  
CCAAGGANGAAATTCANGGGTGAAANGGACTGCTCCGCTCCTGAATTCAGTCTACTCAACCTGANGNTGCA  
GACTGGTCTTGAAGGNACANGGGCCCTCTGGGCCTATTTAAGCANCTTCGGTCGCGAACACGNT

16459.2.edit

AGCGTGNGTCGCGGCCGAGGTGCTGAATAGGCACAGAGGGCACCTGTACACCTTCAGACCAGTCTGCAACCTCA  
GGCTGAGTAGCAGTGAACCTCAGGAGCGGGAGCAGTCCATTACCCCTGAAATTCCTCCTTGNCAGTGCCTTCTC  
AGCAGCAGCCTGCTCTTCTTTTCAATCTCTTCAGGATCTCTGTAGAAGTACAGATCAGGCATGACCTCCCATG  
GGTGTTCACGGGAATGGTGCCACGCATGCGCAGAACTTCCCGAGCCAGCATCCACCACATCAAACCCACTGAG  
TGAGCTCCCTTGTTGTTGCATGGGATGGGCAATGTCCACATAGCGCAGAGGAGAATCTGTGTTACACAGCGCAA  
TGGTAGGTAGGTAAACATAAGATGCCTCCGCGAGAAGCTGGTGGTCAGCCCTGGGGTCAAGTAACCACAAGAAG  
CCGTGGCTCCCGGAAGGCTGCCTGGATCTGGTTAGTGAAGGNTCCAGGAGTGAAGCGGCCAACAAATTGGAGTGG  
CTTCAGTGGCAAGCAGCAAACTTCAGCACAAGCCCTCTGGACCTGCCCGCGCGCCGCTCGA

16460.1.edit

TCGAGCGGCCGCGCGGGCAGGTCCATTTCTCCCTGACGGNCCACTTCTCTCCAATCTTGTAGTTCACACCAT  
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA  
AAGCCTGATTACAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA  
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCNTCCCCGAACCTTATGC  
CTCTGCTGGGCTTTCAGNGCCTCCACTATGATGNTGTAGGGGGGCACCTCTGGNGANGACCTCGGCCGCGACCA  
CGCT

16460.2.edit

AGCGTGGTTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA  
GAGGCATAAGGCTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG  
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC  
TTTAAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGGTCAATTCAGATGTGATTATCTAGATGGTGCCATG  
ACAATGGNGNGAACTACAAGATTGGAGAGAAGTGGNACCNGCAGGGAGAAAATGGACCTGCCCGGGCGGGCCGCT  
CGA

**Fig. 15BB**



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16461.1.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG  
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACA  
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGNTGCA  
ACCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAGTGGCACATCTTGAGGTCACGGCAGGTGC  
GGNCGGGGNTTTTGGGCTGCCCTCTGGNCTTCGGNTGTNCTCNATCTGCTGGCTCA

16461.2.edit

TCGAGCGGCCGCGCCGGGCAGGTCTCGCGGTGCGACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGG  
ACCTCCTGGCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCTGCCCCAGCCACCTCAAGAGAAGG  
CTCAGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC  
ACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGCAGNCGCAAGAACCCCGCCCGCAC  
CTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGCTGCAA  
CCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGG  
CCCAAAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCGGCGAGAACATGACCGAT  
GGATTCCAGTTCGAGTATGGCGGGCAGGGCTCCGACCCTGCCGATGGGGACCTTGGCCGGAACACGCT

16463.1.edit

AGCGTGGNNGCGGCCGAGGTATAAATATCCAGNCCATATCCTCCCTCCACACGCTGANAGATGAAGCTGTNCAA  
AGATCTCAGGGTGGANAAAACCAT

16463.2.edit

TCGAGCGGCCGCGCCGGGCAGGTCTTCAGACTTGGACTGTGTCACTGCCAGGCTTCCAGGGCTCCAACCTTGC  
AGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACCATGGTT  
TTATCCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATATTCTAC  
CTCGGCCGCGACCACGCT

*Fig. 15CC*

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16464.1.edit

CGAGCGGGCGACCGGGCAGGTNCAGACTCCAATCCANANAACCATCAAGCCAGATGTCAGAAGCTACACCATCA  
CAGGTTTACAACCAGGCACTGACTACAAGANCTACCTGCACACCTTGAATGACAATGCTCGGAGCTCCCTGTG  
GTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCTTGCT  
GGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGTACATCATCNAGTATGANAAGCCTGGGCCTCCTCCAG  
AGAAGNGGTCCCTCGGCCCGCCCTGNTGTCCANAGGNTACTATTACTGNGCCNGCAACCGGCAACCGATATC  
NATTTTGNCATTGGCCTTCAACAATAATTA

16464.2.edit

AGCGTGGTTCGCGGCCGANGTCCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAACTGTAAGGGTTC  
TTCATCAGNGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTG  
TCTGAGAGAGAGCTTCTTGNCCTGTCTTTTTCCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCA  
ATGACATAAATTGTATATTCCGGGTCCCGNTCCAGGCCAGTAATAGTANCCTCTGTGACACCAGGGCGGNGCCG  
AGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTAACCGGTAATCCTGGCACGTGGCG  
GCTGCCATGATACCAGCAAGGAATTGGGGTGTGGTGGCCAGGAAACGCAGGTTGGATGGNGCATCAATGGCAGT  
GGAGCGCGTCGATGACCACAGGGGGAGCTCCGACATTGTCAATCAAGGTG

16465.1.edit

AGCGTGGNCGCGGCCGAGGTGCAGCGCGGGCTGTGCCACCTTCTGCTCTCTGCCCAACGATAAGGAGGGTNCCT  
GCCCCAGGAGAACATTAACNTCCCCAGCTCGGCCTCTGCCGG

16465.2.edit

TCGAGCGGCCGCCCCGGGCAGGTTTTTTTTGCTGAAAGTGGNTACTTTATTGGNTGGGAAAGGGAGAAGCTGTGG  
TCAGCCCAAGAGGGAATACAGAGNCCGAAAAAGGGGAGGGCAGGTGGGCTGGAACCAGACGCAGGGCCAGGCA  
GAACTTTCTCTCCTCACTGCTCAGCCTGGTGGTGGCTGGAGCTCANAAATTGGGAGTGACACAGGACACCTTC  
CCACAGCCATTGCGGCCGCATTTTCATCTGGCCAGGACACTGGCTGTCCACCTGGCACTGGTCCCGACAGAAGCC  
CGAGCTGGGGAAAGTTAATGTTACCTGGGGGCAGGAACCCTCCTTATCATTGNGCAGAGAGCAGAAGGTGGCA  
CAGCCCGCGCTGCACCTCGGCCGCGACCACGCT

16466.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACCATAAGTCCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGAT  
TTCTTTCATTGGTCCGGNCTTCTCCTTGGGGGNCACCCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGCG  
TCCACTGGGCGCTCAGGCT

16467.2.edit

TCGAGCGGTTGCCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGA  
TTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGCGGTCCCTCGGCCCGCCCTGGT  
GTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTATTGNCCTGAAGAATAA  
TCANNAANAGCGANCCCCGTGATTGGAAGGA

**Fig. 15DD**



66/101

06\_16471.edit

AGCGTGGTCGCGGCCGAGGTCTGCTGCTTCAGCGAAGGGTTTCTGGCATAACCAATGATAAGGCTGCCAAAGAC  
TGTTCCAATACCAGCACCAGAACCAGCCACTCCTACTGTTGCAGCACCTGCACCAATAAATTTGGCAGCAGTAT  
CAATGTCTCTGCTGATTGCACTGGTCTGAAACTCCCTTTGGATTAGCTGAGACACACCATTCTGGGCCCTGATT  
TTCCTAAGATAGAACTCCAACCTCTTGGCCCTCTAGCACATAGCCATCTGCTCGGTACACTGTCCCGGCCTTGA  
AGCGATGCACGCAAGAAGCTTGCCTGCTGGAAGTCTCCTCCAGGAGACTGCTGATTTTGGCATTCTTTTCC  
TTTCATCATATTTCTTCTGAATTTTTTAGATCGTTTTTGTAAAAATCTTCTTCTCCTCAGGAGTCAGCTTG  
GCCCCGCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGG  
AATTTCTCCTGGGGCTCAGAGTGGTGTACTCGTAAAAACAAGGATCATCGATGGTGNCTACAATGCATCTAATAA  
CGAGCTGGGTGCGACCCAAAGAACCTGGNGAANAATGGATCGNCTCATCGACAGGACACCGTACCCGACAGGG  
GNACGANTCCCACTATGCGCTTGGCCCTGGGCCGCAANAAGGAAAACTGCCCGGGCGGCNTCGAAAGCCCAA  
TTNTGGAAAAATCCATCACACTGGNGGCCNGTCGAGCATGCATNTANAGGGGCCATTCCCCCTNANN

07\_16472.edit

TCGAGCGGCCGCGCGGGCAGGTCCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAG  
ACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAACTGGTACATCAGCAAGAACCCCAA  
GGACAAGAGGCATGTCTGGTTGCGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCG  
ACCCTGCCGATGTGGACCTCGGCCGCGACCACGCT

08\_16472.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG  
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTCTTGCTGATGTACCAGTTCTTCTGGGCCACA  
CTGGGCTGAGTGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGTTGCA  
GCCTTGGTTGGGGACCTGCCCGGGCGGCCGCTCGA

09\_16473.edit

TCGAGCGGCCGCGCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT  
TACCGGTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG  
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT  
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCCAA  
TCTTCATGGACCAGAGATCTTGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTCACCCACCCTGGGTATG  
ACACTGGAAATGGTATTAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAG  
GAACATGGNTTTAGGCGGACCACACCGCCACAACGGCCACCCCATAGGCATAGGCCAAGACCATAACCGCC  
GAATGTAGGACAAGAAGCTNTNTNANCANACCATNTNATGGGCCCATTCAGGACACTTCTGAGTACATCAT  
TTATGNCATCTGTGGCACTTGATGAAAACCTTACAGTTCAGGGTTCTGGAACCTTTACCAGGCCTNTTACAGG  
ACTNGGCCGACNCCTTAAGCCNATTNACCCTGGGGCGTTCTANGGTCCCACTCGNNCACTGGNGAAAATGGC  
TACTGTN

**Fig. 15FF**

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11\_16474.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC  
TAGGAGGGCTTGCTGTGCGGAGGGCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC  
GAGGTTGTGGTGTCTGNAACTCCNAGGACANGAGGGCTAAATTCATGAAGTTTGTGGATGGCCTGATGATC  
CACAATCGGAGACCCTGTAACTACTACCGTCTNACCNCCTGCTGTNCNCCCCCNTTTCTGCTNAANACATNGG  
GNTNNTNCTTGNCNTCCTTGGGTNGAANATNNAATNGCCTNCCCNTTCTANCNCTACTNGNTCCANANTTGG  
CCTTTAANAATCCNCCTTGCCCTNNNCACTGTTCANNTNTTNNTCGTAAACCCTATNANTTNNATTANATNN  
TNNNNNCTCACCCCTCCTCATTNANCCNATANGCTNNAANTCCTNANNCTCCCNCCNNTNCTCCTCCT  
ACTNANTNCTTCTNCCCATTACNNAGCTCTTTCNTTAAANATAATGNNGCCNNGCTCTNCATNTCTACNATNT  
GNNNAATNCCCCNCCCCNANCGNNTTTTGGACCTNNAACCTCCTTTCCTCTCCCTNCNNAATTCNNAN  
TTCNCNTTCCNNTTTTGGNTNNTCCCATNCTTCCANNCTTCANTCTANCNCNCTNCAACTTATTTTCT  
NTCATCCCTTNTTCTTTACANNCCCCCTNNTCTACTCNCNNTTNCATTANATTTGAACTNCCACNCTANTT  
NCCTCCTCTACNNTTTATTTTNCGNTCCTCTACNTAATANTTTAATNANTTNTCN

12\_16474.edit

TCGAGCGGCCGCGCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGCAGGCG  
GCTCTGGCTTCCACCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC  
ACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCCAGGCAGCATGATCTTACCTTGAT  
GCCAGCACACCCTGTCTGAGCAACAGTGGCGCACAAAGCAGTGTCAACGTAGTAAGTTAACAGGGTCTCCGCT  
GTGGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCTCGGAGTTTCCAGACACCACAACT  
CGCAGCCTTTGGCCCCACTCTCCATGATGAACCGCAGCACACCATAGCAGGCCCTCCGCACAAGCAAGCCCTCC  
TAAGAATTTGTAACGCANANACTCTGCTGGCAATGGCACACAACTCTAGTGGACCTCGGNCGCGACCACGC

13\_16475.edit

TCGAGCGGCCGCGCGGGCAGGTCTGGTCCAGGATAGCCTGCGAGTCTCCTACTGCTACTCCAGACTTGACATC  
ATATGAATCATACTGGGGAGAATAGTTCTGAGGACCAGTAGGGCATGATTCACAGATTCCAGGGGGCCAGGAG  
AACCAGGGGACCCTGGTTGTCTGGAATACCAGGGTCACCATTTCTCCAGGAATACCAGGAGGGCCTGGATCT  
CCCTTGGGGCCTTGAGGTCTTGACCATTAGGAGGGCGAGTAGGAGCAGTTGGAGGCTGTGGGCAAACTGCACA  
ACATTCTCCAAATGGAATTTCTGGGTGGGGCAGTCTAATTCCTTGATCCGTACATATTATGTCATCGCAGAGA  
ACGGATCCTGAGTCACAGACACATATTTGGCATGGTTCTGGCTTCCAGACATCTCTATCCGNCATAGGACTGAC  
CAAGATGGGAACATCCTCTTCAACAAGCTTNCCTGTTGTGCCAAAAATAATAGTGGGATGAAGCAGACCGAGAA  
GTANCCAGCTCCCCTTTTGCACAAAGCNTCATCATGTCTAAATATCAGACATGAGACTTCTTTGGGCAAAAAA  
GGAGAAAAAGAAAAAGCAGTTCAAAGTANCCNCCATCAAGTTGGTTCTTGCCNNTTCAGCACCCGGGCCCCGT  
TATAAACACCTNGGGCCGGACCCCCCTT

**Fig. 15GG**

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14\_16475.edit

AGCGTGGTCGCGGCCGAGGTGTTTTATGACGGGCCCGGTGCTGAAGGGCAGGGAACAACCTTGATGGTGCTACTT  
TGAAGTGTCTTTCTTTCTCTTTTGCACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTTGTGCA  
AAAGGGGAGCTGGCTACTTCTCGCTCTGCTTCATCCCACTATTATTTGGCACAACAGGAAGCTGTTGAAGGAG  
GATGTTCCCATCTTGGTCAGTCCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTGTCTGT  
GACTCAGGATCCGTTCTCTGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCCAACCCAGAAATTCC  
ATTTGGAGAATGTTGTGCAGTTTGCCACAGCCTCCAAGTCTCTACTCGCCCTCCTAATGGTCAAGGACCTC  
AAGGCCCCAAGGGAGATCCAGGCCCTCTGGTATTCTGGGAGAAATGGTGACCCTGGTATTCCAGGACAACCA  
GGGTCCCTGGTTCTCTGGCCCCCTGGAATCNGGNGAATCATGCCCTACTGGTCTCAAATATTCTCCCAN  
ATGATTCATATGATGTCAAGTCTGGGATAGCNAGTANGGANGGACTCGCAGGCTATTCTGGACCANACCTGCC  
GGGGGGCGTTGAAAGCCCCAATCTGCANANNTNCNTTCACTGGCGGCCGTGAGCTGCTTTAAAGGGCCA  
TTCNCCTTTAGNGNGGGGGANTACAATTACTNGCGGGCGTTTTANANCGCGNGNCTGGGAAAT

15\_16476.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGE  
TCATGCTCTCGCCGAACCAGACATGCCTCTTGCTTGGGGTCTTGCTGATGTACCAGTTCTTCTGGGCCACA  
CTGGGCTGAGTGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGTTGCA  
GCCTTGGTTGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGTGC  
GGGCGGGGTTCTTGCGGCTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCTCAGGCTCTTGAGGGTGGTE  
TCCACCTCGAGGTACGGTCACGAACCACATTGGCATCATCAGCCGGTAGTAGCGGCCACCATCGTGAGCCTT  
CTCTTGANGTGGCTGGGGCAGGAAGTGAAGTCGAACCAGCGCTGGGAGGACCAGGGGGACCAANAGGTCCAGE  
AAGGGCCCGGGGGGACCAACAGGACCAGCATCACCAGTGCGACCCGCGAGAACCTGCCCGGCCGNCCGCTCE  
AA

16\_16476.edit

TCGAGCGNCGCCCGGGCAGGTCTCGCGGTGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGE  
ACCTCCTGGTCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGE  
CTCACGATGGTGGCCGCTACTACGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC  
ACCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCAGAGGGCAGCCGCAAGAACCCCGCCGCAC  
CTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCA  
ACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTE  
GCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGA  
TGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCACCCCTGCCGATGTGGACCTCCGGCCGCGACCAACCTT

**Fig. 15HH**

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17\_16477.edit

TNGAGCGGCCGCCGGGCAGGNTGNNAACGCTGGTCTGCTGGTCTCTGGCAAGGCTGGTGAAGATGGTCAC  
CCTGGAAAAACCGGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAACTCC  
TGGACTTCTGGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCCGGTGCTCCTG  
GTGTGAAGGGTGAACCTGGTGCCCTGGTGAATGGAATCCAGGTCAAACAGGAGCCCGTGGGCTTCTGGT  
GAGAGAGGACCGTGTTGGTGCCCTGGCCANACCTCGGCCGCGACCACGCTAAGCCCGAATTTCCAGCACACT  
GGNGGCCGTTACTANTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGNGTGA  
AATTGTTATCCGCTCACAATTTACACANCATACGAAGCCGGAAAGCATAAAGTGTAAGCCTTGGGGTGCTAA  
TGAGTGAGCTAACTCNCATTAATTTGCGTTGCGCTCACTGCCGCTTTTCCANNNGGAAACNTGGCNTNGCC  
NGCTTG CNTTAANTGAAATCCGCCNACCCCCGGGGAAAAGNCGGTTTGCGTATTGGGGCNCCTTTTCCCTTTC  
CTCGGNTTACTTGANTTANTGGGCTTTGGNCGNTTCGGGTTGNGGCGANCNGGTTCAACNTCACNCCAAAGNG  
GNAANACGGTTTTCCANAATCCGGGGGNTANCCCAANGNAAAACATNNGNCNAANGGGCT

18\_16477.edit

AGCGTGGTTNGCGGCCGAGGTCTGGGCCAGGGGCACCAACACGTCCTCTCTCACCAGGAAGCCACGGGCTCCT  
GTTTGACCTGGAGTTCCATTTTACCAGGGGCACAGGTTTACCCTTCACACCAGGAGCACGGGGCTGTCCCTT  
CAATCCATNCAGACATTGTGNCCTTAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCCAGGAAACACCGA  
GCACCTGTGGTCCAACACTCCTCTCTCACCAGGTGTCGGGTTTTCCAGGGTGACCATCTTACCAGCCTT  
GCCAGGAGGACCAGCAGGACCAGCGTTACCAACCTGCCGGGGCGGCGCTCGA

21\_16479.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT  
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA  
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA  
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTTTCGGAACCTTATGCC  
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCAG  
CT

22\_16479.edit

AGCGTGGTGCAGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGAGGCACTGAAAGACCAGCA  
GAGGCATAAGGTTCCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG  
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC  
TTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAAGATGTGATTATCTAGATGGTGCCATG  
ACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCCGGCCGC  
TCGA

**Fig. 15II**

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24\_16480.edit

TCGAGCGNNCGCCCGGGCAGGTCCAGTAGTGCCTTCGGGACTGGGTTACCCCCAGGTCTGCGGCAGTTGTCAC  
AGCGCCAGCCCCGCTGGCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGCCACTGTTCT  
CCTACGTGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCTCCTTTTCCGTT  
CCCAAGACATGTGCAGCTCATTTGGCTGGCTCTATAGTTTGGGAAAGTTTGTGAAACTGTGCCACTGACCTT  
TACTTCCTCCTTCTCTACTGGAGCTTTCGTACCTTCCACTTCTGCTGTTGGTAAATGGTGGATCTTCTATCAA  
TTTCATTGACAGTACCCACTTCTCCAAACATCCAGGAAAATAGTGATTTAGAGCGATTAGGAGAACCAAATT  
ATGGGGCAGAAATAAGGGGCTTTTCCACAGGTTTTCTTTGGAGGAAGATTTAGTGGTGACTTTAAAAGAATA  
CTCAACAGTGTCTTATCCCATAGCAAAAGAAGAAACNGTAAATGATGGAANGCTTCTGGAGATGCCNNCATT  
TAAGGGACNCCCAGAACTTCACCATCTACAGGACCTACTTCAGTTTACANNAAGNCACATANTCTGACTCANAA  
AGGACCCAGTAGCNCCATGGNCAGCACTTTNAGCCTTTCCCTGGGGAAAANNTTACNTTCTTAAANCCTNGG  
CCNNGACCCCTTAAGNCCAAATTNTGGAAGAAANTTCNTNCNNCTGGGGGGCNGTTCNACATGCNTTTNAAGGG  
CCCAATTNCCCCNT

25\_16481.edit

TCGAGCGGCCGCCCCGGGCAGGTGTGCGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA  
TTGCTCTCCCACTCCACGGCGATGTGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGACCTGGTTCTT  
GGTCATCTCCTCCCGGATGGGGGCAGGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTGGCTTTGGAGATGG  
TTTTCTCGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTACTCCTTGCCATTGAGCCAGTCTGG  
TGCAGGACGGTGAGGACGCTGACCACACGGTACGTGCTGTTGTACTGCTCCTCCCGCGGCTTTGTCTTGGCATT  
ATGCACCTCCACGCCGTCCACGTACAGTTGAACCTTGACCTCAGGGTCTTCGTGGCTCACGTCCACCACCACGC  
ATGTAACCTCAGACCTCGGCCGCGACACGCT

26\_16481.edit

AGCGTGGTGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGACGTGAGCCACGAAGACCCTGAGGTCAAGT  
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCACG  
TACCGTGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTC  
CAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAAGCCCCGAGAACCACAGGTG  
TACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTA  
TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAACAAGACCACGCCTCCCGTGC  
TGGACTCCGACACCTGCCCGGGCGGCCGCTCGA

27\_16482.edit

TCGAGCGGCCGCCCCGGGCAGGTTGAATGGCTCCTCGCTGACCACCCCGGTGCTGGTGGTGGGTACAGAGCTCCG  
ATGGGTGAAACCATTGACATAGAGACTGTCCCTGTCCAGGGTGTAGGGGCCAGCTCAGTGATGCCGTGGGTCA  
GCTGGCTCAGCTTCCAGTACAGCCGCTCTCTGTCCAGTCCAGGGCTTTTGGGGTCAGGACGATGGGTGCAGACA  
GCATCCACTCTGGTGGCTGCCCCATCCTTCTCAGGCTGAGCAAGGTGAGTCTGCAACCAGAGTACAGAGAGCT  
GACACTGGTGTCTTGAACAAGGGCATAAGCAGACCCTGAAGGACACCTCGGCCGCGACACGCT

**Fig. 15JJ**



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28\_16482.edit

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTCTGCTCTCTG  
TACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCAC  
CCATCGTCCTGACCCCAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACG  
GCATCACTGAGCTGGGCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCT  
GTACCCACCACCAGCACCGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

29\_16483.edit

AGCGTGGTCGCGGCCGAGGTGTCCTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAACTGTAAGGGTTCT  
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCATGAGATGGTTGT  
CTGAGAGAGAGCTTCTTGTCTACATTCGGCGGGTATGGTCTTGGCCTATGCCCTATGGGGTGGCGTTGTGG  
GCGGTGTGGTCCGCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACTGGGTGCTGACCAGAAAGTG  
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGTCTTTGAACTGTGGAAGG  
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAAGTTGGGGAAGCTCGTCTGTCTTTT  
TCCTTCCAATCAGGGGCTCGCTCTTCTGATTATCTTCAGGGCAATGACATAAATTGTATATTCGGTCCCGGTT  
CCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGGCCGAGGGACCCTTCTNTTGAAGAGACCAGCTTC  
TCATACTTGATGATGAGNCCGGTAATCCTGGCAGCTGGNGGTTGCATGATNCCACCAAGGAAATNGGNGGGGN  
GGACCTGCCCGGGCGGCTTCNAAAGCCCAATTCACACACTTGGNGGCCGTACTATGGATCCCACTCNGTCCA  
ACTTGGNGGAATATGGCATAACTTTT

31\_16484.edit

TCGAGCGGCCGCGGCCGAGGTGTCCTTGACCTTTTCAGCAAGTGGGAAGGTGTAATCCGTCTCCACAGACAAGGC  
CAGGACTCGTTTGTACCGTTGATGATAGAATGGGGTACTGATGCAACAGTTGGGTAGCCAATCTGCAGACAGA  
CACTGGCAACATTGCGGACACCCTCCAGGAAGCGAGAATGCAGAGTTTCTCTGTGATATCAAGCACTTCAGGG  
TTGTAGATGCTGCCATTGTGGAACACCTGCTGGATGACCAGCCCAAAGGAGAAGGGGGAGATGTTGAGCATGTT  
CAGCAGCGTGGCTTCGCTGGCTCCACTTTGTCTCCAGTCTTGATCAGACCTCGGCCGCGACCACGCT

37\_16487.edit

AGCGTGGTCGCGGCCGAGGTCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT  
CCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA  
GTTGAGCCCAAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTC  
AGTCTTCTCTTCCCCGCATCCCCCTTCAAACCTGCCCGGGCGGCCGCTCG

**Fig. 15KK**

72/101

38\_16487.edit

CGAGCGGCCGCCCGGGCAGGTTTGAAGGGGGATGCGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTCA  
GGTGTCTGGGCACGGTGGGCATGTGTGAGTTTGTCAAGATTGGGCTCAACTCTCTTGTCCACCTTGGTGT  
GCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGGTGCCGAAGTTGCTGGAGGGCAGGTCACCAAGCTGC  
TGAGGAGTAGAGTCTGAGGACTGTAGGACAGACCTCGGCCGCGACCACGCT

39\_16488.edit

NGGNNGGTCCGNCNGNCAGGACCACTCNTCTTCGAAATA

41\_16489.edit

AGCGTGGTCGCGGCCGAGGTCCTCACTTGCCTCCTGCAAAGCACCGATAGCTGCGCTCTGGAAGCGCAGATCTG  
TTTAAAGTCTGAGCAATTTCTCGCACCAGACGCTGGAAGGGAAGTTTGCGAATCAGAAGTTCAGTGGACTTC  
TGATAACGTCTAATTTACGGAGCGCCACAGTACCAGGACCTGCCCGGGCGGCCGCTCGA

42\_16489.edit

TCGAGCGGCCGCCCGGGCAGGTCCACATCGGCAGGGTGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC  
TTCTGATTGCAAACCTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCTGCGCTTC  
CAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGACCTCGGCCGCGACCACGCT

45\_16491.edit

TCGAGCGGCCGCCCGGGCAGGTCCACATCGGCAGGGTGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC  
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTTGGGGTCTTGCTGATGTACCAGTCTTCTGGGCCA  
CACTGGGCTGAGTGGGTACAGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG  
CAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGT  
GCGGGCGGGGTTCTTGACCTCGGCCGCGACCACGCT

***Fig. 15LL***

73/101

46\_16491.edit

GTGGGNTTGAACCCNTTTNANCTCCGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGA  
ATTCGGCTTAGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCGCACCTGCCGTGACCTCAAGATGTGCCACTC  
TGA CTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCA  
ACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCAGAGAAGTGGTACATCAGCAAG  
AACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCA  
GGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

47\_16492.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC  
AGGAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC  
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATT  
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTTACGGACAACAGCATTAG  
TGTCAGTGGCTGCCTTCAAGTTCCTGTTACTGGTTACAGAGTAACCACTCCCAAAAATGGACCAGGAC  
CAACAAAACTAAACTGCAGGTCCAGATCAACAGAAATGACTATTGAAGGCTTGACGCCACAGTGGAGTAT  
GTGGTTAAGTGTCTATGCTCAGAATCAAGCGGAGAGAAGTCAGCCTCTGGTTCAGACTGNAAGTAACCAACAT  
TGATCGCCTAAAGGACTGGCATTCACTGATGNGGATGCCGATTCCATCAAAATTGNTTGGGAAAACCCACAGGG  
GCAAGTTTNCANGTCNAGGNGGACCTACTCGAGCCCTGAGGATGGAATCCTTGACTNNTCCTTNNCTGATGGG  
GAAAAAAACCTTNAAACTTGAAGGACCTGCCCGGGCGGCCGTNCAAAACCAATTCCACCCCTTGGGGGCG  
TTCTATGGGNCCCACTCGGACCAAACTTGGGGTAAN

48\_16492.edit

TCGAGCGGCCGCCCGGGCAGGTCTTGACGCTCTGCAGTGTCTTCTTACCATCAGGTGCAGGGAATAGCTCAT  
GGATTCCATCCTCAGGGCTCGAGTAGGTACCCCTGTACCTGGAACTTGCCCCTGTGGGCTTTCCAAGCAATT  
TTGATGGAATCGGCATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC  
CAGAGGCTGACTCTCTCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT  
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTTGTGGTCTGGTCCATTTTTGGGAGTGGTG  
GTTACTCTGTAACAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGCTCTGAACATCGGT  
CACTTGATCTGGGATGGTTTGTCAATTTCTGTTGGTAATTAATGGAAATTGGCTTGCTGCTTGCGGGGCTTG  
TCTCCACGGCCAGTGACAGCATACAGTGATGGTATAATCAACTCCAGGTTTAAGCCGCTGATGGTAGCTGAA  
ACTTTGCTCCAGGCACAAGTGAACCTCTGACAGGGCTATTTCTNCTGTTCTCGTAAGTGATCCTGTAATATC  
TCACTGGGACAGCAGGANGCATTCCAAACTTCGGGCGNGACCCCTAAGCCGAATTNTGCAATATNCATCACA  
CTGGCGGGGCGCTCGANCATTCAATAAAGGCCCAATCNCCTATAGGGAGTNTANTACAATTNG

**Fig. 15MM**

74/101

49\_16493.edit

TCGAGCGGCCGCCCGGGCAGGTCACTTTTGGTTTTTGGTCATGTTGGTTGGTCAAAGATAAAAACTAAGTTTG  
AGAGATGAATGCAAAGGAAAAAATATTTTCCAAAGTCCATGTGAAATTGTCTCCCATTTTTTGGCTTTTGAG  
GGGGTTCAAGTTTGGGTTGCTTGTCTGTTTCCGGGTTGGGGGAAAGTTGGTTGGGTGGGAGGGAGCCAGGTTGG  
GATGGAGGGAGTTTACAGGAAGCAGACAGGGCCAACGTCG

55\_16496.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA  
GAGGCATAAGGTTGCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG  
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC  
TTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTATCTAGATGGTGCCATGA  
CAATGGTGTGAACATAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTC  
GA

56\_16496.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT  
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACAGTTTA  
AAGCCTGATTAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA  
GTCATCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCC  
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCAG  
CT

59\_16498.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCATAAGTCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGAT  
TTCTTTTATTGGTCCGGTCTTCTCCTTGGGGGTCAACCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGTG  
TCCACTGGGCGCTCAGGCTTGTGGGTGTGACCTGAGTGAACCTTCAGGTCAAGTTGGTGCAGGAATAGTGGTTACT  
GCAGTCTGAACCAGAGGCTGACTCTCTCCGCTTGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGG  
CTGCAAGCCTTCAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTTGTGGTCTGCTGCTGCT  
TGGGAGTGGTGGTTACTCTGTAACCAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGTCC  
TGAACATCGGTCACTTGATCTGGGATGGTTTGNCAATTTCTGTTCCGTAATTAATGGAAATTGGCTTGCTGCT  
TGCGGGGCTGTCTCCACGGCCAGTGACAGCATACAGNGATGGNATNATCAACTCCAAGTTTAAGGCCCTGAT  
GGTAACCTTTAACTTGCTCCAGCCAGNGAAGTTCCGGACAGGGTATTTCTTCTGGTTTTCCGAAAGNGANCCT  
GGAATNNTCTCCTTGGANCAGAAGGANCNTCCAAAACCTGGGCCGGAACCCCTT

**Fig. 15NN**

75/101

60\_16473.edit

AGCGTGGTCGCGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCCCTGAACTGTAAGGGTTCT  
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGCTGGAATGGGGCCCATGAGATGGTTGT  
CTGAGAGAGAGCTTCTTGTCCTACATTCGGCGGGTATGGTCTTGGCCTATGCCCTATGGGGGTGGCCGTTGTGG  
GCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGTTGCTGACCAGAAGTG  
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTGAACTGTGGAAGG  
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGTCTGTCTTTT  
TCCTTCCAATCAGGGGCTCGCTCTTCTGATTATCTTCAGGGCAATGACATAAATTGTATATTGGTTCCCGGT  
TCCAGGCCAGTAATAGTAGCCTCTTGACACCAGGCGGGGCCANGGACCACTTCTCTGGGANGAGACCCAGC  
TTCTCATACTTGATGATGTAACCCGGTAATCCTGCACGTGGCGGCTGNCATGATACCANCAAGGAATTGGGTGN  
GGNGGACCTGCCCGGGCGGCCCTCNA

60\_16498.edit

AGCGTGGTCGCGGCCGAGGTCGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC  
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCCTAAAC  
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGAAGCAGCAAGCCAATT  
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTGAGGACAACAGCATTAG  
TGTAAGTGCGTGCCTTCAAGTTCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGAC  
CAACAAAACTAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGACGCCACAGTGGAGTAT  
GTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTGAGACTGCAGTAACCACTATTCC  
TGCACCAACTGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCCGCCAGTGGACACCACCCAATGTTCC  
ACTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCCGGACCCATGAAAGAAATCAACCTTGCTCCT  
GACAGCTCATCCGNGGGTGTATCAGGACTTATGGGGGACTGCCCGGCGNGGCCGNTCGAAANCGAATTNTGAAA  
TTTCCTTCNCACTGGGNGGCCGNTTCGAGCTTNCTNTANANGGCCCAATTCNCCTNTAGNGGGTCGTN

61\_16499.edit

AGCGTGGTCGCGGCCGAGGTCNAGGA

62\_16483.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT  
TACCGGTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTG  
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT  
CAGAAGAGCGAGCCCCGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCCAA  
TCTTCATGGACCAGAGATCTTGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTACCCACCCTGGGTATG  
ACACTGGAAATGGTATTGAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAG  
GAACATGGTTTTAGGCGGACCACACCGCCACAACGGGCACCCCATAGGNATAGGCCAAGACCATAACCCGC  
CGAATGTAGGACAAGAAGCTCTNTCTCAACAACCATCTCATGGGCCCATTCAGGACACTTCTGAGTACATCA  
TTTCATGTCATCCTGGTGGGCACTTGATGAANAACCTTACAGTTCAGGGTCTGGAACCTTCTACCAGNGCCA  
CTTCTGACAGGANCTTGGGCGNGACCACCT

**Fig. 1500**

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63\_16500.edit

AGCGTGGTCGCGGCCGAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCATTG  
TCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAA  
GCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGAGT  
CATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCGAACCTTATGCCTC  
TGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTGCCCCGGCGGCCCGCT  
CGA

64\_16493.edit

AGCGTGGTCGCGGCCGAGGTGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAA  
CTCCCTCCATCCCAACCTGGCTCCCTCCACCCAACCAACTTCCCCCAACCCGGAACAGACAAGCAACCCA  
AACTGAACCCCTCAAAGCCAAAAAATGGGAGACAATTTACATGGACTTTGGAAAAATTTTTTCTTTG  
CATTATCTCTCAAACCTTAGTTTTATCTTTGACCAACCGAACATGACCAAAACCAAAAGTGACCTGCCCGGG  
CGGCCGCTCGA

64\_16500.edit

TCGAGCGGCCGCCCCGGGCAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAG  
CAGAGGCATAAGGTTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGA  
TGACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAG  
GCTTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTATCTAGATGGTGCCAT  
GACAATGGTGTGAACCTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTCGGCCGCGACCACG  
CT

***Fig. 15PP***

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16501.edit

TCGAGCGGCCGCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACCTCACCATCAACAACC  
TGCGGTATGAGGAGAACATGCAGCACCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTTCAGGGCCTG  
CTCAGGTCCCTGTTCAAGAGCACCAGTGTGGCCCTCTGTAAGTCTGGCTGCAGACTGACTTTGCTCAGACCTGA  
GAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCTCCGCTTGATCCCACTGGTNCCTGGACTGGACA  
NANAGCGGCTATACTTGGGAGCTGANCCNAACCTTTGGCGGNGACNCCNCTT

16501.2.edit

GAGGACTGGCTCAGCTCCAGTATAGCCGCTCTCTGTCCAGTCCAGGACCAGTGGGATCAAGGCGGAGGGTGCA  
GATGGCGTCCACTCCAGTGGCTGCCCCATGTTTCTCAAGTCTGAGCAAAGNCAGTCTGCAGCCAGAGTACAGAG  
GGCCAACACTGGTGCTCTTGAACAGGGACCTGAGCAGGCCCTGAAGGACCCTCTCGTGGTGTTGAACCTTCCTG  
GAGCCAGGGTGCTGCATGTTCTCCTCATACCGCAGGTTGTTGATGGTGAAGTTCAGTGTGAATGGCTCCTCGCT  
GACCACCC

16502.1.edit

AGCGTGGTCGCGGCCGAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTA  
CCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTC  
ACAGAGGCTACTATTACTGGCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCA  
GAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCCTCCACACCCCAATC  
TTCATGGACCANANANCTTGGATNGTCCTTTCACNGGTTNAAAAAACCTTTTCGCCCCCCCACCTTGGGGATT  
AACCTTGGGAAANGGGGATTTNACCNTTCC

16502.2.edit

TCGAGCGGCCGCCGGGCAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCCTGAACTGTAAGGGTT  
CTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCATGAGATGGTT  
GTCTGAGAGAGAGCTTCTTGTCCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCGTTGT  
GGGCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGTTGCTGACCAGAAG  
TGCCAGGAAGCTGAATACCATTTCCAGTGTATACCCAGGGNGGGTGACCAAAGGGGGTNTTTNGACCTGGNG  
AAAGGAACCATCCAAAANCTCTGNCCCATG

**Fig. 15QQ**

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16503.1.edit

AGCGTGGNCGCGGCCGAGGTCTGAGGATGTAACTCTTCCCAGGGGAAGGCTGAAGTGCTGACCATGGTGCTAC  
TGGGTCTTCTGAGTCAGATATGTGACTGATGNGAACTGAAGTAGGTACTGTAGATGGTGAAGCTGGGTGTCC  
CTAAATGCTGCATCTCCAGAGCCTTCCATCATTACCGTTTCTTCTTTTGCTATGGGATGAGACACTGTTGAGTA  
TTCTCTAAAGTCACCACTGAAATCTTCTCCAAAGGAAAACCTGTGGAAAAGCCCCATTATTTCTGCCCCATAAT  
TTGGTTCTCCTAATCNCCTGAAATCACTATTTCCCTGGAANGTTTGGGAAAAANNGGCNACCTGNCANTGGA  
AANTGGATANAAAGATCCCACCATTTTACCCAACNAGCAGAAAGTGGGAANGGTACCGAAAAGCTCCAAGTAAN  
AAAAAGGAGGGAAGTAAAGGTCAAGTGGGCACCAAGTTTCAAACAACTTTCCCCAACTATANAACCCA

16503.2.edit

AAGCGGCCGCGCCGGGCAGGNNCAGNAGTGCCTTCGGGACTGGGNTCACCCCAGGTCTGCGGCAGTTGTCACAG  
CGCCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGCCACTGTTCTCC  
TACGTGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCTCCTTTTCCGTTCC  
CAAGACATGTGCAGCTCATTGGCTGGCTCTATAGTTTGGGGAAAGTTTGTGAAACTGTGCCACTGACCTTTA  
CTTCTCCTTCTCTACTGGAGCTTTCGTACCTTCCACTTCTGCTGNTGGNAAAAAGGGNGGAACNTCTTATCA  
ATTTCAATGGACAGTANCCCNCTTCTNCCCAAACATNCAAGGGAAAATATTGATTNCNAGAGCGGATTAAGG  
AACAACCCNAATTATGGGGGCCAGAAATAAAGGGGGCTTTTCCACAGGTNTTTTCT

16504.1.edit

TCGAGCGGCCGCGCCGGGCAGGTCTGCAGGCTATTGTAAGTGTTCTGAGCACATATGAGATAACCTGGGCCAAGC  
TATGATGTTGATACGTTAGGTGTATTAAATGCACTTTTGAAGTCCATCTCAGTGGATGACAGCCTTCTCACTG  
ACAGCAGAGATCTTCTCACTGTGCCAGTGGGCAGGAGAAAGAGCATGCTGCGACTGGACCTCGGCCGCGACCA  
CGCT

16504.2.edit

AGCGTGGTCCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTCTCCTGCCCACTGGCACAGTGAGGAAGATCTCTG  
CTGTCACTGAGAAGGCTGTCACTGAGATGGCAGTCAAAAGTGCAATTAATACACCTAACGTATCGAACAT  
CATAGCTTGGCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCGGGCGGCCGC  
TCGA

**Fig. 15RR**



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16505.1.edit

CGAGCGGCCGCCCGGGCAGGTCCAGACTCCAATCCAGAGAACCACCAAGCCAGATGTCAGAAGCTACACCATCA  
CAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTG  
GTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCT  
GGTATCATGGCAGCGGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCA  
GAGAAGTGGTCCCTCGGCCCGCCCTGGTGNCACAGAAGCTACTATTACTGGCCTGGAACCGGGAACCGAATAT  
ACAATTTATGTCATTGCCCTGAAGAATAATCANAAGAGCGAGCCCCTGATTGGAAGG

16505.2.edit

AGCGTGGTCGCGGCCGAGGTCCCTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCCCTGAACTGTAAGGGTTCT  
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCATGAGATGGTTGT  
CTGAGAGAGAGCTTCTTGCTCTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAA  
TGACATAAATTGTATATTCGGTTCCCGGTTCCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGCCGA  
GGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTANCCGGTAATCCTGGCACCGTGGCG  
GCTGCCATGATACCAGCAAGGAATTGGGTGTGGTGGCCAAGAAACGCAGGTTGGATGGTGCATCAATGGCAGTG  
GAGGCGTCGATNACCACAGGGGAGCTCCGANCATTGTCAATTCAAGGTGGACAGGTAGAATCTTGTAAATCAGGTG  
CCTGGTTTGTAACCTG

16506.1.edit

TCGAGCGGCCGCCCGGGCAGGTTTCGTGACCGTGACCTCGAGGTGGACACCACCCCTCAAGAGCCTGAGCCAGCA  
GATCGAGAACATCCGGAGCCAGAGGGCAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCC  
ACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTC  
TGCAACATGGAGACTGGTGAGACCTGCGTGATCCCACTCAGCCAGTGTGGCCAGAAGAACTGGTACATCAG  
CAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCGGCGAAAGCATGACCGATGGATTCCAGTTCGAGTATGGCG  
GCCAGGGCTCCGACCCTGCCGATGTGGACCTCGGCCGCGACACGCTAAGCCCGAATTCAGCACACTGGCGGC  
CGTTACTAGTGGGATCCGAGCTTCGGTACCAAGCTTGGCGTAATCATGGGNCATAGCTGTTTCCTGNGTGAAAA  
TGGTATTCCGCTTCACAATTTCCAC

16506.2.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG  
TCATGCTCTCGCCGAACCAGACATGCCTCTTGCTTGGGGTCTTGCTGATGTACCAGTCTTCTGGGCCACA  
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA  
GCCTTGTTGGGGTCAATCCAGTACTCTCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGTGC  
GGGCGGGGTTCTTGCGGTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCTCAAGCTCTTGAGGGTGGT  
GTCCACCTCGAGGTACGGTCACGAAACCTGCCGGGCGGCCGCTCGA

**Fig. 15SS**

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16507.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAA  
GAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGA  
CTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAGAAGAACTGGTACATCAGCAAGAACCCCAAG  
GACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGA  
CCCTGCCGATGTGGACCTGCCCGNGCCGNGCCGCTCGAAAAGCCNAATTTCCAGNCACACTTGGCCGGCCGTT  
ACTACTG

16507.2.edit

TCGAGCGGCCGCGCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC  
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA  
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG  
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGT  
GCGGGCGGGGTTCTTGACCTCGGCCGCGACCACGCT

16508.1.edit

CGAGCGGCCGCGCCGGGCAGGTCCCCCCCCCTTT  
TTTTTTTTTTTTTTTTTT

16508.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGCATTCTTCGACTTCTCTCCAGCCGAGCTTCCAGAACATCACATATCAC  
TGCAAAAATAGCATTGCATACATGGATCAGGCCAGTGGAATGTAAAGAAGGCCCTGAAGCTGATGGGGTCAAA  
TGAAGGTGAATTCAAGGCTGAAGGAAATAGCAAATTCACCTACACAGTTCTGGAGGATGGTTGCACGAAACACA  
CTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAACACGCAAGGCTGTGAGACTACCTATTGTAGATATTGCA  
CCCTATGACATTGGTGGTCTGATCAAGAATTTGGTGTGGACGTTGGCCCTGTTTGCTTTTATAAACCAAACCT  
CTATCTGAAATCCCAACAAAAAATTTAACTCCATATGTGNTCCTCTTGTTCTAATCTTGGCAACCAAGTGCAA  
GTGACCGACAAAATCCAGTTATTTATTTCCAAAATGTTTGGAAACAGTATAATTTGACAAAGAAAAAGGATA  
CTTCTCTTTTTTTGGCTGGTCCACCAAATACAATTCAAAAGGCTTTTTGGTTTTATTTTTTANCCAATTCAA  
TTTCAAATGTCTCAATGGNGCTTATAATAAAATAAACTTTCACCCTNTTTTNTGAT

**Fig. 15TT**

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16509.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC  
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCCTTAAAC  
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATT  
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTTACAGGACAACAGCATTAG  
TGTCAGTGCGCTGCCTTCAAGTTCCTGTTACTGGTTACAGAAGTAACCACCACTCCCAAAAATGGACCAGGA  
CCAACAAAACTAAACTGCAGGTCCAGATCAAACAGAAAATGGACTATTGAAGGCTTGACGCCACAGTGGAA  
GTATGTGGNTAGNGTCTATGCTCAGAATCCCAAGCCGAGAAAGTCAGCCTTCTGGTTTAGACTGCAGTAACC  
AACATTGATCGCCCTAAAGGACTGGNCATTCACTTGGATGGTGGATGTCCAATTC

16509.2.edit

TCGAGCGGCCGCGCCGGGCAGGTCTTGCAGCTCTGCAGNGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCAT  
GGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCTGTGGGCTTTCCCAAGCAATT  
TTGATGGAATCGACATCCACATCAGNGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC  
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT  
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGTCCTGNCCATTTTTGGGAAGTGG  
GGGGTTACTCTGTAACCAAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGCTCTGAACATC  
GGTCACTTGATCTGGGGATGGTTTTGACAATTTCTGGTTCGGCAAATTAATGGAAATTGGCTTGCTGCTTGGC  
GGGGCTGNCTCCACGGGCCAGTGACAGCATACT

16510.1.edit

TCGAGCGGCCGCGCCGGGCAGGTCTTGCAGCTCTGCAGTGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCAT  
GGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCTGTGGGCTTTCCCAAGCAATT  
TTGATGGAATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC  
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT  
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGNCCTGNCCATTTTTGGGGAAGGG  
GTGGTTACTCTTGTAAACCAAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGGTGGCCTGAACATC  
GGTCACTTGATCTGGGATGGTTTTGGTCAATTTCTGTTCCGTAATTAATGGGAAATTGGCTTACTGGCTTGCGG  
GGGCTGTCTCCACGGNCAGTGACAAGCATACACAGNGATGGGTATAATCAACTCCAGGTTTAAGGCCNCTGAT  
GGTA

16510.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC  
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCCTTAAAC  
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGTAAGCCAATT  
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTTACAGGACAACAGCATTAG  
TGTCAGTGCGCTGCCTTCAAGTTCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGGACCAGGA  
CCAACAAAACTAAACTGCANGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGACGCCACAGTGGAG  
TATGTGGGTTAGTGTCTATGCTCAGAATNCCAAGCGGAGAGTCAAGCCTCTGGTTCAGACT

**Fig. 15UU**

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16511.1.edit

TCGAGCGGCCGCGCCGGGCAGGTCAGCGCTCTCAGGACGTACCACCATGGCCTGGGCTCTGCTCCTCCTCACCC  
TCCTCACTCAGGGCACAGGGTCCTGGGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGA  
CAGTCAGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGCTTATGAATTTGTCTCCTGGTACCAACA  
ACACCCAGGCAAGGCCCCCAAACCTCATGATTTCTGAGGTCACTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCT  
CTGGCTCCAAGTCTGGCAACACGGCTCCCTGACCGTCTCTGGGCTCCANGCTGAGGATGANGCTGATTATTAC  
TGGAAGCTCATATGCAGGCAACAACAATTGGGTGTTGCGCGGAAGGGACCAAGCTGACCGTNCTAAGGTCAAGC  
CCAAGGCTTGCCCCCTCGGTCACTCTGTTCCACCTCCTCTGAAGAAGCTTCAAGCCAACAANGNCACACT  
GGGTGTGTCTCATAAGTGGACTTTCTACCC

16511.2.edit

AGCGTGGTCGCGGCCGAGGTCGTAGCTTCTGTGGGACTTCCACTGCTCAGGCGTCAGGCTCAGGTAGCTGCTG  
GCCGCGTACTTGTTGTTGCTTTGNTTGGAGGGTGTGGTGGTCTCCACTCCCGCTTGACGGGGCTGCTATCTGC  
CTTCCAGGCCACTGTACGGCTCCCGGGTAGAAGTCACTTATGAGACACACCAGTGTGGCCTTGTTGGCTTGAA  
GCTCCTCAGAGGAGGGTGGGAACAGAGTGACCGAGGGGCGAGCCTTGGGCTGACCTAGGACGGTCAGCTTGGTC  
CCTCCGCGGAACACCCAATTGTTGTTGCCTGCATATGAGCTGCAGTAATAATCAGCCTCATCCTCAGCCTGGAG  
CCCAGAGACNGTCAAGGGAGGCCCGTGTTTGCCAAGACTTGGAAGCCAGANAAGCGATCAGGGACCCCTGAGGG  
CCGCTTTACNGACCTCAAAAAATCATGAATTTGGGGGCGCTTTCCTGGGNGTTGGTTGGTNACCAGNAAAACA  
AAATTTCATAAAGCACCAACGTCACTGCTGGTTCCAGTGCANGAANATGGTGAAGTGAANTGTCC

16512.1.edit

AGCGTGGTCGCGGCCGAGGTCAGCATCAGGAGCCCCGCTTGCCGGCTCTGGTCATCGCCTTCTTTTGTGG  
CCTGAAACGATGTATCAATTCGCAGTAGCAGAACTGCCGTCTCCACTGCTGTCTTATAAGTCTGCAGCTTCAC  
AGCCAATGGCTCCCATATGCCAGTTCCTTCATGTCCACCAAAGTACCGTCTCACCATTTACACCCAGGTCT  
CACAGTTCTCCTGGGTGTGCTTGGCCGAAGGGAGGTAAGTANACGGATGGTGCTGGTCCCACAGTTCTGGATC  
AGGGTACGAGGAATGACCTCTAGGGCTGGGCNACAAGCCCTGTATGGACCTGCCCGGGCGGGCCGCTCGA

16512.2.edit

TCGAGCGGCCGCGCCGGGCAGGTCCATACAGGGCTGTTGCCAGGCCCTAGAGGNCATTCTTGTAACCTGATCC  
AGAACTGTGGGACCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAACTGTGAGACC  
TGGGTGTAAATGGNGAGACGGTACTTTGGTGGACATGAAGGAACTGGGCATATGGGAGCCATTGGCTGNGAA  
GCTGCANACTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATGACATCGTTTCAGGCCACA  
AAAAGAAAGGCGATGACCANAGCCGGCAAGCGGGGCTTCTGATGCTGGACCTCGGCCGCCGACCAGCTT

**Fig. 15VV**

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16514.1.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCCAGGCAGAGTCTCTGCGTTACAACTCC  
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC  
GAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATGGCCTGATGATCCA  
CAGCGGAGACCCTGTTAACTACTACGTTGACACTGCTGTGCGCCACGTGTTGCTCANACAGGGTGTGCTGGGCA  
TCAAGGTGAAGATCATGCTGCCCTGGGACCCANCTGGCAAAAATGGCCCTTAAAAACCCCTTGCCNTGACCAGG  
TGAACCATTTGTGNGAACCCCAAGATGAANATACTTGCCACCACCCCCATTTC

16514.2.edit

TGAGCGGCCGCGCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGCAGGCG  
GCTCTGGCTTCCACCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC  
ACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCAGGGCAGCATGATCTTCACCTTGAT  
GCCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAGCAGTGTCAACGTAGTAGTTAACAGGGTCTCCGCTGT  
GGATCATCAGGCCATCCAAAACTTCATGGATTAGCCCTCTGTCTCGGAGTTTCCAAAACACCACAACCTC  
GCCAGCCTTTGGGCCCCACTTCTTCATGAATGAAACCGCAGCACACCATTANCAAGGCCCTTCCGCACAGGNAA  
GCCCTTCTTAAGGAGTTTGTAAACGCAAAAACCTCTTGCTGGGGCAAATGGGCACACAGACCTNTANTNGGA  
CCTTGGNCCGGAACCACCGCTT

16515.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCCCTCCTGGCAAGGCTGGTGAAGATGGTCACCCTGGAAAACCCGGACGAC  
CTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTTCCCTGGAATCCTGGACTTCCTGGCTTCAA  
GGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCCGGTGCTCCTGGTGTGAAGGGTGAACCTGG  
NGCCCTGGTGAAAATGGAATCCAGGTCAAACAGGAGCCCGNGGGCTTCTGGNGAGAGAGGACGTGTTGGTG  
CCCCTGGCCCANACCTGCCCGGGCGGCGCTCNAAAAGCCGAAATCCAGNACACTGGCGGCCGNTACTANTGGA  
ATCCGAACTTCGGTACCAAAGCTTGGCCGTAATCATGGCCATAGCTTGTTCCCTGGGGNGGAAATTTGGTATTCC  
GCTNCCAATTCACACAACATACCGAACC CGGAAAGCATTAAAGTGTAAAAGCCCTGGGGGGGCTAAATGANG  
TGAGCNTAACTCNCATTTAATTGGCGTTGCGCTTCACTGCCCCGCTTTTCCAGTCCGGGNA

16515.2.edit

TGAGCGGCCGCGCCGGGCAGGTCTGGGCCAGGGGCACCAACACGTCTCTCTCACCAGGAAGCCACGGGCTCC  
TGTTTGACCTGGAGTTCCATTTTACCAGGGGCACCAGGTTACCCCTTACACCAGGAGCACC GGCTGTCCCT  
TCAATCCATCCAGACCATTGTGNNCCCTAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCCAGGGAAACCACGA  
GCACCCTGTGGTCCAACAACCTCTCTCTCACCAGGTCGTCCGGGTTTTCCAGGGTGACCATCTTACCAGCCTT  
GCCAGGAGGGCCAGACCTCGGCCGCGACCACGCT

**Fig. 15WW**

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16516.1.edit

ANCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGNCACCTACAACATCATAGTGGAGGCACTGAAAGACCANCA  
GAGGCATAAGGTTTCGGGAAGAGG

16516.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT  
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACAGTTTA  
AAGCCTGATTACAGACATTCGTTCCCACTCATCTCAAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA  
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGTCCACGGTAACAACCTCTTCCCGAACCTTATGCC  
TCTGCTGGTCTTTCACTGCCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCNGNCCNGAACAAC  
GCTTAAGCCCGNATTCTGCAGAATAATCCCATCACACTTGGCGGCCGCTTCGANCATGCATNTAAAAGGGGCC  
CCAATTTCCCTTATAAGNGAANCCGTATTTNCCAATTTCACTGGNCCCGCCGNTTTTACAAACGNCGGTGAA  
CTGGGGAAAAACCCTGGCGGTTACCCAACTTTAATCGCCNTTGGCAGCACAATCCCCCTTTTCGNCCANCNTG  
GGCGTAAATAACCGAAAA

16517.1.edit

ANCGNGGTGCGGGCCGANGTNTTTTTCTTNTTTTTT

16518.1.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT  
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG  
TACCGGGNGGTGAGCGTCCTCACCGTCCTGCACCAGAATTGGTTGAATGGCAAGGAGTACAAGNGCAAGGTTTC  
CAACAAAGCCNTCCAGCCCCNTCGAAAAAACCATTTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT  
ACACCCTGCCCCATCCCGGGAGGAAAAGANCAANAACCNGGTTAGCCTTAACCTTGCTTGGTCNAANGCTTTT  
TATCCCAACGNACTTCCCCNTGGAANTGGGAAAAACCAATGGGCCAANCCGAAAAACAATTACAANAACCCC

16518.2.edit

TCGAGCGGCCGCCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA  
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGACCTGGTTCTT  
GGTCATCTCCTCCCGGATGGGGCAGGGTGAACACCTGGGGTTCTCGGGGCTTGCCCTTTGGTTTTGAANATG  
GTTTTCTCGATGGGGGCTGGAAGGGCTTTGTTGNAACCTTGCACTTGACTCCTTGCCATTACCCAGNCCTGG  
NGCAGGACGGNGAGGACNCTNACCACACGGAACCGGGCTGGTGGACTGCTCC

**Fig. 15XX**

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16519.1.edit

AGCGTGGTCGCGGACGANCTCCTGTCAGAGTGGNACTGGTAGAAGTTCCANGAACCCCTGAACTGTAAGGGTTCT  
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGNGNCCTGGAATGGGGCCCATGANATGGTTGC  
C

16519.2.edit

TCGAGCGGCCGCGCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT  
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTG  
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT  
CAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCCTCCACACCCCAA  
TCTTCATGGACCAGAGATCTTGATGTTCTTCCACAGTTCAAAGACCCCTTCGGCACCCCCCTGGGTATG  
AACCTGGGAAAANGGNANTTAANCTTCTGGCA

16520.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC  
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC  
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATT  
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTTCAAGACAACAGCATTAG  
TGTCAGTGCTGCCTTCAAGGTNCCCTGGTACTGGGTACAGANTAACCACCACTCCAAAAATGGACCAGGA  
ACCACAAAACTTAACTGCAGGGTCCAGATCAAAACAGAAATGACTATTGAANGCTTGACGCCACAGTGGGA  
GTATGNGGGTAGTGNCTATGCTTCAGAATCAAAGCGGAAAAANGTCAAGCCTTNTGGGTCAA

16520.2.edit

TCGAGCGGCCGCGCGGGCAGGTCTTGAGCTCTGCAGTGTCTTCTTACCATCAGGTGCAGGGAATAGCTCAT  
GGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCCTGTGGGCTTTCCTAAGCAATT  
TTGATGGAATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGNCTGAAC  
CAGAGGCTGACTCTCTCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAANCCTT  
CAATAANNCATTTCTGTTTGATCTGGACC

16521.2.edit

TCGAGCGGCCGCGCGGGCAGGTCTGGTGGGGTCTGGCACACGCACATGGGGGNGTTGNTCTNATCCAGCTGCC  
CAGCCCCATTGGCGAGTTTGAGAAGGTGTGCAGCAATGACAACAANACCTTCGACTCTTCTGCCACTTCTTT  
GCCACAAAGTGACCCCTGGAGGGCACCAAGAAGGGCCACAAGCTCCACCTGGACTACATCGGGCCTTGCAAATA  
CATCCCCCTTGCTGGACTCTGAGCTGACCGAATCCCCCTTGCGCATGCGGGACTGGCTCAAGAACCGTCTT  
GGCACCTTGTATGANAGGGATGAAGACACNACCC

**Fig. 15YY**

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16522.1.edit

AGCGTGGTCGCGGCCGAGGTCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT  
CCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA  
GTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTC  
AGTCTTCCTCTTCCCCCGCATCCCCCTTCCAAACCTGCCGGGGCGCCGCTCGAAAGCCGAATTCCAGCACACT  
GGCGGCCGGTACTAGTGGANCCNAACCTTGGNANCCAACCTGGNGGAANTAATGGGCATAANCTGTTTCTGGGGG  
GAAATTGGTATCCNGTTTACAATTCCCNCAACATACGAGCCGGAAGCATAAAAGNGTAAAAGCCTGGGGGNG  
GCCTANTGAAGTGAAGCTAACTCACATTAATNGCGTTGCCGCTCACTGGCCCGCTTTTCCAGC

16522.2.edit

TCGAGCGGCCGCCCCGGGCAGGTTTGAAGGGGGATGCGGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTC  
AGGTGCTGGGCACGGTGGGCATGTGTGAGTTTGTGACAAAGATTTGGGCTCAACTCTTTGTCCACCTTGGTGT  
TGCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGGNGCCGAAGTTGCTGGAGGGCACGGTCACCACGCTG  
CTGAGGGAGTAGAGTCCTGAGGACTGTANGACAGACCTCGGCCGNGACCACGCTAAGCCGAATTCTGCAGATAT  
CCATCACACTGGCGGCCGCTCCGAGCATGCATTTAGAGG

16523.1.edit

AGCGTGGNCGCGGACGANGACAACAACCCC

16523.2.edit

TCGAGCGGCCGCCCCGGGCAGGNCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC  
GGTCATGCTCTTGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGNACCAGTTCTTCTGGGCCA  
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG  
CAGCCTTGTTGGGGTCAATCCAGTACTCTCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGT  
GCGGGCGGGTTCTTGACCT

16524.1.edit

AGCGTGGTCGCGGCCGAGGTCCAGCCTGGAGATAANGGTGAAGGTGGTGCCCCCGGACTTCCAGGTATAGCTGG  
ACCTCGTGGTAGCCCTGGTGAGAGAGGTGAAACTGCCCTCCAGGACCTGCTGGTTTCCCTGGTGCTCCTGGAC  
AGAATGGTGAACCTGGNGGTAAAGGAGAAAGAGGGGCTCCGGNTGANAAAGGTGAAGGAGGCCCTCCTGNATTG  
GCAGGGGCCCCANGACTTAGAGGTGGAGCTGGCCCCCTGGCCCCGAAGGAGGAAAGGGTGCTGCTGGTCTCCTC  
TGGGCCACCTGG

***Fig. 15ZZ***



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16524.2.edit

TCGAGCGGCCGCCGGGCAGGTCTGGGCCAGGAGGACCAATAGGACCAGTAGGACCCCTTGGGCCATCTTTCCC  
TGGGACACCATCAGCACCTGGACCGCCTGGTTCAACCTTGTCAACCTTTGGACCAGGACTTCCAAGACCTCCTC  
TTTCTCCAGGCATTCTTGCAGACCAGGAGTACCANCAGCACCAGGTGGCCAGGAGGACCAGCAGCACCTTT  
CCTCCTTCGGGACCAGGGGGACCAGCTCCACCTCTAAGTCCTGGGGCCCTGCCAATCCAGGAGGGCCTCCTTC  
ACCTTTCTACCCGGAGCCCCTCTTTCT

16526.1.edit

TCGAGCGGCCGCCGGGCAGGTCCACCGGGATATTCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAA  
GGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTCTTACCTGGACAGAGTGAGGAGCCTGGAGACCGACAACC  
GGAGGCTGGAGAGCAAAATCCGGGAGCACTTGGAGAAGAAGGGACCCAGGTCAGAGACTGGAGCCATTACTTC  
AAGATCATCGAGGACCTGAGGGCTCANATCTTCGCAAATACTGCNGACAATGCCCG

16526.2.edit

ATGCGNGGTGCGGGCCGANGACCANCTCTGGCTCATACTTGACTCTAAAGNCNTCACCAGNANTTACGGNCATT  
GCCAATCTGCAGAACGATGCGGGCATTGTCCGCANTATTTGCGAAGATCTGAGCCCTCAGGNCCTCGATGATCT  
TGAAGTAANGGCTCCAGTCTCTGACCTGGGGTCCCTTCTTCTCCAAGTGCTCCCGGATTTTGCTCTCCAGCCTC  
CGGTTCTCGGTCTCCAAGNCTTCTCACTCTGTCCAGGAAAAGAGGCCAGGCGNCGATCAGGGCTTTTGCATGG  
ACT

16527.1.edit

AGCGTGGTGC GGCCGAGGTTGTACAAGCTTT  
TT

16527.2.edit

TCGAGCGGCCGCCGGGCAGGTCTGCCAACCAAGATTGGCCCCCGCCGCATCCACACAGTTNGTGTGCGGGG  
AGGTAACAAGAAATACCGTGGCCTGAGGNTGGACGNGGGGAATTTCTCCTGGGGCTCAGAGTGTGTACTCGTA  
AAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAAT  
TGCATCGTGCTCATNGACAGCACACCGTACCGACAGTGGGTACCGAAGTCCCACTATGCNCCT

***Fig. 15AAA***

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16528.1.edit

TCGAGCGGCCGCGCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT  
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG  
TCACAGAGGCTACTATTACTGGCCTGGAACCGGAACCGAATATACAATTTATGTCATTGCCCTGAAG

16528.2.edit

AGCGTGNTCNCGGCCGAGGATGGGGAAGCTCGNCTGTCTTTTTCTTCCAATCAGGGGCTNNNTCTTCTGATTA  
TTCTTCAGGGCAANGACATAAATTGTATATTCGGNTCCCGGTTCCAGNCCAGTAATAGTAGCCTCTGTGACACC  
AGGGCGGGGCGGAGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGAAGCCGGTAATCC  
TGGCACGTGGGCGGCTGCCATGATACCAANGAATTGGGTGTGGTGGACCTGCCCGGGCGGGCCGCTCGAAA  
ANCCGAATTCNTGCAAGAATATCCATCACACTTGGGCGGGCCGNTCGAACCATGCATCNTAAAGGGCCCCAAT  
TTCCCCCTATTAGNGAAGCCNCATTTAACAATTCCACTTGG

16529.1.edit

TCGAGCGGCCGCGCGGGCAGGTCTCGCGGTGCGACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGG  
ACCTCCTGGTCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGG  
CTCAGGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC  
ACCCTCAAGAGCCTTGAGCCAGCAGAATCGAAAACATTCGGAACCCAAGAAGGGCAAGCCGCAAAGAAACCCC  
GCCCCGACCTGGCCGNGAACCTCCAAGAANGTGCCACNTCTTGACTGGGAAAAAAGGGAAAANTACTTGGAA  
TTGGAC

16529.2.edit

AGCGTGGTGC GGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG  
TCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTGGGGTCTTGCTGATGTACCAGTTCTTCTGGGCCACA  
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA  
GCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTCCAGTCAGAAGTGGCACATCTTGAGGTACGGCAGGGT  
GCGGGCGGGGTTCTTGCGGGCTGCCCTCTGGGCTCCCGGAATGTTCTNNGAACTTGCTGG

***Fig. 15BBB***

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16530.1.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCCAGGCAGAGTCTCTGCGTTACAACTCC  
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC  
GAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATGGCCTGATGATCCA  
CAGCGGAGACCCTGTAACTACTACGTTGACACTTGCTTGTGCGCCACGTGTTGCTCANACANGGGTGGGCTGG  
GCATCAAGGNG

16530.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGCAGGCG  
GCTCTGGCTTCCACCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC  
ACGTGGTCAGGCAGGGGCTTCTAGGGCCAATCTTACCAGTTGGGTCCAGGGCAGCATGATCTTACCTTGAT  
GCCCAGCACACCCTGTCTGAGCAACAGTGGCGCACAGCAAGTGTCAACGTAAGTAAGTTAACAGGGTCTCCG  
TGTGGATCATCAGGCCATCCACAACTTCATGGATTTAACCTCTGTCCTCGGAG

16531.1.edit

TCGAGCGGCCGCCCGGGCAGGTGTTTCAGAGGTTCCAAGGTCCACTGTGGAGGTCCCAGGAGTGCTGGTGGTGG  
GCACAGAGGTCCGATGGGTGAAACCATTTGACATAGAGACTGTTCTGTCCAGGGTGTAGGGGCCAGCTCTTTG  
ATGCCATTGGCCAGTTGGCTCAGCTCCCAGTACAGCCGCTCTCTGTTGAGTCCAGGGCTTTTGGGGTCAAGATG  
ATGGATGCAGATGGCATCCACTCCAGTGGCTGCTCCATCCTTCTCGGACCTGAGAGAGGTGAGTCTGCAGCCAG  
AGTACAGAGGGCCAACACTGGTGTCTTTGAATA

16531.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTACTGGGAGCTAAGCAAACCTGACCAATGACATTGAAGAGCTGGGCCCTAC  
ACCCTGGACAGGAACAGTCTCTATGTCAATGGTTTACCCATCAGAGCTCTGTGNCCACCACCAGCACTCCTGG  
GACCTCCACAGTGGATTTAGAACCTCAGGGACTCCATCCTCCCTCTCCAGCCCCACAATTATGGCTGCTGGCC  
CTCTCCTGGTACCATTACCCTCAACTTCACCATCACCACCTGCAGTATGGGGAGGACATGGGTACCCTGNC  
TCCAGGAAGTTCAACACCACA

16532.1.edit

TCGAGCGGCCGCCCGGACAGGTCTGGGCGGATAGCACCGGCATATTTTGGAAATGGATGAGGTCTGGCACCTG  
AGCAGTCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCAGGNTCTGAGNCT  
GTGGGATAGCTGCCATGAAGTAACCTGAAGGAGGTGCTGGCTGGTANGGGTTGATTACAGGGTTGGGAACAGCT  
CGTACACTTGCCATTCTCTGCATATACTGGTTAGTGAGGTGAGCCTGGCCCTCTCTTTTG

***Fig. 15CCC***

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01\_16558.3.edit

AGCGTGGTCGCGGCCGAGGTGAGCCACAGGTGACCGGGGCTGAAGCTGGGGCTGCTGGNCCTGCTGGTCCTG

02\_16558.4.edit

CAGCNGCTCCNACGGGGCCTGNGGGACCAACAACACCGTTTTACCCTTAGGCCCTTTGGCTCCTCTTTCTCCT  
TTAGCACCAGGTTGACCAGCAGCNCCANCAGGACCAGCAAATCCATTGGGGCCAGCAGGACCACCTCACCAGG  
TTCACCAGGGCTTCCCGAGGACCAGCAGGACCAGCAGGACCAGCAGCCCAGCTTCGCCCCGGTCACCTGTGG  
CTCACCTCGGCCGCGACACGCT

03\_16535.1.edit

TCGAGCGGTGCCCCGGGCGAGGTCCACCGGGATAGCCGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAA  
GGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTCTTACCTGGACAGAGTGAGGAGCCTGGAGACCGANAACC  
GGAGGCTGGANAGCAAAATCCGGGAGCACTTGGAGAAGAAGGGACCCAGGTCAAGAGACTGGAGCCATTACTT  
CAAGATCATCGAGGGACCTGGAGG

04\_16535.2.edit

AGCGNGGTGCGGGCCGAGGTCCAGCTCTGTCTCATACTTGACTCTAAAGTCATCAGCAGCAAGACGGGCATTGT  
CAATCTGCAGAACGATGCGGGCATTGTCCGCAGTATTTGCGAAGATCTGAGCCCTCAGGTCTCGATGATCTTG  
AAGTAATGGCTCCAGTCTCTGACCTGGGGTCCCTTCTTCTCCAAGTGCTCCCGGATTTTGCTCTCCAGCCTCCG  
GTTCTCGGTCTCCAGGCTCCTCACTCTGTCCAGGTAAGAAGGCCAGGCGGTGTTTCAAGGCTTTGCATGGTCTC  
CTTCTCGTTCTGGATGCCTCCCATTCCTGCCAGACCC

05\_16536.1.edit

TCGAGCGGCCGCCCCGGGCGAGGTGAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCAACCTGTGCTG  
CGGACATCTCCAGGGAGTGACAGAGGGAAGCAGGTCAAACCTGCTCAGATCAGTCAGACTGGCTGTTCTCAGTTC  
TCACCTGAGCAAGGTGAGTCTGCAGCCAGAGTACAGAGGGCCAACTGGTGTCTTGAACAAGGGCTTGAGCA  
GACCTGCAGAACCTCTTCCGTGGTGTGAACTTCCTGGAACCAGGGTGTTGCATGTTTTCTCATAATGC  
AAGGTTGGTGATGG

***Fig. 15DDD***

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07\_16537.1.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG  
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACA  
CTGGGCTGAGTGGGGTACACCGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGC  
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08\_16537.2.edit

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***Fig. 15EEE***

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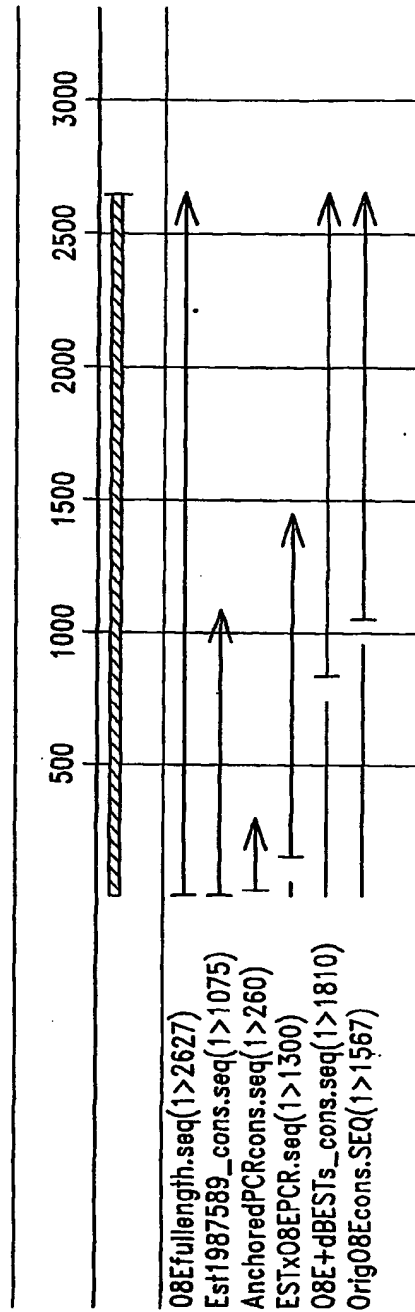


Fig. 16

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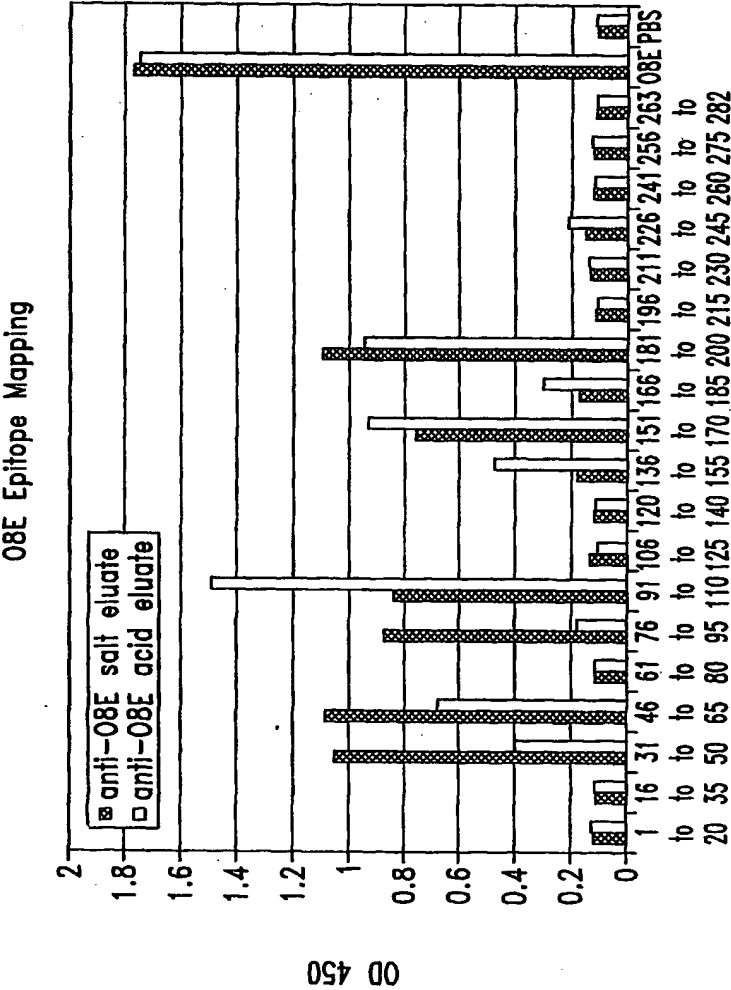
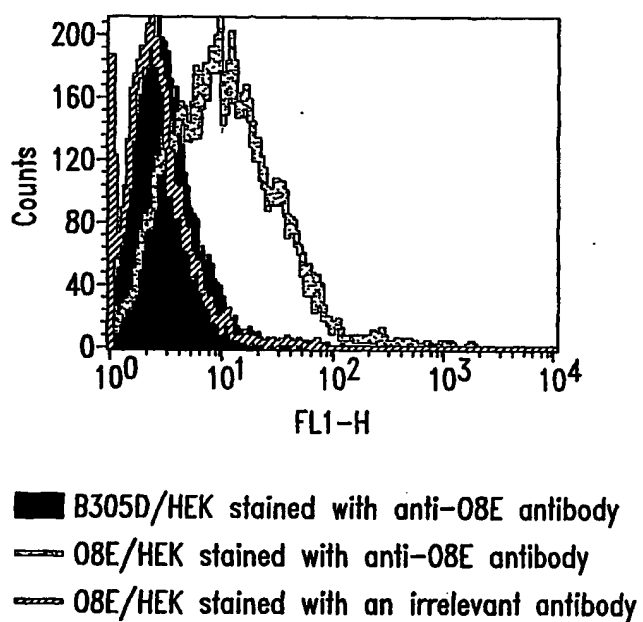


Fig. 17

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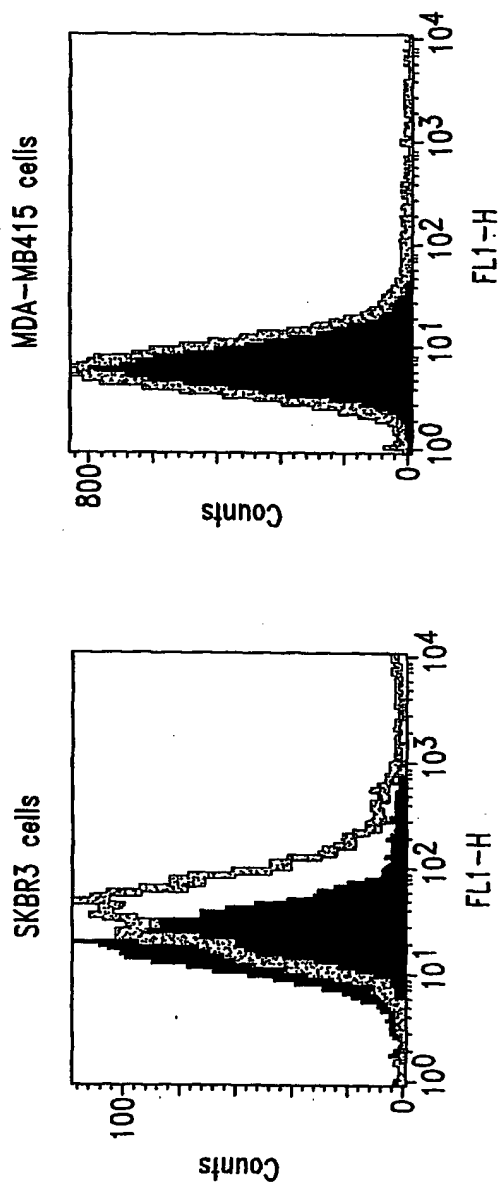
## O8E Surface Expression

*Fig. 18*



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Surface expression of O8E

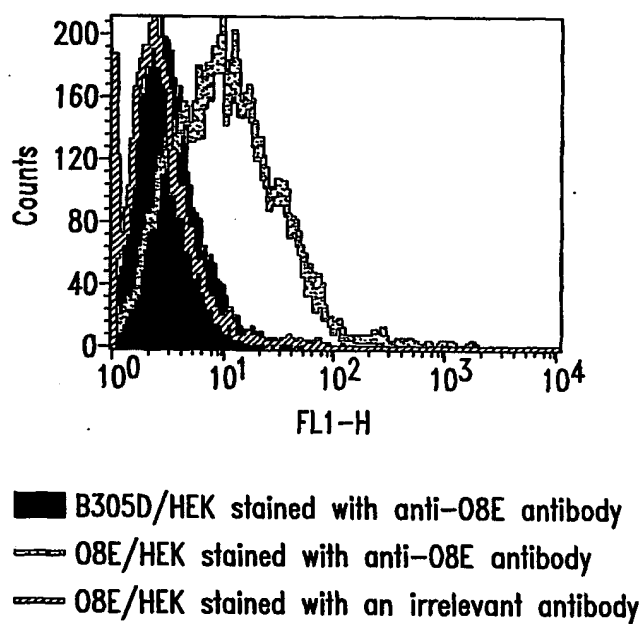


Black; irrelevant antibody  
Light gray; anti-O8E antibody

*Fig. 19*

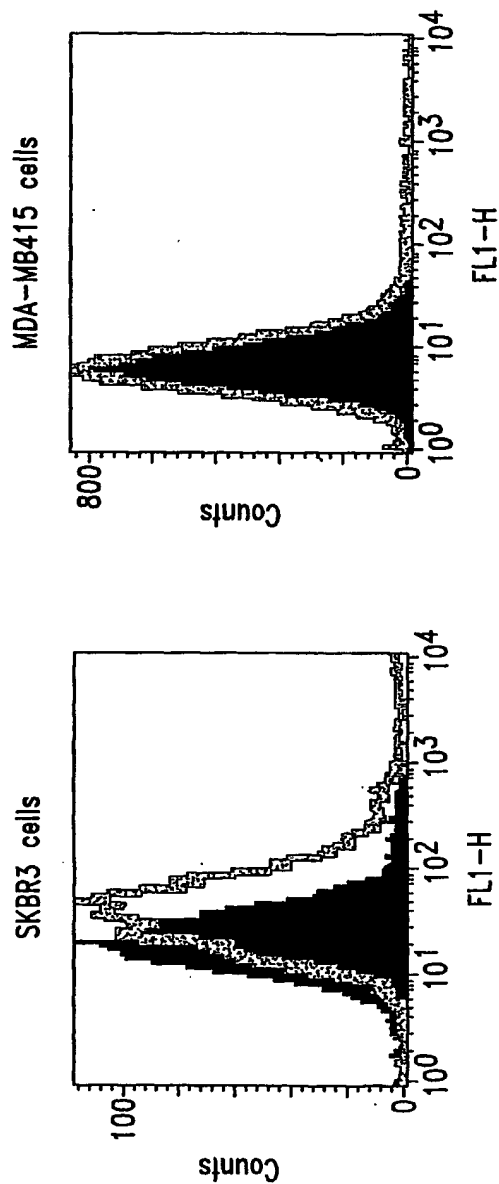
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## O8E Surface Expression

*Fig. 20*

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Surface expression of O8E

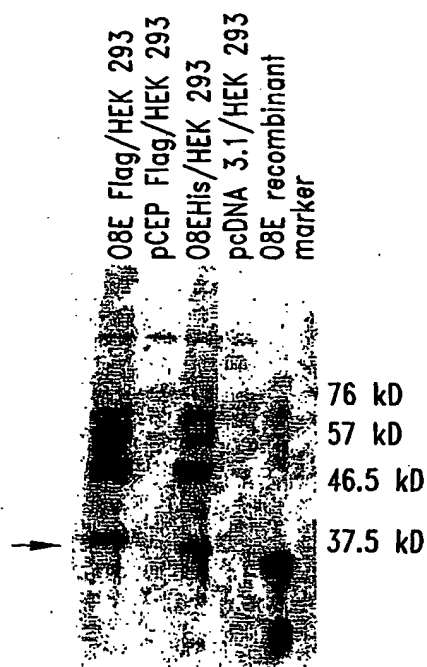


Black; Irrelevant antibody  
Light Grey; Anti-O8E antibody

*Fig. 21*

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O8E expression in HEK293 Cells  
(probed with anti-O8E rabbit polyclonal sera #2333L)



*Fig. 22*

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O8E Rabbits 01212000

Date: 1/21/99

| Antigen<br>on Plate | Sera Sample                      | Antibody Dilutions |        |        |        |         |         |         |          |          |          |           |           |      |  |
|---------------------|----------------------------------|--------------------|--------|--------|--------|---------|---------|---------|----------|----------|----------|-----------|-----------|------|--|
|                     |                                  | 1:1000             | 1:2000 | 1:4000 | 1:8000 | 1:16000 | 1:32000 | 1:64000 | 1:128000 | 1:256000 | 1:512000 | 1:1024000 | 1:2048000 |      |  |
| O8E<br>(#632-24)    | Preimmune sera (#2576L):1/10/99  | 0.13               | 0.09   | 0.08   | 0.07   | 0.07    | 0.07    | 0.07    | 0.06     | 0.07     | 0.07     | 0.07      | 0.07      | 0.07 |  |
|                     | Average                          | 0.10               | 0.08   | 0.07   | 0.07   | 0.07    | 0.07    | 0.07    | 0.06     | 0.06     | 0.07     | 0.06      | 0.06      | 0.07 |  |
|                     | $\alpha$ -O8E (#2576K):1/11/2000 | 0.11               | 0.08   | 0.07   | 0.07   | 0.07    | 0.07    | 0.07    | 0.06     | 0.07     | 0.07     | 0.07      | 0.06      | 0.07 |  |
|                     | Average                          | 2.92               | 2.81   | 2.74   | 2.70   | 2.58    | 2.08    | 1.61    | 1.01     | 0.68     | 0.40     | 0.24      | 0.15      |      |  |
|                     | Preimmune sera (#2333L):1/10/99  | 2.93               | 2.77   | 2.74   | 2.69   | 2.48    | 2.08    | 1.57    | 1.00     | 0.66     | 0.40     | 0.23      | 0.16      |      |  |
|                     | Average                          | 2.93               | 2.79   | 2.74   | 2.69   | 2.53    | 2.08    | 1.59    | 1.00     | 0.67     | 0.40     | 0.23      | 0.16      |      |  |
|                     | Preimmune sera (#2333L):1/10/99  | 0.09               | 0.07   | 0.06   | 0.06   | 0.07    | 0.07    | 0.07    | 0.07     | 0.07     | 0.07     | 0.07      | 0.07      | 0.07 |  |
|                     | Average                          | 0.08               | 0.07   | 0.06   | 0.07   | 0.10    | 0.07    | 0.07    | 0.07     | 0.07     | 0.07     | 0.07      | 0.07      | 0.07 |  |
|                     | $\alpha$ -O8E (#2333L):1/11/2000 | 0.08               | 0.07   | 0.06   | 0.06   | 0.08    | 0.07    | 0.07    | 0.07     | 0.07     | 0.07     | 0.07      | 0.07      | 0.07 |  |
|                     | Average                          | 2.73               | 2.75   | 2.64   | 2.48   | 2.30    | 1.78    | 1.41    | 0.92     | 0.58     | 0.32     | 0.20      | 0.14      |      |  |
|                     | Preimmune sera (#2333L):1/10/99  | 2.73               | 2.76   | 2.51   | 2.60   | 2.37    | 1.93    | 1.44    | 0.88     | 0.58     | 0.35     | 0.20      | 0.14      |      |  |
|                     | Average                          | 2.73               | 2.76   | 2.57   | 2.54   | 2.33    | 1.85    | 1.43    | 0.90     | 0.58     | 0.33     | 0.20      | 0.14      |      |  |

Fig. 23

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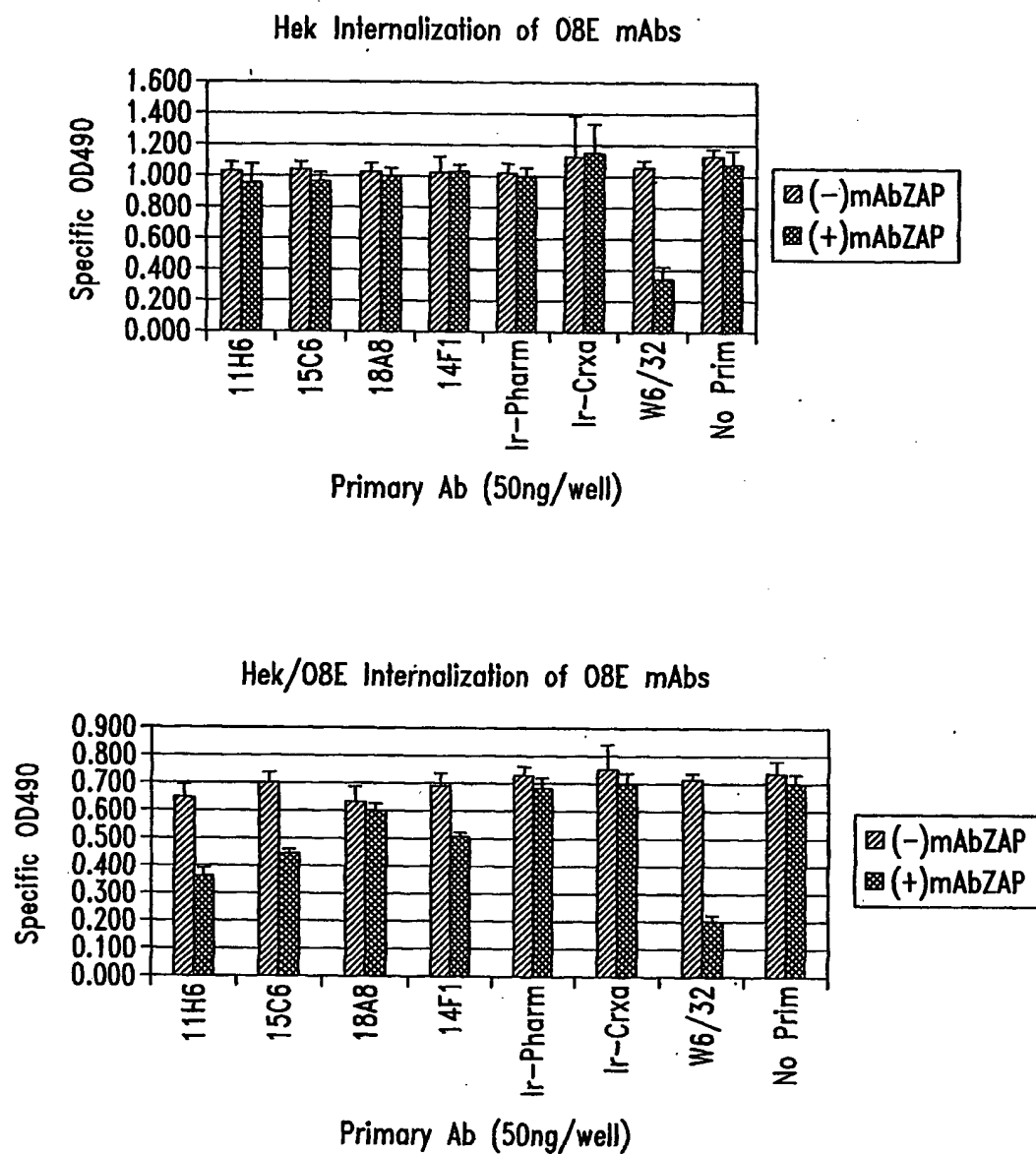
affi-pure O8E #2576L 739.87A&amp;B

| Date: 5/2/2000                   |                                  |                    |        |        |        |         |         |         |          |          |          |           |           |  |
|----------------------------------|----------------------------------|--------------------|--------|--------|--------|---------|---------|---------|----------|----------|----------|-----------|-----------|--|
| Antibody Name                    |                                  | O8E polyclonal     |        |        |        |         |         |         |          |          |          |           |           |  |
| Rabbit #, Bleed Date             |                                  | 2576L, 1/11/2000   |        |        |        |         |         |         |          |          |          |           |           |  |
| Purification Method              |                                  | affinity           |        |        |        |         |         |         |          |          |          |           |           |  |
| Buffer                           |                                  | PBS                |        |        |        |         |         |         |          |          |          |           |           |  |
| Notebook                         |                                  | #705, p150         |        |        |        |         |         |         |          |          |          |           |           |  |
| lot #                            | 739.87A                          | 739.87B            |        |        |        |         |         |         |          |          |          |           |           |  |
| Antibody Concentration           | 1.4mg/ml                         | 1.7mg/ml           |        |        |        |         |         |         |          |          |          |           |           |  |
| Initial Amount                   | 18mg                             | 3mg                |        |        |        |         |         |         |          |          |          |           |           |  |
| Antigen on Plate                 | Sera Sample                      | Antibody Dilutions |        |        |        |         |         |         |          |          |          |           |           |  |
| O8E #632-24                      | preimmune sera (2576L)           | 1:1000             | 1:2000 | 1:4000 | 1:8000 | 1:16000 | 1:32000 | 1:64000 | 1:128000 | 1:256000 | 1:512000 | 1:1024000 | 1:2048000 |  |
|                                  |                                  | 0.15               | 0.11   | 0.09   | 0.08   | 0.08    | 0.07    | 0.07    | 0.07     | 0.07     | 0.08     | 0.07      | 0.08      |  |
|                                  |                                  | 0.14               | 0.10   | 0.09   | 0.08   | 0.07    | 0.07    | 0.07    | 0.07     | 0.07     | 0.07     | 0.07      | 0.07      |  |
|                                  | Average                          | 0.14               | 0.10   | 0.09   | 0.08   | 0.07    | 0.07    | 0.07    | 0.07     | 0.07     | 0.08     | 0.07      | 0.08      |  |
|                                  | $\alpha$ -O8E (2576K):2/8/2000   | 2.74               | 2.71   | 2.63   | 2.49   | 2.29    | 1.87    | 1.39    | 0.92     | 0.57     | 0.33     | 0.20      | 0.14      |  |
|                                  |                                  | 2.72               | 2.68   | 2.64   | 2.47   | 2.26    | 1.93    | 1.42    | 0.94     | 0.57     | 0.34     | 0.21      | 0.14      |  |
|                                  | Average                          | 2.73               | 2.70   | 2.63   | 2.48   | 2.27    | 1.90    | 1.41    | 0.93     | 0.57     | 0.34     | 0.21      | 0.14      |  |
|                                  | affinity pure $\alpha$ -O8E poly | 2.69               | 2.60   | 2.50   | 2.21   | 1.83    | 1.34    | 0.99    | 0.64     | 0.38     | 0.22     | 0.15      | 0.11      |  |
|                                  | salt peak 739-87A                | 2.59               | 2.48   | 2.38   | 2.21   | 1.82    | 1.33    | 1.00    | 0.62     | 0.37     | 0.22     | 0.14      | 0.11      |  |
|                                  | Average                          | 2.64               | 2.54   | 2.44   | 2.21   | 1.83    | 1.34    | 1.00    | 0.63     | 0.37     | 0.22     | 0.15      | 0.11      |  |
| affinity pure $\alpha$ -O8E poly | 2.46                             | 2.39               | 2.40   | 2.34   | 2.08   | 1.73    | 1.29    | 0.81    | 0.49     | 0.29     | 0.19     | 0.13      |           |  |
| acid peak 739-67B                | 2.65                             | 2.66               | 2.61   | 2.45   | 2.14   | 1.76    | 1.30    | 0.82    | 0.48     | 0.29     | 0.19     | 0.13      |           |  |
| Average                          | 2.56                             | 2.53               | 2.51   | 2.39   | 2.11   | 1.74    | 1.30    | 0.81    | 0.49     | 0.29     | 0.19     | 0.13      |           |  |

Fig. 24

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Anti-O8E mAb Binding to O8E Amino Acids  
61-80 Induces Ligand Internalization

*Fig. 25*

## SEQUENCE LISTING

<110> Corixa Corporation  
Mitcham, Jennifer L.  
King, Gordon E.  
Algate, Paul A.  
Fling, Steven P.  
Retter, Marc W.  
Fanger, Gary Richard  
Reed, Steven G.  
Vedvick, Thomas S.  
Carter, Darrick  
Hill, Paul  
Albone, Earl

<120> COMPOSITIONS AND METHODS FOR THE THERAPY  
AND DIAGNOSIS OF OVARIAN CANCER

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<213> Homo sapiens

<400> 12  
ctgggatcat ttctcttgat gtcataaaag actcttcttc ttcctcttca tctcttctt 60  
catcctcttc tgtacagtgc tgccgggtac aacggctatc ttgtcttta tcttgagatg 120  
aagatgatgc ttctgtttct cctaccataa ctgaagaaat ttcgctggaa gtcgtttgac 180  
tggctgtttc tctgacttca ccttctttgt caaacctgag tctttttacc tcatgccct 240  
cagcttccac agcatcttca tctggatgtt tatttttcaa agggctcact gaggaaactt 300  
ctgattcaga ggtcgaagag tcaactgtgat ttttctctc attttgcctgc aaatttgcct 360  
ctttgctgtc tgtgctctca ggcaacccat ttgttgcac gggggctgac aaagaaacct 420  
ttggtcgatt aagtggcctg ggtgtcccag gccatttat attagacctc tcagtatagc 480  
ttggtgaatt tccaggaaac ataacacccat tcattcgatt taaactattg gaattgggtt 540  
t 541

<210> 13  
<211> 441  
<212> DNA  
<213> Homo sapiens

<400> 13  
gagggttggt ggtagcggct tggggaggtg ctgcgtctgt cggctcttgc ctctcgcacg 60  
cttcccccg ctcccttcgt ttccccccc eggtcgccctg cgtgccggag tgtgtgcgag 120  
ggagggggag ggcgtcgggg ggggtggggg aggcgttccg gtccccaaga gaccgcgga 180  
gggagcgga ggcgtgaggg gactccggga agccatggac gtcgagaggc tccaggaggc 240  
gctgaaagat ttgagaaga ggggaaaaa ggaagtgtt cctgtcctgg atcagtttct 300  
ttgtcatgta gccaaagact gagaaacaat gattcagtgg tcccaattta aaggctattt 360  
tattttcaaa ctggagaaag tgatggatga ttccagaact tcagctcctg agccaagagg 420  
tcctccaac cctaattgtc a 441

<210> 14  
<211> 131  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 126  
<223> n = A,T,C or G

<400> 14  
aagcaggcgg ctccccgcgt cgcagggccg tgccacctgc ccgcccgcc gctcgtctgc 60  
tcgcccgcgg cgccgcgctg ccgaccgcca gcatgtgcc gagagtgggc tgccccgcgc 120  
tgccgntgcc g 131

<210> 15  
<211> 692  
<212> DNA  
<213> Homo sapiens

<400> 15  
atctcttgta tgccaaatat ttaatatataa tctttgaaac aagttcagat gaaataaaaa 60  
tcaaagtttg caaaaacgtg aagattaact taattgtcaa atattcctca ttgccccaaa 120  
tcagtatttt ttttatttct atgcaaaagt atgccttcaa actgcttaaa tgatatatga 180  
tatgatacac aaaccagttt tcaaatagta aagccagtca tcttgcaatt gtaagaaata 240  
ggtaaaagat tataagacac cttacacaca cacacacaca cacacacgtg tgcacgcaa 300  
tgacaaaaaa caatttggcc tctcctaaaa taagaacatg aagaccctta attgctgcc 360

```

ggaggggaaca ctgtgtcacc cctccctaca atccaggtag tttcctttaa tccaatagca 420
aatctgggca tatttgagag gagtgattct gacagccacg ttgaaatcct gtggggaacc 480
attcatgtcc acccactggg gccctgaaaa aatgccataa atttttcgct cccacttctg 540
ctgctgtctc ttccacatcc tcacatagac cccagaccgg ctggcccctg gctgggcatc 600
gcattgtctg tagagcaagt cataggtctc gtctttgacg tcacagaagc gatacaccaa 660
attgcctggg cggtcattgt cataaccaga ga                                     692

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```

<210> 16
<211> 728
<212> DNA
<213> Homo sapiens

```

```

<400> 16
cagacgggggt ttcactatgt tggctaggct ggtcttgaac tcctgacttc aggtgatctg 60
cctgccttgg cctcccaaag tgctgggatt acaggcataa gccactgcgc ccggctgatc 120
tgatggttcc ataaggcttt tccccctttt gctcagcact tctccttcct gccgccatgt 180
gaagaaggac atgtttgctt ccccttccac cagcattgta agttgtttcc tgaggcctcc 240
ccggccatgc tgaactgtga gtcaattaaa cctctttcct ttataaatta tccagttttg 300
ggtatgtctt tattagtaga atgagaacag actaatacaa cccttaaagg agactgacgg 360
agaggattct tcctggatcc cagcacttcc tctgaatgct actgacattc ttcttgagga 420
ctttaaactg ggagatagaa aacagattcc atggctcagc agcctgagag cagggaggga 480
gccaagctat agatgacatg ggcagcctcc cctgaggcca ggtgtggccg aacctgggca 540
gtgctgccac ccacccaccc agggccaagt cctgtccttg gagagccaag cctcaatcac 600
tgctagcctc aagtgtcccc aagccacagt ggctaggggg actcagggaa cagttccca 660
tctgccctac ttctcttacc tttacccctc atacctccaa agtagaccat gttcatgagg 720
tccaaagg                                     728

```

```

<210> 17
<211> 531
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 518, 528
<223> n = A,T,C or G

```

```

<400> 17
aagcaggagaa gccactgcgg ctctggctg aaaagcggcg ccaggctcgg gaacagaggg 60
aacgcgaaga acaggagcgg aagctgcagg ctgaaaggga caagcgaatg cgagaggagc 120
agctggcccc ggaggctgaa gcccgggctg aacgtgaggc cgaggcgcg agacgggagg 180
agcaggaggg tcgagagaag gcgcaggctg agcaggagga gcaggagcga ctgcagaagc 240
agaaagagga agccgaagcc cgggtcccggg aagaagctga gcgccagcgc caggagcggg 300
aaaagcactt tcagaaggag gaacaggaga gacaagagcg aagaaagcgg ctggaggaga 360
taatgaagag gactcggaaa tcagaagccg ccgaaaccaa gaagcaggat gcaaaggaga 420
ccgcagctaa caattccggc ccagaccctt gtgaaagctg tagagactcg gccctctggg 480
cttcagaaaa ggattctatt gcagaaagga aggagctnng ccccccangg a 531

```

```

<210> 18
<211> 1041
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 544
<223> n = A,T,C or G

```

&lt;400&gt; 18

```

ctctgtggaa aactgatgag gaatgaattt accattaccc atgtttctcat cccaagcaa 60
agtgtctgggt ctgattactg caacacagag aacgaagaag aacttttcct catacaggat 120
cagcagggcc tcatcacact gggctggatt catactcacc ccacacagac cgcgtttctc 180
tccagtgtcg acctacacac tcaactgctct taccagatga tgttgccaga gtcagtagcc 240
attgtttgct cccccaagtt ccaggaaact ggattcttta aactaactga ccatggacta 300
gaggagattt ctctctgtcg ccagaaagga ttcatccac acagcaagga tccacctctg 360
ttctgtagct gcagccacgt gactgttggt gacagagcag tgaccatcac agaccttcga 420
tgagcgtttg agtccaacac ctccaagaa caacaaaacc atatcagtgt actgtagccc 480
cttaatttaa gctttctaga aagctttgga agtttttgta gatagtagaa aggggggcat 540
cacntgagaa agagctgatt ttgtatttca ggtttgaaaa gaaataactg aacatatttt 600
ttaggcaagt cagaaagaga acatggtcac ccaaaagcaa ctgtaactca gaaattaagt 660
tactcagaaa ttaagtagct cagaaattaa gaaagaatgg tataatgaac ccccatatac 720
cttccttctt ggattacca attgttaaca ttttttcct ctcagctatc cttctaattt 780
ctctctaatt tcaatttgtt tatatttacc tctgggctca ataaggcat ctgtgcagaa 840
atttggaagc catttagaaa atcttttgga ttttcctgtg gtttatggca atatgaatgg 900
agcttattac tggggtgagg gacagcttac tccatttgac cagattgttt ggctaacaca 960
tcccgaagaa tgattttgtc aggaattatt gttatttaat aaatatttca ggatattttt 1020
cctctacaat aaagtaacaa t 1041

```

&lt;210&gt; 19

&lt;211&gt; 1043

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

```

ctctgtggaa aactgatgag gaatgaattt accattaccc atgtttctcat cccaagcaa 60
agtgtctgggt ctgattactg caacacagag aacgaagaag aacttttcct catacaggat 120
cagcagggcc tcatcacact gggctggatt catactcacc ccacacagac cgcgtttctc 180
tccagtgtcg acctacacac tcaactgctct taccagatga tgttgccaga gtcagtagcc 240
attgtttgct cccccaagtt ccaggaaact ggattcttta aactaactga ccatggacta 300
gaggagattt ctctctgtcg ccagaaagga ttcatccac acagcaagga tccacctctg 360
ttctgtagct gcagccacgt gactgttggt gacagagcag tgaccatcac agaccttcga 420
tgagcgtttg agtccaacac ctccaagaa caacaaaacc atatcagtgt actgtagccc 480
cttaatttaa gctttctaga aagctttgga agtttttgta gatagtagaa aggggggcat 540
cacctgagaa agagctgatt ttgtatttca ggtttgaaaa gaaataactg aacatatttt 600
ttaggcaagt cagaaagaga acatggtcac ccaaaagcaa ctgtaactca gaaattaagt 660
tactcagaaa ttaagtagct cagaaattaa gaaagaatgg tataatgaac ccccatatac 720
cttccttctt ggattacca attgttaaca ttttttcct ctcagctatc cttctaattt 780
ctctctaatt tcaatttgtt tatatttacc tctgggctca ataaggcat ctgtgcagaa 840
atttggaagc catttagaaa atcttttgga ttttcctgtg gtttatggca atatgaatgg 900
agcttattac tggggtgagg gacagcttac tccatttgac cagattgttt ggctaacaca 960
tcccgaagaa tgattttgtc aggaattatt gttatttaat aaatatttca ggatattttt 1020
cctctacaat aaagtaacaa tta 1043

```

&lt;210&gt; 20

&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

```

ggacgacaag gccatggcga tatcggatcc gaattcaagc ctttggaatt aaataaacct 60
ggaacaggga aggtgaaagt tggagtgaga tgtcttccat atctatacct ttgtgcacag 120
ttgaatggga actgtttggg tttagggcat cttagagttg attgatggaa aaagcagaca 180
ggaactgggt ggaggtcaag tggggaagtt ggtgaatgtg gaataactta cttttgtgct 240
ccacttaaac cagatgtgtt gcagctttcc tgacatgcaa ggatctactt taattccaca 300
ctctcattaa taaattgaat aaaagggaat gttttggcac ctgatataat ctgccaggct 360
atgtgacagt aggaaggaat ggtttccctt aacaagccca atgcactggg ctgactttat 420

```

aaattattta ataaaatgaa ctattatc

448

<210> 21

<211> 411

<212> DNA

<213> Homo sapiens

<400> 21

```

ggcagtgaca ttcacccatca tgggaaccac cttccctttt cttcaggatt ctctgtagtg 60
gaagagagca cccagtgttg ggctgaaaac atctgaaagt agggagaaga acctaaaata 120
atcagtatct cagagggtc taagggtcca agaagtctca ctggacattt aagtgccaac 180
aaaggcatac tttcgggaatc gccaaagtcaa aactttctaa cttctgtctc tctcagagac 240
aagtgagact caagagtcta ctgctttagt ggcaactaca gaaaactggt gttaccacaga 300
aaaacaggag caattagaaa tggttccaat atttcaaagc tccgcaaaca ggatgtgctt 360
tcctttgccc atttaggggt tcttctcttt ctttctctt tattaaccac t 411

```

<210> 22

<211> 896

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 230, 320

<223> n = A,T,C or G

<400> 22

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tgcgctgaaa acaacggcct cttttactgt taaaatgcag ccacaggtgc ttagccgtgg 60
gcatctcaac caccagcctc tgtggggggc aggtggggtt ccctgtgggc ctctggggccc 120
acgtccagcc tctgtcctct gccttccgtt cttcgacagt gttcccggca tccctgggtca 180
cttgggtactt ggctggggcc tctgtgtctg ctccagcagc tccctcaggc ggctggggccc 240
cttcaccgca gcctcatgtt gtgtccggag gctgtctcag gcctcctcct tctctggcag 300
ggctgtcttc accctccggc gcacctcctc cagctccagc tgcctggcgg cctgcagcgt 360
ggccagctcg gccttggcct gccgcgtctc ctctcarag gctgccagcc ggctcctcga 420
ctcctggcgg atcacctggg ccaggttget gcgtcgtcta gaaagctgct cgttcaccgc 480
ctgcgcatcc tccagcgccc gctccttctg ccgcacaagg ccctgcagac gcagattctc 540
gcctcgggcc tcccaagct ggcccttcag ctccgagcac cgctcctgaa gcttccgctc 600
cgactgctcc agctcggaga gctcggcctc gtacttgtcc cgtaagcgtt tgatgcggct 660
ctcggcagcc ttctcactct cctccttggc cagcgccatg tcggcctcca gccggtgaat 720
gaccagctca atctccttgt cccggccttt ccggatttct tccctcagct cctgttcccg 780
gttcagcagc cagcctcct ccttctggt gcggccggcc tcccacgcct gcctctccag 840
ctccagctgc tgettcaggg tattcagctc catctggcgg gcctgcagcg tggcca 896

```

<210> 23

<211> 111

<212> DNA

<213> Homo sapiens

<400> 23

```

caacttatta cttgaaatta taatatagcc tgtccgtttg ctgtttccag gctgtgatat 60
attttcctag tgggttgact ttaaaaataa ataaggttta attttctccc c 111

```

<210> 24

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature  
<222> 472, 494  
<223> n = A,T,C or G

<400> 24  
tgcaagtcac gggagtttat ttatttaatt tttttcccca gatggagact ctgtcgccca 60  
ggctggagtg caatgggtgtg atcttggtc actgcaacct ccacctcctg gggtcaagcg 120  
attctcctgc cacagcctcc cgagtagctg ggattacagg tgcccgccac cacaccagc 180  
taatttttat atttttagta aagacagggg ttcccatgt tggccaggct ggtcttgaac 240  
ttctgacctc aggtgatcca cctgcctcgg cctcccaaag tgttgggatt acaggcgtga 300  
gctaccctg cctggccagc cactggagtt taaaggacag tcatgttggc tccagcctaa 360  
ggcggcattt tcccccata gaaagccgc ggctcctgta cctcaaaata gggcacctgt 420  
aaagtcagtc agtgaagtct ctgctctaac tggccaccgg gggccattgg cntctgacac 480  
agccttgcca ggagcctgc atctgcaaaa gaaaagttca cttcctttcc g 531

<210> 25  
<211> 471  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 377  
<223> n = A,T,C or G

<400> 25  
cagagaatct kagaaagatg tcgcgttttc ttttaatgaa tgagagaagc ccatttgtat 60  
ccctgaatca ttgagaaaag gcggcggttg cgacagcggc gacctaggga tcgatctgga 120  
gggacttggt gagcgtgcag agacctctag ctcgagcggc agggacctcc cgccgggatg 180  
cctggggagc agatggaccc tactggaagt cagtggatt cagatttctc tcagcaagat 240  
actccttgcc tgataattga agattctcag cctgaaaagc aggttctaga ggatgattct 300  
ggttctcact tcagtatgct atctcgacac cttcctaata tccagacgca caaagaaaat 360  
cctgtgttg atgttgngtc caatccttga acaaacagct ggagaagaac gaggagaccg 420  
gtaatatgtg gttcaatgaa catttgaaag aaaaccaggt tgagaccct g 471

<210> 26  
<211> 541  
<212> DNA  
<213> Homo sapiens

<400> 26  
gactgtcctg aacaagggac ctctgaccag agagctgcag gagatgcaga gtggtggcag 60  
gagtgaagc caaagaacac ccaccttctt cccttgaagg agtagagcaa ccatacagaag 120  
atactgtttt attgctctgg tcaaacaagt ctctctgagt tgacaaaacc tcaggctctg 180  
gtgacttctg aatctgcagt ccactttcca taagttcttg tgcagacaac tgttcttttg 240  
cttccatagc agcaacagat gctttggggc taaaaggcat gtcctctgac cttgcagggtg 300  
gtggattttg ctctttttaca acatgtacat ccttactggg ctgtgctgtc acagggatgt 360  
ccttgctgga ctgttctgct atggggatat cttcgttgga ctgttcttca tgcttaattg 420  
cagtattagc atccacatca gacagcctgg tataaccaga gttggtggtt actgattgta 480  
gctgctcttt gtccacttca tatggcacia gtattttcct caacatcctg gctctgggaa 540  
g 541

<210> 27  
<211> 461  
<212> DNA  
<213> Homo sapiens

<220>



&lt;221&gt; misc\_feature

&lt;222&gt; 367

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 27

```

gaaatgtata tttaatcatt ctcttgaacg atcagaactc traaatcagt tttctataac 60
arcatgtaat acagtcaccg tggctccaag gtccaggaag gcagtggtta acacatgaag 120
agtgtgggaa gggggctgga aacaaagtat tcttttcctt caaagcttca ttcctcaagg 180
cctcaattca agcagtcatt gtccttgctt tcaaaagtct gtgtgtgctt catggaaggt 240
atatgtttgt tgccttaatt tgaattgtgg ccaggaaggg tctggagatc taaattcaga 300
gtaagaaaac ctgagctaga actcaggcat ttctcttaca gaacttggtc tgcagggtag 360
aatgaangga aagaaactta gaagctcaac aagctgaaga taatcccatc aggcatttcc 420
cataggcctt gcaactctgt tcactgagag atgtttatcct g 461

```

&lt;210&gt; 28

&lt;211&gt; 541

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

```

agtctggagt gagcaaacaa gagcaagaaa caarragaag ccaaaagcag aagggtccaa 60
tatgaacaag ataaatctat cticcaagac atattagaag ttgggaaaat aattcatgtg 120
aactagacaa gtgtgttaag agtgataagt aaaatgcacg tggagacaag tgcattccca 180
gatctcaggg acctccccct gcctgtcacc tggggagtga gaggacagga tagtgcatgt 240
tctttgtctc tgaattttta gttatatgtg ctgtaatgtt gctctgagga agcccctgga 300
aagtctatcc caacatatcc acatcttata ttccacaaat taagctgtag tatgtaccct 360
aagacgtgc taattgactg ccaacttcgca actcaggggc ggctgcattt tagtaatggg 420
tcaaattgatt cactttttat gatgcttccc aagggtgcctt ggcttctctt cccaactgac 480
aatgcccacaa gttgagaaaa atgatcataa ttttagcata aaccgagcaa tcggcgaccc 540
c 541

```

&lt;210&gt; 29

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

```

tagctgtctt cctcactctt atggcaatga ccccatatct taatggatta agataatgaa 60
agtgtatttc ttacactctg tatctatcac cagaagctga ggtgatagcc cgcttgtcat 120
tgtcatccat attctgggac tcaggcggga actttctgga atattgccag ggagcatggc 180
agaggggcac agtgcattct gggggaatgc acattggctc agcctgggta atgagtgata 240
tacattacct ctgttcacaa ctcatgccc agcaccagtc acaaggcccc accaaatacc 300
agagcccaag aaatgtagtc ctgttgatat ggttttgctg tgtcccaacc caaatctcat 360
cttgaattgt aagctcccat aattcccatg tgttggtgga gggacctggt g 411

```

&lt;210&gt; 30

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

```

atcatgagga tgttaccaaa gggatggtac taaaccattt gtattcgtct gttttcacac 60
tgctttgaag atactacctg agactgggta atttataaac aaaagagatt taattgactc 120
acagttctgc atggctgaag aggcctcagg aaacttacag tcatggtgga agggcaagga 180
ggagcaaggc atgtcttaca tgtcagtagg agagagagcg agagcaggag aacctgccac 240
ttataaacca ttcagatctc ataactccct atcatgagaa aaacatggag gaaaccaccc 300
tcatgatcca atcacctccc gccaggtccc tccctcgaca cgtggggatt ataattcagg 360
attagagggga cacagagaca aaccatatca tcattcatga gaaatccacc ctcatagtcc 420

```

aatcagctcc taccaggccc cacctccaac actggggatt gcaattcaac atgagatttg 480  
 gatggggaca cagattcaaa ccatatcata c 511

<210> 31  
 <211> 827  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 catggccttt ctcccttagag gccagagggtg ctgccctggc tgggagtga gctccaggca 60  
 ctaccagctt tcctgatttt cccgtttggt ccatgtgaag agctaccacg agccccagcc 120  
 tcacagtgtc cactcaaggg cagcttggtc ctcttgcct gcagaggcag gctgggtgtga 180  
 ccctgggaac ttgaccggg aacaacagggt ggcccagagt gagtgtggcc tggccctca 240  
 acctagtgtc cgtcctcctc tctcctggag ccagtcttga gtttaaaggc attaatgttt 300  
 agatacaagc tccttgtggc tggaaaaaca cccctctgct gataaagctc agggggcact 360  
 gaggaagcag agggcccttg ggggtgccct cctgaagaga gcgtcaggcc atcagctctg 420  
 tcctctgtgt gctccacgt ctgttctca ccctccatct ctgggagcag ctgcacctga 480  
 ctggccacgc gggggcagt gaggcacagg ctcagggtgg ccgggctacc tggcacccta 540  
 tggcttacia agtagagttg gccagtttc cttccacctg aggggagcac tctgactcct 600  
 aacagtcttc cttgccctgc catcatctgg ggtggctggc tgtcaagaaa ggccgggcat 660  
 gctttctaaa cacagccaca ggaggcttgt agggcatctt ccagggtggg aaacagtctt 720  
 agataagtaa ggtgacttgc ctaaggcctc ccagcaccct tgatcttggg gtctcacagc 780  
 agactgcatg tsaacaactg gaaccgaaaa catgctcag tataaaa 827

<210> 32  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 ccagaacctc cttctctttg gagaatgggg aggcctcttg gagacacaga gggtttcacc 60  
 ttggatgacc tctagagaaa ttgccaaga agcccacctt ctgggtccaa cctgcagacc 120  
 ccacagcagt cagttggtca ggccctgctg tagaaggta cttgggtcca ttgcctgttt 180  
 ccaaccaatg ggcaggagag aaggccttta tttctcgccc acccattctc ctgtaccagc 240  
 acctccggtt tcagtcagyg ttgtccagca acggtaccgt ttacacagtc a 291

<210> 33  
 <211> 491  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 tgcattgact tttatttatg tgttttsgtc tggaaaacca agtgtcccag cagcatgact 60  
 gaacatcact cacttcccct acttgatcta caaggccaac gccgagagcc cagaccagga 120  
 ttccaaacac actgcacgag aatattgttg atccgctgtc aggtaatgtt ccgtcactga 180  
 cccaracgct gttacgtggc acatgactgt acagtgccac gtaacagcac tgtacttttc 240  
 tcccatgaac agttacctgc catgtatcta catgattcag aacattttga acagttaatt 300  
 ctgacacttg aataatccca tcaaaaaccg taaaatcact ttgatgtttg taacgacaac 360  
 atagcatcac tttacgacag aatcatctgg aaaaacagaa caacgaatac atacatctta 420  
 aaaaatgctg ggggtggcca ggcacagctt cagcctgta atcccagcac tttgggaggc 480  
 ttaagcgggt g 491

<210> 34  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> misc\_feature  
 <222> 453, 476, 487  
 <223> n = A,T,C or G

<400> 34  
 tggggcgga agaagccaag gccaaaggagc tgggtcgga gctgcagctg gaggccgagg 60  
 agcagaggaa gcagaagaag cggcagagtg tgctgggcct gcacagatac cttcacttgc 120  
 tggatggaaa tgaaaattac ccgtgtcttg tggatgcaga cggatgatgtg atttccttcc 180  
 caccaataac caacagttag aagacaaagg ttaagaaaac gacttctgat ttgtttttgg 240  
 aagtaacaag tgccaccagt ctgcagattt gcaaggatgt catggatgcc ctcattctga 300  
 aaatggcaag aaatgaaaaa gtacacttta gaaaataaag aggaaggatc actctcagat 360  
 actgaagccg atgcagtctc tggacaactt ccagatccca caacgaatcc cagtgcctgga 420  
 aaggacgggc ccttccttct ggtggtggaa cangtcccg tggatgatct tggaanggaa 480  
 cctgaangtg gtgtaccccg tccaaggccg accttgcca c 521

<210> 35  
 <211> 161  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 18  
 <223> n = A,T,C or G

<400> 35  
 tcccgcgctc gcagggcncg tgccacctgc cygtccgcc gctcgctcgc tgcgccgccg 60  
 cgccgcgctg ccgaccgyca gcagctgcc gagagtgggc tgccccgcgc tgccgctgcc 120  
 gccgccgccg ctgctgccgc tgctgccgct gctgctgctg c 161

<210> 36  
 <211> 341  
 <212> DNA  
 <213> Homo sapiens

<400> 36  
 ggcgggttagg catggaactg agaagaacga agaagctttc agactacgtg gggaagaatg 60  
 aaaaaaccaa aattatcgcc aagattcagc aaaggggaca gggagctcca gcccagagagc 120  
 ctattattag cagtggaggag cagaagcagc tgatgctgta ctatcacaga agacaagagg 180  
 agctcaagag attggaagaa aatgatgatg atgcctattt aaactcacca tgggcggata 240  
 aactgcttt gaaaagacat tttcatggag tgaagacat aaagtggaga ccaagatgaa 300  
 gttcaccagc tgatgacact tccaagaga ttagctcacc t 341

<210> 37  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 516  
 <223> n = A,T,C or G

<400> 37  
 tctgaagggtt aaatgtttca tctaaatagg gataatgrta aacacctata gcatagagtt 60  
 gtttgagatt aaatgagata atacatgtaa aattatgtgc ctggcataca gcaagattgt 120  
 tggtgtgtgt gatgatgatg atgatgatga taatattttt ctatccccag tgcacaactg 180  
 cttgaacctt ttagataatc aatacatgtt tcttgaactg agatcaattt ccccatgttg 240

```

tctgactgat gaagccctac attttcttct agaggagatg acatttgagc aagatcttaa 300
agaaaatcag atgccttcac ctgaccactg cttggtgatc ccatggcact ttgtacatct 360
ctccattagc tctcatctca ccagcccatc attattgtat gtgctgcctt ctgaagcttg 420
cagctggcta ccatcmggta gaataaaaat catcctttca taaaatagtg accctccttt 480
tttatttgca tttcccaaag ccaagcaccg tgggaggta g 521

```

```

<210> 38
<211> 461
<212> DNA
<213> Homo sapiens

```

```

<400> 38
tatgaagaag ggaaaagaag ataatttgtg aaagaaatgg gtccagttac tagtctttga 60
aaagggtcag tctgtagctc ttcttaatga gaataggcag ctttcagttg ctcagggtca 120
gatttcctta gtggtgtatc taatcacagg aaacatctgt ggttccctcc agtctctttc 180
tggtgggactt gggcccatc ctcatttcat ttaattagag gaaatagaac tcaaagtaca 240
atttactgtt gtttaacaat gccacaaaga catggttggg agctatttct tgatttgtgt 300
aaaatgctgt ttttgtgtgc tcataatggt tccaaaaatt ggggtgctggc caaagagaga 360
tactgttaca gaagccagca agaagacctc tgttcattca cccccccggg gatatcagga 420
attgactcca gtgtgtgcaa atccagtttg gcctatcttc t 461

```

```

<210> 39
<211> 769
<212> DNA
<213> Homo sapiens

```

```

<400> 39
tgagggactg attggtttgc tctctgctat tcaattcccc aagcccaactt gttcctgcag 60
cgctctcctt ctcatccctt ttagttgtac cctctctttc atctgagacc tttccttctt 120
gatgtcgctt tttctcttct ttgctttttc tgatgttctg ctccagcatgt tctgggtgct 180
tctcatctgc atcattcctt tcagatgctg tagcttcttc ctctcttttc tgectccttt 240
tctttttctt ttttttgggg ggcttgctct ctgactgcag ttgaggggcc ccagggtcct 300
ggcctttgag acgagccagg aaggcctgct cctgggcctc taggcgagca agcttggcct 360
tcattgtgat cccaagacgg gcagccttgt gtgctgttcg cccctcacag gcttggagca 420
gcattctcat agtcagaate tttggggact tggaccctg gttgtcgtca tcaactgcagc 480
tctccaagtc tttgtttggc ttctctccac ctgaagtcaa tgtagccatc ttcacaaact 540
tctgatacag caagttgggc ttgggatgat tataacgggt ggtctcctta gaaaggctcc 600
ttatctgtac tccatcctgc ccagtttcca ctaccaagtt ggccgcagtc ttgttgaaga 660
gtcattcca ccagtggttt gtgaactcct tggcagggtc atgtcctacc ccatgagtg 720
cttgcttcag ygtcacccctg agagcctgag tgataccatt ctccttcctg 769

```

```

<210> 40
<211> 292
<212> DNA
<213> Homo sapiens

```

```

<400> 40
gacaacatga aataaatcct agaggacaaa attaaactca atagagtgtg gtctagttaa 60
aaactcgaaa aatgagcaag tctggtggga gtggaggaag ggctatacta taaatccaag 120
tggtcctcct gatcttaaca agccatgctc attatacaca tctctgaact ggacatacca 180
cctttacgca ggaaacaggg cttggaactt ctaagggaat ttaacatgca ccaccacat 240
ctaacctacc tgccgggtag gtaccatccc tgcttcgctg aaatcagtcg tc 292

```

```

<210> 41
<211> 406
<212> DNA
<213> Homo sapiens

```

&lt;400&gt; 41

```

ttggaattaa ataaacctgg aacaggggaag gtgaaagtgt gagtgagatg tcttccatat 60
ctataaccttt gtgcacagtt gaatgggaac tgtttgggtt tagggcatct tagagttgat 120
tgatggaaaa agcagacagg aactgggtgg aggtcaagtg gggaagtgtg tgaatgtgga 180
ataacttacc tttgtgctcc acttaaacca gatgtgttgc agctttcctg acatgcaagg 240
atctacttta attccacact ctcattaata aattgaataa aagggaaatgt tttggcacct 300
gatataatct gccaggctat gtgacagtag gaaggaatgg tttcccctaa caagcccaat 360
gcactgggtct gactttataa attatttaat aaaatgaact attatc 406

```

&lt;210&gt; 42

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

```

aaactggacc tgcaacaggg acatgaatth actgcarggt ctgagcaagc tcagcccctc 60
tacctcaggg cccacagacc atgactacct cccccaggag cgggagggtg aagggggcct 120
gtctctgcaa gtggagccag agtggaggaa tgagctctga agacacagca cccagccttc 180
tcgaccagc caagccttaa ctgcctgcct gaccctgaac cagaaccag ctgaactgcc 240
cctccaaggg acaggaaggc tgggggaggg agtttacaac ccaagccatt ccaccccctc 300
ccctgctggg gagaatgaca catcaagctg ctaacaattg ggggaagggg aaggaagaaa 360
actctgaaaa caaatcttg t 381

```

&lt;210&gt; 43

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

```

catgcgttcc accactgttg gccaggctgg tctcgaactc ctggcctcaa gcaatccacc 60
cgctcagacc tccaaaagtg ctgggattac agatgtgagc catggcacca tgccaaaagg 120
ctataatcct ggctctgtgt ttccgagact gcttttaatc ccaacttctc tacatttaga 180
ttaaaaaata ttttattcat ggtcaatctg gaacataatt actgcatctt aagtttccac 240
tgatgtatat agaaggctaa aggcacaatt tttatcaaat ctagtagagt aaccaaacat 300
aaaatcatta attactttca acttaataac taattgacat tectcaaaag agctgttttc 360
aatcctgata ggttctttat tttttcaaaa tatatttgcc atgggatgct aatttgcaat 420
aaggcgcata atgagaatac cccaaactgg a 451

```

&lt;210&gt; 44

&lt;211&gt; 521

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

```

gttggacccc cagggactgg aaagacactt cttgcccgag ctgtggcggg agaagctgat 60
gttccttttt attatgcttc tggatccgaa tttgatgaga tgtttgtggg tgtgggagcc 120
agccgtatca gaaatctttt tagggaagca aaggcgaatg ctcttgtgt tatatttatt 180
gatgaattag attctgttgg tgggaagaga attgaatctc caatgcatcc atattcaagg 240
cagaccataa atcaacttct tgctgaaatg gatggtttta aaccatga aggagtatc 300
ataataggag ccacaaactt cccagaggca ttagataatg ccttaatacc gtccgtgtcg 360
ttttgacatg caagttagc ttccaaggcc agatgtaaaa ggtcgaacag aaattttgaa 420
atggtatctc aataaaaata agtttgatca atcccgttga tccagaaatt atagcctcga 480
ggtactggtg gcttttccgg aagcagagtt gggagaatct t 521

```

&lt;210&gt; 45

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

```

gcctacaaca tccagaaaga gtctaccctg cacctggtgc tscgtctcag aggtgggatg 60
cagatcttcg tgaagaccct gactggtaag accatcactc tcgaagtga gccagtgac 120
accatygaga acgtcaaagc aaagatccar gacaaggaag gcrtycctcc tgaccagcag 180
aggttgatct ttgccggaaa gcagctggaa gatggdcgca ccctgtctga ctacaacatc 240
cagaaagagt cyaccctgca cctggtgctc cgtctcagag gtgggatgca ratcttcgtg 300
aagaccctga ctggtaagac catcaccctc gaggtggagc ccagtgcac catcgagaat 360
gtcaaggcaa agatccaaga taaggaaggc atccctcctg atcagcagag gttgatcttt 420
gctgggaaac agctggaaga tggacgcacc ctgtctgact acaacatcca gaaagagtcc 480
actctgcact tggctctgcg cttgaggggg ggtgtctaag tttccccttt taaggtttcm 540
acaaatttca ttgcactttc ctttcaataa agttgttgca ttccc 585

```

&lt;210&gt; 46

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

```

gaactgggcc ctgagcccaa gtcatgcctt gtgtccgcat ctgccgtgtc acctctgtkc 60
ctgcccctca cccctccctc ctggtcttct gagccagcac catctccaaa tagcctattc 120
cttcctgcaa atcacacaca catgcgggcc acacatacct gctgccctgg agatggggaa 180
gtaggagaga tgaatagagg ccatacatt gtacagaagg aggggcaggt gcagataaaa 240
gcagcagacc cagcggcagc tgaggtgcat ggagcacggt tggggccggc attgggctga 300
gcacctgatg ggcctcatct cgtgaatcct cgaggcagcg ccacagcaga ggagttaagt 360
ggcacctggg ccgagcagag caggagactg agggtcagag tggaggctaa gctgccctgg 420
aactcctcaa tcttgctgc cccctagtat gaagccccct tcctgccctt acaattcctg 480
a 481

```

&lt;210&gt; 47

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 128

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 47

```

atggatctta ctttgcacc caggttgagg tgcagtgtcg caatcttggc tcaactgcagc 60
cttaacctcc caggetcaag ctatcctcct gccaaagcct tccacatagc tgggactaca 120
ggtacacngc caccacaccc agctaaaatt tttgtathtt ttgtagagac gggatctcgc 180
cacgttgccc aggttggtcc catcctgacc tcaagcagat ctgccacct cagcccccca 240
acgtgctagg attacaggcg tgagccaccg caccacgctt ttgttttgct tttaatggaa 300
tcaccagttc ccctccgtgt ctacagagca gctgtgagaa atgctttgca tctgtgacct 360
ttatgaaggg gaacttccat gctgaatgag ggtaggatta catgctcctg tttcccgggg 420
gtcaagaaaag cctcagactc cagcatgata agcagggtga g 461

```

&lt;210&gt; 48

&lt;211&gt; 571

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

```

ataggggctt taaggaggga attcaggttc aatgaggtcg taaggccagg gctcttatcc 60
agtaagactg gggctccttag atgagaaaga gacacccgag gtccttctct ctgccgtgtg 120
aggatgcate aagaaggcgg ccgtctgcaa gcgaaggaga ggccgcacca gaaaccgaca 180

```

```

ccttcacatt ggacttgac cctctagaac tgagaaaata actgtctgtt ggtaagcca 240
cccagtttgt agtattctct tatggcttcc taagcagact aacaaacaaa caccacaaat 300
taactgatgg ctctgctgtc ttctgtaaaa attgctatga gagaactttt cactcactgt 360
tttgagtttt ctccctcagt ccttggttct ttcttctcac ataatcccaa ttcaattta 420
tagttcatgg ccagggcaga gtcattcatc acggcatctc ctgagctaaa ccagcacctg 480
ctctgctcac ttcttgactg gctgctcatc atcagccctc ttgcagagat ttcatttcct 540
cccgtgccag gtacttcacg caccaagctc a 571

```

<210> 49  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

```

<400> 49
ggataatgaa gttgttttat ttagcttggc caaaaaggca ttttcttata 60
caacaaatat ccccaaaata aagcaagcat atatatcttg aatgtgtaat aatccagtga 120
taaacagagc cagtacttta aaagaaaaaa aaatatgtat ttctgtcagg ttaaatgag 180
aatcaaaacc atttactctg ctaactcatt attttttgct ttctttttgg ttaagagagg 240
caatgcaata cactgaaaaa ggtttttatc ttatctggca ttggaattag acatattcaa 300
acccagcccc ccatttccaa actttaagac cacaacaaag taatttactt ttctgaacat 360
tggttttttc tggaaaatgg gaattataaa atagactttg cagactctta tgagattaaa 420
taagataatg tatgaaattc tttcttcttt tttacttctt tttccttttt gagatggagt 480
ctcaccocgt caccagaggt ggagtacagt g 511

```

<210> 50  
 <211> 561  
 <212> DNA  
 <213> Homo sapiens

```

<400> 50
ccactgcact ccagcctggg tgacggagtg agactctgtc tcaaaaaaac aaacaaacaa 60
acaaacaaaa aactgaaaag gaaatagagt tcctctttcc tcatatatga atatattatt 120
tcaacagatt gttgatcacc taccatagtc ttggtattgt tctaattgct ggggatacag 180
caagagggtc tgagaaactt catggagcat gaaagtaaat aaacaaagtt aatttcaagg 240
ccaggcatgg ttgctcacac cttagtccc agcactttgg gaggtgagg cagggtggatc 300
actgggccc aggagttcaa ggctgcagtg agccaagatt gtgccactac tctccaggtc 360
gggcaacaga gcaagacct gtctcagggg gaacaaaaag ttaatttcag attttgtaa 420
gtgctgtaaa ggaagtaaat aggttgatat tcaagagagc acctgaaggc caggcgtggt 480
ggctcacgcc tgtggtctaa cgctttggga agcccagcgg ggcggatcac aaggctcagg 540
gaattttggc caggcatggt g 561

```

<210> 51  
 <211> 451  
 <212> DNA  
 <213> Homo sapiens

```

<400> 51
agaatccatt tattgggttt taaactagtt acacaactga aatcagtttg gcactacttt 60
atacagggat tacgcctgtg tatgccgaca cttaataact gtaccaggac cactgctgtg 120
cttaggtctg tattcagtca ttcagcatgt agatactaaa aatatactgt agtggttcct 180
taagggaagc tgtacagggg gtgttgcaag atgacattca ccaatttggt aattatttca 240
accagaaga tacctttcac tctataaact tgtcataggc aaacatgtgg tgtagcatt 300
gagagatgca cacaaaaatg ttacataaaa gttcagacat tctaatagata agtgaactga 360
aaaaaaaaaa aacccacat ctcaattttt gtaacaagat aaagaaaata atttaaaaac 420
acaaaaaatg gcattcagtg ggtacaaagc c 451

```

<210> 52  
 <211> 682

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

```

caaatattta atataaatct ttgaaacaag ttcagakgaa ataaaaatca aagtttgcaa 60
aaacgtgaag attaaactta ttgtcaaata ttcctcattg ccccaaata gtattttttt 120
tatttctatg caaaagtatg ccttcaaact gcttaaatga tatatgatat gatacacaaa 180
ccagttttca aatagtaaag ccagtcattc tgcaattgta agaaataggt aaaagattat 240
aagacacctt acacacacac acacacacac acacacacgt gtgcaccgcc aatgacaaaa 300
aacaatttgg cctctcctaa aataagaaca tgaagaccct taattgctgc caggagggaa 360
cactgtgtca cccctcccta caatccaggt agtttccttt aatccaatag caaatctggg 420
catatttgag aggagtgatt ctgacagcca csgettgaat cctgtgggga accattcatg 480
tccacccact ggtgccctga aaaaatgccataaataattttc gctccactt ctgctgctgt 540
ctcttcacata tcctcacata gacccagac ccgctggccc ctggctgggc atcgctgtgc 600
tggtagagca agtcattaggt ctgctctttg acgtcacaga agcgatacac caaattgcct 660
ggtcgggtcat tgtcataacc ag                                     682

```

&lt;210&gt; 53

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 208

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 53

```

tttgacttta gttaggggtct gaactattta ttttactttg ccmgtaatat ttaraccyta 60
tatatctttc attatgccat cttatcttct aatgbcaagg gaacagwtgc taamctggct 120
tctgcattwa tcacattaaa aatggctttc ttggaaaatc ttcttgatat gaataaagga 180
tcttttavag ccatcattta aagcmggnnt ctctccaaca cgagtctgct sasgggggk 240
gagctgtgaa ctctggctga aggctttccc atacacactg caatgacmtg gtttctgacc 300
agbgtgaagt a                                     311

```

&lt;210&gt; 54

&lt;211&gt; 561

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 54

```

agagaagccc cataaatgca atcagtgtgg gaaggccttc agtcagagct caagcctttt 60
cctccatcat cgggttcata ctggagagaa accctatgta tgtaatgaat gcggcagagc 120
ctttggtttt aactctcatc ttactgaaca cgtaaggatt cacacaggag aaaaacccta 180
tgtttgtaat gagtgcggca aagcctttcg tcggagttcc actcttggtc agcatcgaag 240
agttcacact ggggagaagc cctaccagtg cgttgaatgt gggaaagctt tcagccagag 300
ctcccagctc accctacatc agccgagttc acactggaga gaagccctat gactgtggtg 360
actgtgggaa ggccttcagc cggaggtcaa ccctcattca gcatcagaaa gttcacagcg 420
gagagactcg taagtgcaga aaacatggtc cagcctttgt tcatggctcc agcctcacag 480
cagatggaca gattccact ggagagaagc acggcagaac ctttaacat ggtgcaaatt 540
tcattctgcg ctggacagtt c                                     561

```

&lt;210&gt; 55

&lt;211&gt; 811

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 55



```

gagacagggg ctcactttgt caccagggct ggaatgcagt ggtgcgatct tacgtagctc 60
actgcagccc tgacctcctg gactcaaaca attctcctgc ctcagccctg caagtagctg 120
ggactgtggg tgcattgccac catgcctggc taacttttgt agtttttgta aagatggggg 180
tttgccatgt tgcacatgct ggtcttgaac tctgagctc aaacgatctg cccacctcgg 240
cctcccagaa tgttgggatt acaggggtaa accaccacgc ctggcccat tagggatttc 300
ttagcatcca ctgtctcact gagattaatc ataagagatg ataagcactg gaagaaaaaa 360
atttttacta ggctttggat attttttccc tttttcagct ttatacagag gattggatct 420
ttagttttcc ttttaactgat aataaaacat tgaaaggaaa taagtttacc tgagattcac 480
agagataacc ggcattcact ccttgcctca ttccagtctt taccacatca attattttca 540
gaggtgcagg ataaaggcct ttagtctgct ttgcgacttt ttcttccact tttttgtaaa 600
cctgttgccg gacaaatgga attgacagcg tatgccatga ctattccatt tgtcaggcat 660
acgctgtcaa tttttccacc aatcccttgt ctctctttgg agagatcttc ttatcagcta 720
gtcctttggc aaaagtaatt gcaacttctt ctagggtattc tattgtccgt tccactgggtg 780
gaaccctggg gaccaggact aaaacctcca g                                     811

```

<210> 56

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 45, 477, 490, 561

<223> n = A,T,C or G

<400> 56

```

atctcatata tatattttctt cctgacttta tttgcttgct tctgncacgc atttaaaata 60
tcacagagac caaaatagag cggctttctg gtggaacgca tggcagtcac aggacaaaat 120
acaaaactag ggggctctgt cttctcatac atcatacaat ttccaagtat tttttttatg 180
tacaaagagc tactctatct gaaaaaaaat taaaaaataa atgagacaag atagtttatg 240
catcctagga agaaagaatg ggaagaaaga acggggcagt tgggtacaga ttctgtccc 300
ctgttcccag ggaccactac cttcctgccg ctgagttccc ccacagcctc acccatcatg 360
tcacagggca agtgccaggg taggtgggga ccagtgagga caggaaccag caacatactt 420
tggcctggaa gataaggaga aagtctcaga aacacactgg tgggaagcaa tcccacnggc 480
cgtgccccan gagcttccca cctgctgctg gctccctggg tggttttggg aacagcttgg 540
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<210> 57

<211> 481

<212> DNA

<213> Homo sapiens

<400> 57

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tttacctctt tacaaattaa ataagcaagt aactggatcc acaatttata atacctgtca 180
attttttctg tattaaacct ctatcatagt ttaagcctat tagggactt aatccttaca 240
aataaacagg tttaaaatca cctcaatagg caactgcctt tctggttttc ttctttgact 300
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ctgtattcca gacttcttaa attatagaaa aaggaatgta cactttttgt attctttctg 420
agcagggccg ggaggcaaca tcatctacca tggtagggac ttgtatgcat ggactacttt 480
a                                     481

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<210> 58

<211> 141

<212> DNA

<213> Homo sapiens

<400> 58  
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 acaggwtcat gccattctcc tgcctcagca tctggagtag ctgggactac aggcgccagc 120  
 caccatgccc agctaatttt t 141

<210> 59  
 <211> 191  
 <212> DNA  
 <213> Homo sapiens

<400> 59  
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 acaagacttg ggagtgttc acacctggaa caacatactg gacttcacac tggabagaaa 120  
 ccttacaagt gtaatgagtg tggcaaagcc tttggcaagc agtcaacact tattcaccat 180  
 caggcaattc a 191

<210> 60  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 60  
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 tattacatct gaagaacgta ctaagcatga taaacagttt gataacctca aaccttcagg 120  
 aggttacata acagggtgatc aagcccgtag ttttttccta cagtcaggtc tggcggtccc 180  
 ggtttttagct gaaatatggg ccttatcaga tctgaacaag gatgggaaga tggaccagca 240  
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 agtcctccct cctatcatga aacaaccccc tatgttctct ccactaatct ctgctcgttt 360  
 tgggatggga agcatgccc atctgtccat tcatcagcca ttgcctccag ttgcacctat 420  
 agcaacaccc ttgtcttctg ctacttcagg gaccagtatt cctccctaata gatgcctgct 480

<210> 61  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
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 agcttagatg cagtttcttt ttcaagagca tctaattgtt ctttaagtct ttggcataat 180  
 tcttcctttt ctgatgactt tctatgaagt aaactgatcc ctgaatcagg tgtgttactg 240  
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 ttattttgat attccttaag ctcttggtga agttgttoga tttccataat ttccagggtca 360  
 cactggttat cccaaacttc t 381

<210> 62  
 <211> 906  
 <212> DNA  
 <213> Homo sapiens

<400> 62  
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 taggggaagg gcccgcgtag tcctcgcagg gccccagagc tggagtcggc tccacagccc 180  
 cgggcccgtcg gcttctcact tcctggacct ccccgcgccc cgggcctgag gactggctcg 240  
 gcggagggag aagaggaaac agacttgagc agctccccgt tgtctcgcaa ctccactgcc 300  
 gaggaactct catttcttcc ctgcgtcctt caccctccac ctcatgtaga aaggtgctga 360

```

agcgtccgga ggggaagaaga acctgggcta ccgtcctggc cttcccmccc ctttcccggg 420
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ctgggggaact tttttccctt cttcaggtea ggggaaaggg aatgcccaat tcagagagac 540
atgggggcaa gaaggacggg agtggaggag cttctggaac ttgacagccg tcacgaggag 600
gcggcagctc taacagcaga gagcgtcacc gcttggtatc gaagcacaag cggcataagt 660
ccaaacactc caaagacatg gggttggtga cccccgaagc agcatccctg ggcacagtta 720
tcaaaccctt ggtggagtat gatgatatca gctctgattc cgacaccttc tccgatgaca 780
tggccttcaa actagaccga agggagaacg acgaacgtcg tggatcagat cggagcgacc 840
gcctgcacaa acatcgtcac caccagcaca ggcgttcccg ggacttacta aaagctaaac 900
agaccg                                     906

```

<210> 63  
 <211> 491  
 <212> DNA  
 <213> Homo sapiens

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<400> 63
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tgcttcacga gaggatggg acagctctca ggtcagaatc caggctgaga aggccatgct 120
ggttgggggc ccccggaagc acggtccgga tcctccctgg catcagcgta gaccgctgc 180
tcaggcttgg ggtaccaaac tcagtctctg tactgttttg gccccatgag gtgagaggaa 240
aacctagaaa aagattggtc gtgctaagga atcagctgcc cctcatcct ccgcatccaa 300
tgctgggtgac aacatattcc ctctcccagg acacagactc ggtgactcca cactgggctg 360
agtggcctct ggaggctcgt ggcctaaggc agggctccgt aaggctgatc ggctgaactg 420
ggtggggtga gggtttctga cccttcgctt cccatcccat aaccgctgtc aatgagctca 480
cactgtggtc a                                     491

```

<210> 64  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

```

<400> 64
gatggcatgg tcgttgctaa tgtgcctgct gggatggagc acttctcct gtgagcccag 60
gggacccgcc tgcctctgga gcttggggca aggagggaag agtgatacca ggaagggtgg 120
gctgcagcca gggccagag tcagttcagg gagtggctct cggccctcaa agctctccg 180
gggactgctc aggagtgatg gtgccctgga gtttgccca acttccctgg ccaccctgga 240
aggtgcctgg ctgtccagg cctctaggct gggctgatgg gtttctccag gacacaagta 300
tcattaaagc caccctctcc tcagcttgct aggccgcaca tgtgggacag gctgtgctca 360
caacccctc gcctgcctg ccctccatca ggaggagcca gtggaacctt cggaaagctc 420
ccagcatctc agcagccctc aaaagtcgtc ctggggcaag ctctggttct cctgactgga 480
ggtcatctgg gcttggcctg ctctctctcg c                                     511

```

<210> 65  
 <211> 394  
 <212> DNA  
 <213> Homo sapiens

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<400> 65
taaaaaagtg taacaaagggt ttatttagac tttcttcatg cccccagatc caggatgtct 60
atgtaaaccg ttatcttaca aagaaagcac aatatttggg ataaactaag tcagtgaactt 120
gcttaactga aatagcgtcc atccaaaagt gggtttaagg taaaactacc tgacgatatt 180
ggcggggatc ctgcagtttg gactgcttgc cgggtttgtc cagggttccg ggtctgttct 240
tggcactcat ggggacaggc atctgctcgt tctgtggggc cccgctggag cccttacgtg 300
aagctgaagg tatcgaccst agggggctct agggcagtg gaccttcac cggaaactaac 360
aagggtcggg gagaggcctc ttgggctatg tggg                                     394

```

<210> 66

<211> 359  
 <212> DNA  
 <213> Homo sapiens

<400> 66  
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 tcacgttwaa gacactaggt cgggcgccac agtgccaccc aaggagaaga agaatttgga 120  
 atttttccat gaagatgtac ggaaatctga tgttgaatat gaaaatggcc cccaaatgga 180  
 attccaaaag gttaccacag gggctgtaag acctagtac cctcctaagt gggaaagagg 240  
 aatggagaat agtatttctg atgcatcaag aacatcagaa tataaaactg agatcataat 300  
 gaaggaaaat tccatatcca atatgagttt actcagagac agtagaaact attcccagg 359

<210> 67  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 425  
 <223> n = A,T,C or G

<400> 67  
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 taatgccctt tcctctcctt ctgcacagga gacacagatg ggtaacatag aggcatggga 120  
 agtggaggag gacacaggac tagccaccca ccttctcttc ccggtctccc aagatgactg 180  
 cttatagagt ggaggaggca aacagggtccc ctcaatgtac cagatgggtca cctatagcac 240  
 cagctccaga tggccacgtg gttgcagctg gactcaatga aactctgtga caaccagaag 300  
 atacctgctt tgggatgaga gggaggataa agccatgcag ggaggatatt taccatccct 360  
 accctaagca cagtgcgaagc agtgagcccc cggctccag tacctgaaaa accaaggcct 420  
 actgncctttt ggatgctctc ttgggccacg 450

<210> 68  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
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 gctgagaggc aagaccgtct ccctcctgct gcagctgctt cccagcagc cactgctggg 120  
 cacagcagaa acgccagcag agaaaatggg agccgagagt ccttagccct ggagctgagg 180  
 ctgctctggg gctgacccgc tggctgtacg tggccagaac tggggttggc atctggcatc 240  
 catttgaggc caggggtggag gaaagggagg ccaacagagg aaaacctatt cctgctgtga 300  
 caacacagcc cttgtccac gcagcctaag tgcaggagc gtgatgaagt caggcagcca 360  
 gtcggggagg acgaggtaac tcagcagcaa tgtcaccttg tagcctatgc gctcaatggc 420  
 ccggaggggc agcaaccccc cgcacacgtc agccaacagc agtgccctctg caggcaccaa 480  
 gagagcgatg atggacttga gcgccgtgtt c 511

<210> 69  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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 tatctgtcca ccatcttgcc ttgcccttcc tggggctgag gcagacaaag gaaaggtaat 120  
 gaggttaggg cccccagggc ggctaagtgc tattggcctg ctccctgtca aagagagcca 180  
 tagccagctg ggcacggccc cctagcccct ccaggttgct gaggcgagc cgggtggtaga 240

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gttcttcact gagccgtggg ctgcagtctc gcaggagaa cttctgcacc agccctggct 300
ctacggcccc aaagagggtg agccctgaga accggaggaa aacatccatc acctccagcc 360
cctccagggc ttctctctct tcttggcctg ccagttcacc tgccagccgg gctcgggccc 420
ccaggtagtc agcgtttag aagcagccct ccgcagaagc ctgccggtca aatctccccg 480
ctataggagc cccccgggag gggtcagcac c 511

```

&lt;210&gt; 70

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

```

caagttgaac gtcaggcttg gcagagggtg agtgtagatg aaaacaaagg tgtgattatg 60
aagaggatgt gagtcctttg ggtgtaggag agaaaggctg ttgagcttct atttcaagat 120
acttttacct gtgcaaaaag cacattttcc acctccttct catggcattt gtgtaagggtg 180
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gattagcaag ggaccctca ctaagtgttg atggagttag gacagagctc agctgtttga 300
atctcagagc ccaggcagct ggagctgggt aggatcctgg agctggcact aatgtgaggt 360
gcattccctc caaccaggc tcagatccgg aacctgaccg tgctgacccc cgaaggggag 420
gcagggtga gctggcccg tgggtccct gtccttttca caccacactc tcgcttttag 480
gtgctgggct gggactactt cacagagcag c 511

```

&lt;210&gt; 71

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

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tggcctgggc aggattggga gagaggtagc taccgggatg cagtcctttg ggatgaagac 60
tatagggtat gaccccatca tttcccaga ggtctcgcc tcctttggtg ttcagcagct 120
gcccctggag gagatctggc ctctctgtga tttcatcact gtgcacactc ctctcctgcc 180
ctccacgaca ggcttgctga atgacaacac ctttgcccag tgcaagaagg ggggtgcgtgt 240
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tggccagtgt gccggggctg cactggacgt gtttacggaa gagccgccac gggaccgggc 360
cttggtggac catgagaatg tcatcagctg tcccacctg ggtgccagca ccaaggaggc 420
tcagagccgc tgtggggagg aaattgctgt tcagttcgtg gacatggtga aggggaaatc 480
tctcacgggg gttgtgaatg cccaggccct t 511

```

&lt;210&gt; 72

&lt;211&gt; 2017

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

agccagatgg ctgagagctg caagaagaag tcaggatcat gatggctcag tttcccacag 60
cgatgaatgg agggccaaat atgtgggcta ttacatctga agaacgtact aagcatgata 120
aacagtttga taacctcaaa ccttcaggag gttacataac aggtgatcaa gcccgactt 180
ttttctaca gtcaggctctg ccggccccgg ttttagctga aatatgggcc ttatcagatc 240
tgaacaagga tgggaagatg gaccagcaag agttctctat agctatgaaa ctcatcaagt 300
taaagtgtga gggccaacag ctgcctgtag tcctccctcc tatcatgaaa caaccccta 360
tgttctctcc actaatctct gctcgttttg ggatgggaag catgcccaat ctgtccattc 420
atcagccatt gcctccagtt gcacctatag caacaccctt gtcttctgct acttcaggga 480
ccagtattcc tcccctaata atgcctgctc ccctagtgc ttctgttagt acatcctcat 540
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aggcccagtc tctgattgat ttaggatcta gtagtcaac ttctcaact gcttccctct 720
cagggaactc acctaaagaca gggacctcag agtggcagt tcctcagcct tcaagattaa 780
agtatcgga aaaatttaat agtctagaca aaggcatgag cggatacctc tcaggttttc 840

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aagctagaaa tgcccttctt cagtcaaate tctctcaaac tcagctagct actatttggg 900
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ataatacaca gcagttagcc cttgaacaac ttcataaaat caaacgtgac aaattgaagg 1980
aaatcgaaag aaaaagatta gagcaaaaaa aaaaaaa 2017

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&lt;210&gt; 73

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

```

atggcagtg cattcaccat catgggaacc accttccctt ttcttcagga ttctctgtag 60
tggaagagag caccagtggt tgggctgaaa acatctgaaa gtaggagaa gaacctaaaa 120
taatcagtat ctcaagggc tctaagggtc caagaagtct cactggacat ttaagtcca 180
acaaaggcat actttcggaa tcgccaagtc aaaactttct aacttctgtc tctctcagag 240
acaagtgaga ctcaagagtc tactgttcta gtggcaacta cagaaaactg gtgttaccca 300
gaaaaacagg agcaattaga aatggttcca atatttcaaa gctccgcaa caggatgtgc 360
tttcttttgc ccatttaggg tttcttctct ttcctttctc tttattaacc acta 414

```

&lt;210&gt; 74

&lt;211&gt; 1567

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 74

```

atatctagaa gtctggagtg agcaaacaag agcaagaagc aaaaagaagc caaaagcaga 60
aggctccaat atgaacaaga taaatctatc ttcaaagaca tattagaagt tgggaaaata 120
attcatgtga actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 180
gcatccccag atctcaggga cctccccctg cctgtcacct ggggagtgag aggacaggat 240
agtgcagtgt cttgtctct gaatttttag ttatatgtgc tgtaatgttg ctctgaggaa 300
gcccctggaa agtctatccc aacatatcca catcttatat tccacaaatt aagctgtagt 360
atgtacccta agacgtgct aattgactgc cacttcgcaa ctacggggcg gctgcatttt 420
agtaatgggt caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 480
ccaactgaca aatgccaaa ttgagaaaaa tgatcataa tttagcataa acagagcagt 540
cggcgacacc gattttataa ataaactgag caccttcttt ttaaacaaac aaatgcgggt 600
ttattttctc gatgatgttc atccgtgaat ggtccaggga aggaccttc accttgacta 660
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acaggacgtc tcccattac aactacccaa tccgaagtgt caactgtgtc aggactaaga 960
aaccctgggt ttgagtagaa aagggcctgg aaagagggga gccacaaat ctgtctgctt 1020

```

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cctcacatta gtcattggca aataagcatt ctgtctcttt ggtgctgcc tcagcacaga 1080
gagccagaac tctatcgggc accaggataa catctctcag tgaacagagt tgacaaggcc 1140
tatgggaaat gcctgatggg attatcttca gcttggtgag cttctaagtt tctttccctt 1200
cattctaccc tgcaagccaa gttctgtaag agaaatgcct gagttctagc tcagggttttc 1260
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cactcttcat gtgttaacca ctgccttcct ggaccttgga gccacggtga ctgtattaca 1500
tggtgttata gaaaactgat tttagagttc tgatcgttca agagaatgat taaatataca 1560
tttccta 1567

```

&lt;210&gt; 75

&lt;211&gt; 240

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 75

```

tcgagcggcc gcccgggcag gtccttcaga cttggactgt gtcacactgc caggcttcca 60
gggtccaac ttgcagacgg cctggtgtgg gacagtctct gtaatcgca aagcaaccat 120
ggaagacctg ggggaaaaca ccatggtttt atccaccctg agatctttga acaacttcat 180
ctctcagcgt gcggaggagg gctctggact ggatatttct acctcgccg cgaccacgct 240

```

&lt;210&gt; 76

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 288

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 76

```

tagcgyggtc gcggccgagg yctgcttytc tgtccagccc agggcctgtg gggtcagggc 60
ggtgggtgca gatggcatcc actccggtgg cttcccatc tttctctggc ctgagcaagg 120
tcagcctgca gccagagtac agagggccaa cactggtgtt cttgaacaag ggccttagca 180
ggcctgaag grccctctct gtagtgttga acttcctgga gccaggccac atgttctcct 240
cataccgcag gytagygatg gtgaagttga ggggtgaaata gtattmangr agatggctgg 300
caracctgcc cgggcggccg ctcsaaatcc 360

```

&lt;210&gt; 77

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 77

```

agcgtggctg cggccgaggt gtccttcagg gtctgcttat gcccttggtc aagaacacca 60
gtgtcagctc tctgtactct ggttcagac tgacctgct caggcctgag aaggatgggg 120
cagccaccag agtggatgct gtctgcaccc atcgtcctga ccccaaaagc cctggactgg 180
acagagagcg gctgtactgg aagctgagcc agctgaccca cggcatcact gagctgggcc 240
cctacaccct ggacagggac agtctctatg tcaatgggtt caccatcgg agctctgtac 300
ccaccaccag caccgggggtg gtcagcgagg agccattcaa cctgcccggg cggccgctcg 360
a 361

```

&lt;210&gt; 78

&lt;211&gt; 356

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 7, 346, 350, 353

<223> n = A,T,C or G

<400> 78

```

ttggggnttt mgagcggccg cccggggcagg taccgggggtg gtcagcgagg agccattcac 60
actgaacttc accatcaaca acctgcggta tgaggagaac atgcagcacc ctggctccag 120
gaagttcaac accacggaga gggtccttca gggcctgctc aggtccctgt tcaagagcac 180
cagtgttggc cctctgtact ctggctgcag actgactttg ctcagacttg agaaacatgg 240
ggcagccact ggagtggacg ccatctgcac cctccgcctt gatccactg gtcctggact 300
ggacagagag cggctatact gggagctgag ccagtcctct ggcgngacn ccnctt 356

```

<210> 79

<211> 226

<212> DNA

<213> Homo sapiens

<400> 79

```

agcgtggtcg cggccgaggt ccagtcgcag catgctcttt ctctgcccc ctggcacagt 60
gaggaagatc tctgctgtca gtgagaaggc tgtcatccac tgagatggca gtcaaaagtg 120
catttaatac acctaacgta tcgaacatca tagcttgccc caggttatct catatgtgct 180
cagaacactt acaatagcct gcagacctgc ccgggcggcc gctcga 226

```

<210> 80

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 23

<223> n = A,T,C or G

<400> 80

```

tgtggtgttg aacttcctgg agncagggtg acccatgtcc tccccatact gcaggttggt 60
gatggtgaag ttgagggtga atggtaccag gagaggcca gcagccataa ttgtsgrgck 120
gsmgmssgag gmwggwgtty cwgaggttcy rarrtccact gtggagggtc caggagtgtc 180
ggtggtgggc acagagstcy gatgggtgaa accattgaca tagagactgt tcctgtccag 240
ggtgtagggg cccagctctt yratgycatt ggycagttkg ctyagctccc agtacagccr 300
ctctckgyyg mgwccagsgc ttttggggtc aagatgatgg atgcagatgg catccactcc 360
agtggctgct ccatccttct cggacctgag agaggtcagt ctgcagccag agtacagagg 420
gccaacactg gtgttctttg aata 444

```

<210> 81

<211> 310

<212> DNA

<213> Homo sapiens

<400> 81

```

tcgagcggcc gcccgggcag gtcaggaagc acattggtct tagagccact gcctcctgga 60
ttccacctgt gctgcggaca tctccaggga gtgcagaagg gaagcaggtc aaactgctca 120
gatcagtcag actggctgtt ctcaattctc acctgagcaa ggtcagtctg cagccagagt 180
acagagggcc aacactggtg ttcttgaaca agggcttgag cagaccctgc agaaccctct 240
tccgtggtgt tgaacttctt ggaaaccagg gtgttgcagt tttttcctca taatgcaagg 300
ttggtgatgg 310

```



<210> 82  
<211> 571  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 202  
<223> n = A,T,C or G

<400> 82  
acggtttcaa tggacacttt tattgtttac ttaatggatc atcaattttg tctcactacc 60  
tacaaatgga atttcatctt gtttccatgc tgagtagtga aacagtgaca aagctaataca 120  
taataaccta catcaaaaga gaactaagct aacactgctc actttctttt taacaggcaa 180  
aatataaata tatgactctt anaatgcaca atggtttagt cactaaaaaa ttcaaattggg 240  
atcttgaaga atgtatgcaa atccagggtg cagtgaagat gagctgagat gctgtgcaac 300  
tgtttaaggg ttcttggcac tgcattctct ggccactagc tgaatcttga catggaaggt 360  
tttagctaata gccaaagtga gatgcagaaa atgctaagtt gacttagggg ctgtgcacag 420  
gaactaaaag gcaggaaagt actaaatatt gctgagagca tccaccccag gaaggacttt 480  
accttccagg agctccaaac tggcaccacc cccagtgtct acatggctga ctttatcctc 540  
cgtgttccat ttggcacagc aagtggcagt g 571

<210> 83  
<211> 551  
<212> DNA  
<213> Homo sapiens

<400> 83  
aaggctggtg ggtttttgat cctgctggag aacctccgct ttcattgtga ggaagaaggg 60  
aagggaag atgcttctgg gaacaagggt aaagccgagc cagccaaaat agaagctttc 120  
cgagcttcac tttccaagct aggggatgct tatgtcaatg atgcttttgg cactgctcac 180  
agagcccaca gctccatggt aggagtcaat ctgccacaga aggctggtgg gtttttgatg 240  
aagaaggagc tgaactactt tgcaaaggcc ttggagagcc cagagcgacc ctctctggcc 300  
atctctggcg gagctaaagt tgcaagaaag atccagctca tcaataatat gctggacaaa 360  
gtcaatgaga tgattattgg tggaggaaat gcttttacct tccttaaggt gctcaacaac 420  
atggagattg gcaactctct gtttgatgaa gagggagcca agattgtcaa agacctaatg 480  
tccaaagctg agaagaatgg tgtgaagatt accttgctg ttgactttgt cactgctgac 540  
aagtttgatg a 551

<210> 84  
<211> 571  
<212> DNA  
<213> Homo sapiens

<400> 84  
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taagttctga ttccaactta gctaattcat tctgagaact gtggtatagg tggcgtgtct 120  
cttctagctg ggacaaagt tctttgtttt cccctgtag agtatcacag accttctgtc 180  
gaagctggac ctctgtctgg gccttggact cccaaatctg cttgtcatgt tcaagcctgg 240  
aatgttaat ctttaattct tccatatgga tggacatctg tctaagttga tccttttagaa 300  
cactgcaatt atcttctttg agtctaattt ctcttctttt gctttgaatc gcatcactaa 360  
acttctctc ccatttctta gtttcatcta tcacctgtc acgatcatcc tggagggaag 420  
acatgctctt agtaaaggct gcaagctggg tcacagtact gtccaagttt tcctgaagtt 480  
gctgaacttc cttgtctttc ttgttcaaag taacctgaat ctctccaatt gtctcttcca 540  
agtggacttt ttctctgcgc aaagcatcca g 571

<210> 85

<211> 561  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
 .tcattgcctg tgatggcatc tggaatgtga tgagcagcca ggaagttgta gatttcattc 60  
 aatcaaagga ttcagcatgt ggtggaagct gtgaggcaag agaaacaaga actgtatggc 120  
 aagttaàgaa gcacagaggc aaacaagaag gagacagaaa agcagttgca ggaagctgag 180  
 caagaaatgg aggaaatgaa agaaaagatg agaaagtttg ctaaactctaa acagcagaaa 240  
 atcctagagc tggagaaga gaatgaccgg cttagggcag aggtgcaccc tgcaggagat 300  
 acagctaaag agtgtatgga aacactttctt tcttccaatg ccagcatgaa ggaagaactt 360  
 gaaagggtca aaatggagta tgaaaccctt tctaagaagt ttcagtcttt aatgtctgag 420  
 aaagactctc taagtgaaga ggttcaagat ttaaagcatc agatagaagg taatgtatct 480  
 aaacaagcta acctagaggc caccgagaaa catgataacc aaacgaatgt cactgaagag 540  
 ggaacacagt ctataccagg t 561

<210> 86  
 <211> 795  
 <212> DNA  
 <213> Homo sapiens

<400> 86  
 aagccaataa tcaccattta ttacttaata tatgccaacc actgtacttg gcagttcaca 60  
 aattctcacc gttacaacaa ccccatgagg tattttattcc cattctatag ataggggaaac 120  
 cacagctcaa gtaagttagg aaactgagcc aagtatacac agaatacga gtggcaaaac 180  
 tagaaggaaa gactgacact gctatctgct ggccctccagt gtccctggctc ttttcacacg 240  
 ggttcaatgt ctccagcgct gctgctgctg ctgcattacc atgccctcat tgtttttctt 300  
 cctctggtgt tcaactgcat ccttcaaaga atctaactca ttccagagac cacttatttc 360  
 tttctctctt tctgaaatta cttttaataa ttcttcatga gggggaaaag aagatgcctg 420  
 ttggtagttt tgttgtttaa gctgctcaat ttgggactta aacaatttgt tttcatcttg 480  
 tacatcctgt aacagctgtg ttttgctaga aagatcactc tccctctctt ttagcatggc 540  
 ttctaacctc ttcaattcat tttccttttc tttcaacaca atctcaagtt cttcaaactg 600  
 tgatgcagaa gaggcctctt tcaagttatg ttgtgctact tcctgaacat gtgcttttaa 660  
 agattcaatt tcttcttgaa gatcctgtaa ccacttcctt gtattggcta ggtctttctc 720  
 tttctcttcc aaaacagcct tcatgggtatt catctgttcc tcttttcctt ttaataagtt 780  
 caggagcttc agaac 795

<210> 87  
 <211> 594  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
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 caactggggt tatgtcttca tattttatat ttttgtaa taaaaaatt acaagtttta 120  
 aatagccaat ggctgggtat attttcagaa aacatgatta gactaattca ttaatgggtg 180  
 cttcaagctt ttcttattg gctccagaaa attcaccac cttttgtccc ttcttaaaaa 240  
 actggaatgt tggcatgcat ttgacttcac actctgaagc aacatcctga cagtcatcca 300  
 catctacttc aagggaatgc acgttggaat acttttcaga gagggaaatga aagaaaggct 360  
 tgatcatttt gcaaggccca caccacgtgg ctgagaagtc aactactaca agtttatcac 420  
 ctgcagcgtc caaggcttcc tgaaaagcag tcttgctctc gatctgcttc accatcttgg 480  
 ctgctggagt ctgacgagcg gctgtaagga ccgatggaaa tggatccaaa gcaccaaaaca 540  
 gagcttcaag actcgtgct tggcttgaat tcggatccga tatcgccatg gcct 594

<210> 88  
 <211> 557  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 88

```

aagtgttagc attaatgttt tattgtcacg cagatggcaa ctgggtttat gtcttcatat 60
tttatatttt tgtaaattaa aaaaattmca agtttttaaat agccaatggc tggttatatt 120
ttcagaaaac atgattagac taattcatta atgggtggctt caagcttttc cttattggct 180
ccagaaaatt caccacacctt ttgtcccttc ttaaaaaact ggaatgttgg catgcatttg 240
acttcacact ctgaagcaac atcctgacag tcatccacat ctacttcaag gaatatcacg 300
ttggaatact tttcagagag ggaatgaaag aaaggcttga tcattttgca aggccacac 360
cacgtggctg agaagtcaac tactacaagt ttatcacctg cagcgtccaa ggcttcctga 420
aaagcagtct tgctctcgat ctgcttcacc atcttggctg ctggagtctg acgagcggct 480
gtaaggaccg atggaaatgg atccaaagca ccaaacagag cttcaagact cgctgcttgg 540
catgaattcg gatccga 557

```

&lt;210&gt; 89

&lt;211&gt; 561

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 544, 551

&lt;223&gt; n = A, T, C or G

&lt;400&gt; 89

```

tacaaacttt attgaaacgc acacgcgcac acacacaaac acccctgtgg atagggaaaa 60
gcacctggcc acaggggtcca ctgaaacggg gaggggatgg cagcttgtaa tgtggctttt 120
gccacaaccc cttcttgaca gggaaggcct tagattgagg cccacacctc catggtgatg 180
gggagctcag aatgggggtcc agggagaatt tggttagggg gaggtgctag ggaggcatga 240
gcagaggggca ccctccgagt ggggtcccga gggctgcaga gtcttcagta ctgtccctca 300
cagcagctgt ctcaaggctg ggtccctcaa aggggcgtcc cagcgcgggg cctccctgcg 360
caaacacttg gtaccctcgg ctgcgagcgc gaagccagca ggacagcagt ggcgcgcgac 420
agcacaacag acgccctggc ggtagggaca gcaggcccag ccctgtcggg tgtctcggca 480
gcaggtctgg ttatcatggc agaagtgtcc ttcccacact tcacgtcctt cacaccacg 540
tganggctac nggccaggaa g 561

```

&lt;210&gt; 90

&lt;211&gt; 561

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

```

cccgtgggtg ccatccacgg agttgttacc tgatcttttg aagcaggatc gcccgtctgc 60
actgcagtgg aagcccctg ggcagcagtg atggccatcc ccgcatgcca cggcctctgg 120
gaaggggcag caactggaag tccctgagac ggtaaagatg caggagtggc cggcagagca 180
gtgggcatca acctggcagg ggccaccag atgcctgctc agtgttgtgg gccatttgc 240
cagaagggga cggcagcagc tgtagctggc tctccgggg tccaggcagc aggccacagg 300
gcagaactga ccatctgggc accgcgttcc agccaccagc cctgctgtta aggccacca 360
gtcaccagg gtccacatgg tctgcctgcg tccgactccg cggtccttgg gccctgatg 420
ttctacctgc tgtgagctgc ccagtgggaa gtatggctgc tgccaatgcc caacgccacc 480
tgtgtctccg atcacctgca ctgctgcccc aagacactgt gtgtgacctg atccagagta 540
agtgcctctc caaggagaac g 561

```

&lt;210&gt; 91

&lt;211&gt; 541

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc\_feature  
 <222> 480, 491  
 <223> n = A,T,C or G

<400> 91  
 gaatcacctt tctggttttag ctagtacttt gtacagaaca atgaggtttc ccacagcgga 60  
 gtctccctgg gctctgtttg gctctcggtta aggcaggcct acaccttttc ctctcctcta 120  
 tggagagggg aatatgcatt aagggtgaaa gtcaccttcc aaaagtgaga aagggattcg 180  
 attgctgctt caggactgtg gaattatttg gaatgtttta caaatggttg ctacaaaaca 240  
 acaaaaaagg taattacaaa atgtgtacat cacaacatgc tttttaaaga cattatgcat 300  
 tgtgtccaca ttcccttaaa tgttgtttcc aaagggtgctc agcctctagc ccagctggat 360  
 tctccgggaa gaggcagaga cagtttggcg aaaaagacac agggaaggag ggggtggtga 420  
 aaggagaaag cagccttcca gttaaagatc agccttcagt taaaggtcag cttcccgcga 480  
 gctggcctca ngcggagtct gggtcagagg gaggagcagc agcagggtgg gactggggcg 540  
 t 541

<210> 92  
 <211> 551  
 <212> DNA  
 <213> Homo sapiens

<400> 92  
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 gtgaagcgca agatccaggt tctgcagcag caggcagatg atgcagagga gcgagctgag 120  
 cgctccagc gagaagttga gggagaaaagg cgggcccggg aacaggctga ggctgaggtg 180  
 gctccttga accgtaggat ccagctggtt gaagaagagc tggaccgtgc tcaggagcgc 240  
 ctggccactg ccctgcaaaa gctggaagaa gctgaaaaag ctgctgatga gagtgaagaga 300  
 ggtatgaagg ttattgaaaa ccgggcctta aaagatgaag aaaagatgga actccaggaa 360  
 atccaactca aagaagctaa gcacattgca gaagaggcag ataggaagta tgaagaggtg 420  
 gctcgtaagt tggatgatcat tgaaggagac ttggaacgca cagaggaaacg agctgagctg 480  
 gcagagtcct gttgccgaga gatggatgag cagattagac tgatggacca gaacctgaag 540  
 tgtctgagtg c 551

<210> 93  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 93  
 gagaacttgg cctttattgt gggcccagga gggcacaaag gtcaggaggc ccaagggagg 60  
 gatctggttt tctggatagc caggtcatag catgggtatc agtaggaatc cgctgtagct 120  
 gcacaggcct cacttgctgc agttccgggg agaacacctg cactgcatgg cgttgatgac 180  
 ctctgggtac acgacagagc cattggtgca gtgcaagggc acgcgcatgg gctccgtcct 240  
 cgagggcagg cagcaggagc attgctcctg cacatcctcg atgtcaatgg agtacacagc 300  
 tttgctggca cactttccct ggcagtaatg aatgtccact tcctcttggg acttacaatc 360  
 tcccaactttg atgtactgca ccttggtgtg gatgtctttg caatcaggct cctcacatgt 420  
 gtacacagcag gtgcctggaa ttttcacgat tttgcctcct tcagccagac acttggtgtc 480  
 atcaaatggt gggcagcccc tgacctctt ctcccagatg tactctctc t 531

<210> 94  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 517  
 <223> n = A,T,C or G

&lt;400&gt; 94

```

gcctggacct tgccggatca gtgccacaca gtgacttgct tggcaaattg ccagaccttg 60
ctgcagagtc atcgtgtcaa ttgtgacct ggaccccggc cttcatgtgc caacagccag 120
tctcctgttc ggggtggagga gacgtgtggc tgccgctgga cctgcccttg tgtgtgcacg 180
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tgctcctatg tcatctttca aaacaaggag caggacctgg aagtgtcctt ccacaatggg 300
gcctgcagcc ccggggcaaa acaagcctgc atgaagtcga ttgagattaa gcatgctggc 360
gtctctgctg agctgcacag taacatggag atggcagtg atgggagact ggtccttgcc 420
ccgtacgttg gtgaaaacat ggaagtcagc atctacggcg ctatcatgta tgaagtcagg 480
tttaccatc ttggccacat cctcacatac accgcncaa aacaacgagt t 531

```

&lt;210&gt; 95

&lt;211&gt; 605

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

```

agatcaacct ctgctggtea ggaggaatgc cttccttgte ttggatcttt gctttgacgt 60
tctcgatagt rwcaactkkr ytsramskma agkgyratgr wmttksywgw rasyktmwww 120
rsgraraytt agacaycccm cctcwagagc gsagkaccar gtgcagaggt ggactcttct 180
tggatgttgt agtcagacag ggtgcgtcca tcttcagct gtttccagc aaagatcaac 240
ctctgctgat caggagggat gccttcctta tcttgatct ttgccttgac attctcgatg 300
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tgcacccac ctctgagacg gagcaccagg tgcagggttg actctttctg gatgtttag 420
tcagacaggg tgcgyccatc ttccagctgc tttccsagca aagatcaacc tctgctggte 480
aggaggratg ccttccttgt cytgatctt tgcyytgacr ttctcratgg tgtcactcgg 540
ctccacttcg agagtgatgg tcttaccagt cagggtcttc acgaagatct gcatccacc 600
tctaa 605

```

&lt;210&gt; 96

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

```

aagtcacaaa cagacaaaga ttattaccag ctgcaagcta tattagaagc tgaacgaaga 60
gacagaggtc atgattctga gatgattgga gaccttcaag ctgaattac atctttacaa 120
gaggagggtga agcatctcaa acataatctc gaaaaagtgg aaggagaaag aaaagaggct 180
caagacatgc ttaatcactc agaaaaggaa aagaataatt tagagataga tttaaactac 240
aaacttaa at cattacaaca acggttagaa caagaggtaa atgaacacaa agtaaccaaa 300
gctcgtttaa ctgacaaaaca tcaatctatt gaagaggcaa agtctgtggc aatgtgtgag 360
atggaaaaaa agctgaaaga agaaagagaa gctcgagaga aggctgaaaa tcgggttggt 420
cagattgaga aacagtgttc catgctagac gttgatctga agcaatctca gcagaaacta 480
gaacatttga ctggaaataa agaaaggatg gaggatgaag ttaagaatct a 531

```

&lt;210&gt; 97

&lt;211&gt; 1017

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 963, 995, 1001, 1008, 1010

&lt;223&gt; n = A, T, C or G

&lt;400&gt; 97

```

cgcctccacc atgtccatca gggtagacca gaagtcctac aagggtgcca cctctggccc 60

```

```

ccgggacctc agcagccgct cctacacgag tgggcccggg tcccgcacatca gctcctcgag 120
cttctcccga gtgggcagca gcaactttcg cggtggcctg ggcgggcggt atggtggggc 180
cagcggcacg ggagggcatca ccgcagttac ggtcaaccag agcctgctga gccccctgt 240
cctggaggtg gacccaaca tccaggccgt gcgcacccag gagaaggagc agatcaagac 300
cctcaacaac aagtttgcct ccttcacataga caaggtacgg ttccctggagc agcagaacaa 360
gatgctggag accaagtgga gcctcctgca gcagcagaag acggctcgaa gcaacatgga 420
caacatgttc gagagctaca tcaacarcct tagggcgagc ctggagactc tggggcagga 480
gaagctgaag ctggaggcgg agcttggcaa catgcagggg ctggtggagg acttcaagaa 540
caagtatgag gatgagatca ataagcgtac agagatggag aacgaatttg tcctcatcaa 600
gaaggatgtg gatgaagctt acatgaacaa ggtagagctg gagtctcgcc tggaaagggt 660
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ggctgagagc atgtaccagg tcaagtatga ggagctgcag agcctggctg ggaagcacgg 900
ggatgacctg cggcgacaaa agactgagat ctctgagatg aacccggaac atcagcccgg 960
ctncaggctg agattgaggg cctcaaaggc caganggctt ncctggangn ccgccat 1017

```

<210> 98  
 <211> 561  
 <212> DNA  
 <213> Homo sapiens

```

<400> 98
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tgggtctgga aacccaaacc ctcaaggatg gcctggcgca tgggggaacc agcctgctgg 120
ggcagggggc taccagggg cttcctatcc tggggcctac cccgggcagg ccccccagg 180
ggcttatcct ggacaggcac ctccaggcgc ctaccctgga gcacctggag cttatcccgg 240
agcacctgca cctggagtct acccagggcc acccagcgcc cctggggcct acccatcttc 300
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gccactgatt gtgccttata acctgccttt gcctggggga gtggtgcctc gcatgctgat 420
aacaattctg ggcacggtga agcccaatgc aaacagaatt gctttagatt tccaaagagg 480
gaatgatgtt gccttccact ttaaccacg cttcaatgag aacaacagga gagtcatggt 540
ttgcaataca aagctggata a

```

<210> 99  
 <211> 636  
 <212> DNA  
 <213> Homo sapiens

```

<400> 99
gggaatgcaa caactttatt gaaaggaaag tgcaatgaaa tttgttgaaa ccttaaaagg 60
ggaaacttag acaccccccc tcragcgmag kaccargtgc aragggtggac tctttctgga 120
tggtgtagtc agacagggtr cgwccatctt ccagctgttt yccrgcaaag atcaacctct 180
gctgatcagg aggratgcct tccttatctt ggatctttgc cttgacattc tcgatgggtg 240
cactgggctc cacctcgagg gtgatggtct taccagttag ggtcttcacg aagatytgca 300
tcccacctct gagacggagc accaggtgca gggtrgactc tttctggatg ttgtagtcag 360
acaggggtgcg yccatcttcc agctgcttcc csagcaaaga tcaacctctg ctgggtcagga 420
ggatgcctt ccttgctcyt gatctttgcy ttgacrttct caatgggtgc actcggtccc 480
acttcgagag tgatggtctt accagtcagg gtcttcacga agatctgcat cccacctcta 540
agacggagca ccaggtgcag ggtggactct ttctggatgg ttgtagtcag acaggggtgcg 600
tccatcttcc agctgtttcc cagcaaagat caacct

```

<210> 100  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 100

```

aggttgatct ttgctgggaa acagctggaa gatggacgca cctgtctga ctacaacat 60
ccagaaagag tccaccctgc acctgggtgct ccgtcttaga ggtgggatgc agatcttcgt 120
gaagaccctg actggtaaga ccatcactct cgaagtggag ccgagtgaac ccattgagaa 180
ygtcaargca aagatccarg acaaggaagg catycctcct gaccagcaga ggttgatctt 240
tgctsggaaa gcagctggaa gatggrcgca cctgtctga ctacaacatc cagaaagagt 300
cyaccctgca cctgggtgctc cgtctcagag gtgggatgca ratcttcgtg aagaccctga 360
ctggtaagac catcaccctc gaggtggagc ccagtgcac catcgagaat gtcaaggcaa 420
agatccaaga taaggaaggc atccctcctg atcagcagag gttgatcttt gctgggaaac 480
agctggaaga tggacgcacc ctgtctgact acaacatcca gaaagagtcc acctytgcac 540
ytggtmctbc gtctyagagg kgggrtgcaa atctwmgtkw agacactcac tkkyaagryy 600
atcamcmwtg akktcgakys castkwcact wtcraaamg tyrwgcawa gatccmagac 660
aaggaaggca ttcctcctga ccagcagagg ttgatct 697

```

<210> 101  
 <211> 451  
 <212> DNA  
 <213> Homo sapiens

```

<400> 101
atggagtctc actctgtcga ccaggctgga gcgctgtggt gcgatatcgg ctcaactgcag 60
tctccacttc ctgggttcaa ggcctcctcc tgccctcagcc tcccgagtag ctgggactac 120
aggcaggcgt caccataatt tttgtatttt tagtagagac atggtttcgc catggttggt 180
gggctgggtct cgaactcctg acctcaagt atctgtcctg gcctcccaa gtgttggtg 240
tacaggcgaa agccaacgct cccggccagg gaacaacttt agaataagag aaatatgcaa 300
aagaacatca catcaaggat caattaatta ccatctatta attactatat gtgggtaatt 360
atgactattt cccaagcatt ctacgttgac tgcttgagaa gatgtttgtc ctgcatggtg 420
gagagtggag aagggccagg attcttaggt t 451

```

<210> 102  
 <211> 571  
 <212> DNA  
 <213> Homo sapiens

```

<400> 102
agcgcggtct tccggcgcgga gaaagctgaa ggtgatgtgg ccgccctcaa ccgacgcac 60
cagctcgttg aggagggtt ggacagggtc caggaacgac tggccacggc cctgcagaag 120
ctggaggagg cagaaaaaagc tgcagatgag agtgagagag gaatgaaggt gatagaaaac 180
cgggccatga aggatgagga gaagatggag attcaggaga tgcagctcaa agaggccaag 240
cacattgcgg aagaggctga ccgcaaatac gaggaggtag ctcgtaagct ggtcatcctg 300
gagggtgagc tggagagggc agaggagcgt gcggaggtgt ctgaactaaa atgtggtgac 360
ctggaagaag aactcaagaa tgttactaac aatctgaaat ctctggaggc tgcactgtaa 420
aagtattctg aaaaggagga caaatatgaa gaagaaatta aacttctgtc tgacaaactg 480
aaagaggctg agaccctgac tgaatttgca gagagaacgg ttgcaaaact ggaaaagaca 540
attgatgacc tggaagagaa acttgcccag c 571

```

<210> 103  
 <211> 451  
 <212> DNA  
 <213> Homo sapiens

```

<400> 103
gtgcacagggt cccatttatt gtagaaaata ataataatta cagtgatgaa tagctcttct 60
taaattacaa aacagaaacc acaaagaagg aagaggaaaa accccaggac ttccaagggt 120
gaagctgtcc cctcctccct gccaccctcc caggctcatt agtgtccttg gaaggggcag 180
aggactcaga ggggatcagt ctccaggggc cctgggctga agcgggtgag gcagagagtc 240
ctgaggccac agagctgggc aacctgagcc gcctctctgg cccctcccc caccactgcc 300
caaacctgtt tacagcacct tcgcccctcc cctctaaacc cgtccatcca ctctgcactt 360
cccaggcagg tgggtgggac aggcctcagc catactcctg ggcgcgggtt tcggtgagca 420

```

aggcacagtc ccagaggtga tatcaaggcc t

451

<210> 104

<211> 441

<212> DNA

<213> Homo sapiens

<400> 104

```

gcaaggaact ggtctgctca cacttgctgg cttgcgcac aggactggct ttatctcctg 60
actcacggtg caaagggtga ctctgcgaac gttaagtccg tccccagcgc ttggaatcct 120
acggcccca cagccggatc ccctcagcct tccaggtcct caactcccgt ggacgctgaa 180
caatggcctc catggggcta caggtaatgg gcatcgcgct ggccgtcctg ggctggctgg 240
ccgtcatgct gtgtgcgcg ctgcccattg ggcgctgac ggcttcatc ggcagcaaca 300
ttgtcacctc gcagaccatc tgggagggcc tatggtgaa ctgctgggtg cagagcaccg 360
gccagatgca gtgcaagggtg tacgactcgc tgctggcact gccgcaggac ctgcaggcgg 420
ccccgcct cgtcatcatc a                                     441

```

<210> 105

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 195

<223> n = A,T,C or G

<400> 105

```

tgcaaaagg acacaggggt tcaaaaataa aaattttct tccccctccc caaacctgta 60
ccccagctcc ccgaccacaa ccccttcct cccccggga aagcaagaag gagcaggtgt 120
ggcatctgca gctgggaaga gagaggccgg ggaggtgccg agctcgtgctc tgggtctctt 180
ccaaatataa atacntgtgt cagaactgga aaatcctcca gcaccaccca cccaagcact 240
ctccgttttc tgccggtgtt tggagagggg cggggggcag gggcgccagg caccggctgg 300
ctgcggtcta ctgcatccgc tgggtgtgca ccccgcgagc ctctgctgctc tcattgtaga 360
agagatgaca ctccgggtcc ccccgatgg tgggggctcc ctggatcagc ttcccggtgt 420
tgggggtcac acaccagcac tccccacgt gcccggtcag agacatcttg cactgtttga 480
ggttgtacag gccatgcttg tcacagttg                                     509

```

<210> 106

<211> 571

<212> DNA

<213> Homo sapiens

<400> 106

```

gggttggagg gactggttct ttatttcaaa aagacacttg tcaatattca gtatcaaaac 60
agttgcacta ttgatttctc tttctcccaa tcggcccaa agagaccaca taaaaggaga 120
gtacatttta agccaataag ctgcaggatg tacacctaac agacctcta gaaaccttac 180
cagaaaatgg ggactgggta gggaaggaaa cttaaaagat caacaaactg ccagcccacg 240
gactgcagag gctgtcacag ccagatgggg tggccagggt gccacaaacc caaagcaaag 300
tttcaaaata atataaaatt taaaaagttt tgtacataag ctattcaaga tttctccagc 360
actgactgat acaaagcaca attgagatgg cacttctaga gacagcagct tcaaaccagc 420
aaaagggtga tgagatgagt ttcacatggc taaatcagtg gcaaaaacac agtcttcttt 480
ctttctttct ttcaaggagg caggaaagca attaagtggc cacctcaaca taagggggac 540
atgatccatt ctgtaagcag ttgtgaaggg g                                     571

```

<210> 107

<211> 555

<212> DNA



<213> Homo sapiens

<400> 107

```
caggaaccgg agcgcgagca gtagctgggt gggcaccatg gctgggatca ccaccatcga 60
ggcgttgaag cgcaagatcc aggttctgca gcagcaggca gatgatgcag aggagcgagc 120
tgagcgctc cagcgagaag ttgagggaga aaggcgggcc cggaacagg ctgaggctga 180
ggtggcctcc ttgaaccgta ggatccagct ggttgaagaa gagctggacc gtgctcagga 240
gcgcctggcc actgccctgc aaaagctgga agaagctgaa aaagctgctg atgagagtga 300
gagaggtatg aaggttattg aaaaccgggc cttaaaagat gaagaaaaga tggaaactcca 360
ggaaatccaa ctcaaagaag ctaagcacat tgcagaagag gcagatagga agtatgaaga 420
ggtggctcgt aagttagtga tcattgaagg agacttggaa cgcacagagg aacgagctga 480
gctggcagag tcccgttgcc gagagatgga tgagcagatt agactgatgg accagaacct 540
gaagtgtctg agtgc 555
```

<210> 108

<211> 541

<212> DNA

<213> Homo sapiens

<400> 108

```
atctacgtca tcaatcaggc tggagacacc atgttcaatc gagctaagct gctcaatatt 60
ggctttcaag aggccttgaa ggactatgat tacaactgct ttgtgttcag tgatgtggac 120
ctcattccga tggacgaccg taatgcctac aggtgtttt cgcagccacg gcacatttct 180
gttgcaatgg acaagttggg gtttagcctg ccataatgtt agtattttgg aggtgtctct 240
gctctcagta aacaacagtt tcttgccatc aatggattcc ctaataatta ttgggggttg 300
ggaggagaag atgacgacat ttttaacaga ttagttcata aaggcatgtc tatatcacgt 360
ccaaatgctg tagtagggag gtgtcgaatg atccggcatt caagagacaa gaaaaatgag 420
cccaatcctc agaggtttga ccggatcgca catacaaagg aaacgatgcg cttcgatggg 480
ttgaactcac ttacctacaa ggtgttggat gtcagagata cccgttatat acccaaatca 540
c 541
```

<210> 109

<211> 411

<212> DNA

<213> Homo sapiens

<400> 109

```
ctagacctct aattaaaagg cacaatcatg ctggagaatg aacagtctga ccccgagggc 60
cacagcgaat tttaggggaag gaggcaaaga ggtgagaagg gaaaggaaag aaggaaggaa 120
ggagaacaat aagaactgga gacgttgggt gggtcaggga gtgtggtgga ggctcggaga 180
gatggtaaac aaacctgact gctatgagtt ttcaaccca tagtctaggg ccatgagggc 240
gtcagttctt ggtggctgag ggtccttcca cccagccac ctgggggagt ggagtgggga 300
gttctgccag gtaagcagat gttgtctccc aagtctctga cccagatgtc tggcaggata 360
acgctgacct gttccctcaa caagggacct gaaagtaatt ttgctcttta c 411
```

<210> 110

<211> 451

<212> DNA

<213> Homo sapiens

<400> 110

```
ccgaattcaa gcgtcaacga tccytccctt accatcaaatt caattggcca ccaatggtac 60
tgaacctacg agtacaccga ctacggggcg actaatcttc aactcctaca tacttcccc 120
attattccta gaaccaggcg acctgcgact ccttgacgtt gacaatcgag tagtactccc 180
gattgaagcc cccattcgta taataattac atcacaagac gtcttgcaact catgagctgt 240
ccccacatta ggcttaaaaa cagatgcaat tcccggacgt ctaagccaaa ccactttcac 300
cgctacacga ccgggggtat actacgggtc atgtcttgaa atctgtggag caaaccacag 360
ttcatgccc atcgctcctag aattaattcc ctaaaaaatc tttgaaatag ggcccgtatt 420
```

taccctatag caccctctct acccctcta g

451

<210> 111

<211> 541

<212> DNA

<213> Homo sapiens

<400> 111

```
gctcttcaca cttttattgt taattctctt cacatggcag atacagagct gtcgtcttga 60
agaccaccac tgaccaggaa atgccacttt tacaaaatca tcccccttt tcatgattgg 120
aacagttttc ctgaccgtct gggagcgttg aagggtgacc agcacatttg cacatgcaaa 180
aaaggagtga cccaaggcc tcaaccacac ttcccagagc tcaccatggg ctgcagggtga 240
cttgccaggt ttggggttcg tgagctttcc ttgctgctgc ggtggggagg cctcaagaa 300
ctgagaggcc ggggtatgct tcatgagtgt taacatttac gggacaaaag cgcattatta 360
ggataaggaa cagccacagc acttcatgct tgtgaggggt agctgtagga gcgggtgaaa 420
ggattccagt ttatgaaaat ttaaagcaaa caacggtttt tagctgggtg ggaaacagga 480
aaactgtgat gtcggccaat gaccaccatt tttctgccca tgtgaaggtc cccatgaaac 540
c
```

541

<210> 112

<211> 521

<212> DNA

<213> Homo sapiens

<400> 112

```
caagcgcttg gcgtttggac ccagttcagt gaggttcttg ggttttgtgc ctttggggat 60
tttggtttga cccagggttc agccttagga aggtcttcag gaggaggccg agttccccct 120
cagtaccacc cctctctccc cactttccct ctcccggcaa catctctggg aatcaacagc 180
atattgacac gttggagccg agcctgaaca tgcccctcgg cccagcaca tggaaaacct 240
ccttccttgc ctaagggtgc tgagtttctg gctcttgagg catttcaga cttgaaattc 300
tcatcagtc attgctcttg agtctttgca gagaacctca gatcagggtc acctgggaga 360
aagactttgt cccacttac agatctatct cctcccttgg gaagggcagg gaatggggac 420
ggtgtatgga ggggaaggga tctcctgcgc ccttcattgc cacacttggg gggaccatga 480
acatcttttag tgtctgagct tctcaaatta ctgcaatagg a
```

521

<210> 113

<211> 568

<212> DNA

<213> Homo sapiens

<400> 113

```
agcgtcaaat cagaatggaa aagactcaaa accatcatca acaccaagat caaaaggaca 60
agratccttc aagaaacagg aaaaaactcc taaaacacca aaaggaccta gttctgtaga 120
agacattaaa gcaaaaatgc aagcaagtat agaaaaagggt gtttctcttc ccaaagtgga 180
agccaaattc atcaattatg tgaagaattg cttccggatg actgaccaag aggctattca 240
agatctctgg cagtggagga agtctcttta agaaaatagt ttaaacaatt tgtaaaaaaa 300
ttttccgtct tatttcattt ctgtaacagt tgatatctgg ctgtcctttt tataatgcag 360
agtgagaact ttccctaccg tgtttgataa atgttgcca ggttctattg ccaagaatgt 420
gttgtccaaa atgcctgttt agtttttaaa gatggaactc cacccttgc ttggttttaa 480
gtatgtatgg aatgttatga taggacatag tagtagcggg ggtcagacat ggaaatggtg 540
ggsmgacaaa aatatacatg tgaaataa
```

568

<210> 114

<211> 483

<212> DNA

<213> Homo sapiens

<400> 114

```

tccgaattcc aagcgaatta tggacaaacg attcctttta gaggattact tttttcaatt 60
tcggttttag taatctaggc tttgcctgta aagaatacaa cgatggattt taaatactgt 120
ttgtggaatg tgtttaaagg attgattcta gaacctttgt atatttgata gtatttctaa 180
ctttcatttc tttactgttt gcagttaatg ttcattgttct gctatgcaat cgtttatatg 240
cacgtttctt taattttttt agattttcct ggatgtatag tttaaacaac aaaaagtcta 300
tttaaaactg tagcagtagt ttacagtctt agcaaagagg aaagttgttg gggttaactt 360
tgtattttct ttcttataga ggcttctaaa aaggattttt tatatgttct ttttaacaaa 420
tattgtgtac aacctttaaa acatcaatgt ttggatcaaa acaagacca gcttattttc 480
tgc 483

```

&lt;210&gt; 115

&lt;211&gt; 521

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 115

```

tgtgtggtg cgggctgagg tggaggccca ggactctgac cctgcccctg ccttcagcaa 60
ggcccccggc agcgccggcc actacgaact gccgtgggtt gaaaaatata ggccagttaa 120
gctgaatgaa attgtcggga atgaagacac cgtgagcagg ctagaggtct ttgcaaggga 180
aggaaatgtg cccaacatca tcattgcggg ccctccagga accggcaaga ccacaagcat 240
tctgtgcttg gcccgggccc tgctgggccc agcactcaaa gatgccatgt tggaaactca 300
tgcttcaaag gacaggggca ttgacgttgt gaggaataaa attaaaatgt ttgctcaaca 360
aaaagtcaact cttcccaaag gccgacataa gatcatcatt ctggatgaag cagacagcat 420
gaccgacgga gccagcaag ccttgaggag aaccatggaa atctactcta aaaccactcg 480
ttcgcccttg cttgtaatgc ttcgataag atcatcgagc c 521

```

&lt;210&gt; 116

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

```

ctttgcaaag cttttatttc atgtctgagg catggaatcc acctgcacat ggcattcttag 60
ctgtgaagga gaaagcagtg cagcagaagg aatgagtggg cggaaccaac ggcctccaca 120
agctgccttc cagcagcctg ccaaggccat ggcagagaga gactgcaaac aaacacaagc 180
aaacagagtc tcttcacagc tggagtctga aagctcatag tggcatgtgt gaattctgaca 240
aaattaaaag tgtgcatagt ccattacatg cataaaacac taataataat cctgtttaca 300
cgtgactgca gcaggcaggt ccagctccac cactgccctc ctgccacatc acatcaagtg 360
ccatgggtta gaggggtttt catatgtaat tcttttatc tgtaaaagggt aacaaaatat 420
acagaacaaa actttccctt tttaaaacta atgttacaaa tctgtattat cacttggata 480
taaatagtat ataagctgat c 501

```

&lt;210&gt; 117

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 320

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 117

```

caagggatat atgttgaggg tacrgrgtga cactgaacag atcacaaagc acgagaaaca 60
ttagttctct ccctccccag cgtctccttc gtctccctgg ttttccgatg tccacagagt 120
gagattgtcc ctaagtaact gcatgatcag agtgctgket ttataagact cttcattcag 180
cgtatccaat tcagcaattg cttcatcaaa tgccgttttt gccaggctac aggccttttc 240
aggagagttt agaattctcat agtaaaagac tgagaaattt agtgccagac caagacgaat 300

```

```

tgggtgtgta ggctgcattn ctttcttact aatttcaaat gcttcctggt aagcctgctg 360
ggagttcgac acaagtgggt tgtttgttgc tccagatgcc acttcagaaa gatacctaaa 420
ataatctcct ttcattttca aagtagaaca c                                     451

```

```

<210> 118
<211> 501
<212> DNA
<213> Homo sapiens

```

```

<400> 118
tccggagccg gggtagtcgc cgccgccgcc gccggtgcag ccaactgcagg caccgctgcc 60
gccgcctgag tagtgggctt aggaaggaag aggtcatctc gctcggagct tcgctcggaa 120
gggtctttgt tccctgcagc cctcccacgg gaatgacaat ggataaaaagt gagctggtac 180
agaaagccaa actcgtctgag caggctgagc gatatgatga tatggctgca gccatgaagg 240
cagtcacaga acaggggcat gaactctcca acgaagagag aaatctgctc tctgttgctt 300
acaagaatgt ggtaaggccg cccgccgctc ttcctggcgt gtcactctcca gcattgagca 360
gaaaacagag aggaatgaga agaagcagca gatgggcaaa gagtaccgtg agaagataga 420
ggcagaactg caggacatct gcaatgatgt tctggagctt gttggacaaa tatcttattc 480
caatgctaca caaccagaa a                                     501

```

```

<210> 119
<211> 391
<212> DNA
<213> Homo sapiens

```

```

<400> 119
aaaaagcagc argttcaaca caaaatagaa atctcaaag taggatagaa caaaaccaag 60
tgtgtgaggg gggaagcaac agcaaaagga agaaatgaga tgttgcaaaa aagatggagg 120
agggttcccc tctcctctgg ggactgactc aaacactgat gtggcagtat acaccattcc 180
agagtcaggg gtgttcattc ttttttggga gtaagaaaag gtggggatta agaagacgtt 240
tctggaggct tagggaccaaa ggctggtctc tttccccctt cccaaccccc ttgatccctt 300
tctctgatca ggggaaagga gtcgaatga gggaggtaga gttggaaagg gaaaggattc 360
cacttgacag aatgggacag actccttccc a                                     391

```

```

<210> 120
<211> 421
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 409
<223> n = A,T,C or G

```

```

<400> 120
tggaatagc acagccatcc aggagctctt cargcgcac tcggagcagt tcaactgccat 60
gttcgcccgg aaggccttcc tccactggta cacaggcgag ggcattggac agatggagtt 120
caccgaggct gagagcaaca tgaacgacct cgtctctgag tatcaagcag taccaggatg 180
ccaccgcaga agaggaggag gatttcggtg aggaggccga agaggaggcc taaggcagag 240
ccccatcac ctcaaggcttc tcagttccct tagccgtctt actcaactgc cccttctctc 300
tccctcagaa tttgtgtttg ctgcctctat cttgtttttt gttttttctt ctgggggggt 360
ctagaacagt gcctggcaca tagtaggcgc tcaataaata cttggttgnt gaatgtctcc 420
t                                     421

```

```

<210> 121
<211> 206
<212> DNA
<213> Homo sapiens

```

<400> 121  
 agctggcgct agggctcggt tgtgaaatac agcgtrgtca gcccttgccg tcaagtgtaga 60  
 aacccacgcc tgtaaggctg gtcttcgtcc atctgctttt ttctgaaata cactaagagc 120  
 agccacaaaa ctgtaacctc aaggaaacca taaagcttgg agtgccttaa tttttaacca 180  
 gtttccaata aaacggttta ctacct 206

<210> 122  
 <211> 131  
 <212> DNA  
 <213> Homo sapiens

<400> 122  
 ggagatgaag atgaggaagc tgagtcagct acgggcargc gggcagctga agatgatgag 60  
 gatgacgatg tcgataccaa gaagcagaag accgacgagg atgactagac agcaaaaaag 120  
 gaaaagttaa a 131

<210> 123  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 166, 202, 222, 225  
 <223> n = A,T,C or G

<400> 123  
 gatgaaaatt aaatacttaa attaatcaaa aggcaactag ataccaccta aaacctactg 60  
 cctcagtggc agtakgctaa kgaagatcaa gctacagsac atyatctaata atgaatgtta 120  
 gcaattacat akcargaagc atgtttgctt tccagaagac tatggnacaa tggtcattwg 180  
 ggccaagag gatatttggc cnggaaagga tcaagataga tnaangtaaa g 231

<210> 124  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 284, 412, 513  
 <223> n = A,T,C or G

<400> 124  
 gagtagcaac gcaaagcgct tggatttgag tctgtgggsg acttcggttc cggctctctgc 60  
 agcagccgtg atcgcttagt ggagtgttta gggtagttgg ccaggatgcc gaatatcaaa 120  
 atcttcagca ggcagctccc accaggactt atctcasaaa attgctgacc gcctgggcct 180  
 ggagctaggc aaggtggtga ctaagaaatt cagcaaccag gagacctgtg tggaaattgg 240  
 tgaaagtgtg ccgtggagag gatgtctaca ttgttcagag tggntgtggc gaaatcaatg 300  
 acaatttaata ggagcttttg atcatgatta atgcctgcaa gattgcttca gccagccggg 360  
 ttactgcagt catcccatgc ttcccttatg ccccggcagg ataagaaaga tnagagccgg 420  
 gccgccaatc tcagccaagc ttggtgcaaa tatgctatct gtagcagtgc agatcatatt 480  
 atcaccatgg acctacatgc ttctcaaat canggctttt t 521

<210> 125  
 <211> 341  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 277  
 <223> n = A,T,C or G

<400> 125  
 atgcaaaagg ggacacaggg ggttcaaaaa taaaaatttc ttttccccct ccccaaacct 60  
 gtaccccagc tccccgacca caaccccctt cctcccccg ggaaagcaag aaggagcagg 120  
 tgtggcatct gcagctggga agagagagcg cggggagggtg ccgagctcgg tgctgggtctc 180  
 tttccaaata taaatacgtg tgtcagaact ggaaaatcct ccagcaccca ccaccaagc 240  
 actctccgtt ttctgccggt gtttgagag gggcgnggg caggggcgcc aggcaccggc 300  
 tgggtgcggt ctactgcac cgctgggtgt gcaccccgcg a 341

<210> 126  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 353, 399, 455  
 <223> n = A,T,C or G

<400> 126  
 aggttgagga aggtcatgca ggtgcagatt gtccaggskc agccacaggg tcaagcccaa 60  
 caggcccaga gtggcactgg acagaccatg cagggtgatgc agcagatcat cactaacaca 120  
 ggagagatcc agcagatccc ggtgcagctg aatgccggcc agctgcagta tatccgctta 180  
 gccagcctg tatcaggcac tcaagttgtg cagggacaga tccagacact tgccaccaat 240  
 gctcaacaga ttacacagac agaggtccag caaggacagc agcagttcaa gccagttcac 300  
 aagatggaca gcagctctac cagatccagc aagtcaccat gcctgcgggc cangacctcg 360  
 ccagcccatg ttcatccagt caagccaacc agccctttna cgggcaggcc cccaggtga 420  
 ccggcgactg aagggcctga gctggcaagg ccaangacac ccaacacaat ttttgccata 480  
 cagccccag gcaatgggca cagcctttct tcccagagga c 521

<210> 127  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 127  
 tgagatttat tgcatttcat gcagcttgaa gtccatgcaa aggrgactag cacagttttt 60  
 aatgcattta aaaaataaaa gggaggtggg cagcaaacac acaaagtcct agtttccttg 120  
 gtccctggga gaaaagagtg tggcaatgaa tccaccact ctccacaggg aataaatctg 180  
 tctcttaaat gcaaagaatg tttccatggc ctctggatgc aaatacacag agctctgggg 240  
 tcagagcaag ggatggggag aggaccacga gtgaaaagc agctacacac attcacctaa 300  
 ttccatctga gggaagaac aacgtggcaa gtcttgggg tagcagctgt t 351

<210> 128  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<400> 128  
 tccagacatg ctctgtcct aggcggggag caggaaccag acctgctatg ggaagcagaa 60  
 agagttaagg gaaggtttcc ttctattcct gttccttctc ttttgctttt gaacagtttt 120  
 taaatatact aatagctaag tcatttgcca gccaggcccc ggtgaacagt agagaacaag 180  
 gagcttgcta agaattaatt ttgctgtttt tcacccatt caaacagagc tgccctgttc 240

```

cctgatggag ttccattcct gccagggcac ggctgagtaa cacgaagcca ttcaagaaag 300
gcgggtgtga aatcactgcc accccatgga cagacccctc actcttcctt cttagccgca 360
gcgctactta ataaatatat ttatactttg aaattatgat aaccgatttt tcccatgcgg 420
catcctaagg gcacttgcca gctcttatcc ggacagtcaa gcactgttgt tggacaacag 480
ataaaggaaa agaaaaagaa gaaaacaacc gcaacttctg t 521

```

&lt;210&gt; 129

&lt;211&gt; 521

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

```

tgagacggac cactggcctg gtccccctc atktgctgtc gtaggacctg acatgaaacg 60
cagatctagt ggcagagagg aagatgatga ggaacttctg agacgtcggc agcttcaaga 120
agagcaatta atgaagctta actcaggcct gggacagtgt atcttgaaag aagagatgga 180
gaaagagagc cgggaaaagg catctctgtt agccagtgcg tacgattctc ccatcaactc 240
agcttcacat attccatcat ctaaaactgc atctctccct ggctatggaa gaaatgggct 300
tcaccggcct gtttctaccg acttcgctca gtataacagc tatggggatg tcagcggggg 360
agtgcgagat taccagacac ttccagatgg ccacatgcct gcaatgagaa tggaccgagg 420
agtgtctatg cccaacatgt tggaaccaa gatatttcca tatgaaatgc tcatgggtgac 480
caacagaggg ccgaaaccaa atctcagaga ggtggacaga a 521

```

&lt;210&gt; 130

&lt;211&gt; 270

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

```

tcactttatt tttcttgtat aaaaacccta tgtttagacc acagctggag cctgagtccg 60
ctgcacggag actctggtgt gggctctgac gaggtggtca gtgaactcct gatagggaga 120
cttggatgaat acagtctcct tccagaggtc gggggtcagg tagctgtagg tcttagaaat 180
ggcatcaaag gtggccttgg cgaagttgcc cagggtggca gtgcagcccc gggctgaggt 240
gtagcagtca tcgataccag ccatcatgag 270

```

&lt;210&gt; 131

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 131

```

ctggaatata gaccctgat cgacaaaact ttgaacgagg ctgactgtgc caccgtcccg 60
ccagccattc gtcctactg atgagacaag atgtggtgat gacagaatca gcttttgtaa 120
ttatgtataa tagctcatgc atgtgtccat gtcataactg tcttcatacg cttctgcaact 180
ctggggaaga aggagtacat tgaagggaga ttggcaccta gtggctggga gcttgccagg 240
aaccagtggt ccagggagcg tggcacttac ctttgtccct tgcttcattc ttgtgagatg 300
ataaaaactg gcacagctct taaataaaat ataatgaac a 341

```

&lt;210&gt; 132

&lt;211&gt; 844

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 37

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 132

```

tgaatgggga ggagctgacc caggaaatgg agcttgngga gaccaggcct gcaggggatg 60
gaaccttcca gaagtgggca tctgtggtgg tgcctcttgg gaaggagcag aagtacacat 120
gccatgtgga acatgagggg ctgcctgagc ccctcaccct gagatggggc aaggaggagc 180
ctccttcac caccaagact aacacagtaa tcattgctgt tccggttgtc cttggagctg 240
tggtcatcct tggagctgtg atggcttttg tgatgaagag gaggagaaac acagggtgaa 300
aaggagggga ctatgctctg gctccaggct cccagagctc tgatatgtct ctcccagatt 360
gtaaagtgtg aagacagctg cctgggtgtg acttggtgac agacaatgtc ttcacacatc 420
tcctgtgaca tccagagacc tcagttctct ttagtcaagt gtctgatgtt ccctgtgagt 480
ctgcgggctc aaagtgaaga actgtggagc ccagtccacc cctgcacacc aggaccctat 540
ccctgcactg ccctgtgttc ccttcacag ccaaccttgc tgctccagcc aaacattggt 600
ggacatctgc agcctgtcag ctccatgcta ccctgacctt caactcctca cttccacact 660
gagaataata atttgaatgt ggggtggctg agagatggct cagcgtgac tgctcttcca 720
aaggtcctga gttcaaatcc cagcaaccac atggtggctc acaaccatct gtaatgggat 780
ctaataccct ctctgcagt gtctgaagac asctacagt tacttacata taataataaa 840
taag
844

```

<210> 133  
 <211> 601  
 <212> DNA  
 <213> Homo sapiens

```

<400> 133
ggccgggccc gcgcgcccc gccacacgca cgccgggggt gccagtttat aaaggagag 60
agcaagcagc gagtcttgaa gctctgtttg gtgctttgga tccatttcca tcggtcctta 120
cagccgctcg tcagactcca gcagccaaga tggatgaagc gatcgagagc aagactgctt 180
ttcaggaagc cttggacgct gcaggtgata aactttagt agttgacttc tcagccacgt 240
ggtgtgggccc ttgcaaaatg atcaagcctt tctttcattc cctctctgaa aagtattcca 300
acgtgatatt ccttgaagta gatgtggatg actgtcagga tggtgttcca gagtgtgaag 360
tcaaatgcat gccaaattc cagtttttta agaagggaca aaagggtggg gaattttctg 420
gagccaataa ggaaaagctt gaagccacca ttaatgaatt agtctaata tgttttctga 480
aaatataacc agccattggc tatttaaaac ttgtaatttt ttttaatttac aaaaatataa 540
aatatgaaga cataaaccm gttgccatct gcgtgacaat aaaacattaa tgctaacact 600
t
601

```

<210> 134  
 <211> 421  
 <212> DNA  
 <213> Homo sapiens

```

<400> 134
tcacataaga aatttaagca agttacrcta tcttaaaaaa cacaacgaat gcattttaat 60
agagaaaccc ttccctccct ccacctccct cccccaccct cctcatgaat taagaatcta 120
agagaagaag taaccataaa accaagtttt gtggaatcca tcatccagag tgcttacatg 180
gtgattaggt taatattgcc ttcttataaa atttctatatt taaaaaaaat tataaccctg 240
attgcttatt acaaaaaaat tcagtacaaa agttcaatat attgaaaaat gcttttcccc 300
tccctcacag caccgtttta tatatagcag agaataatga agagattgct agtctagatg 360
gggcaatctt caaattacac caagacgcac agtggtttat ttaccctccc cttctcataa 420
g
421

```

<210> 135  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

```

<400> 135
ggaaaggatt caagaattag aggacttgct tgctrragaa aaagacaact ctcgtcgcat 60
gctgacagac aaagagagag agatggcgga aataagggat caaatgcagc aacagctgaa 120
tgactatgaa cagcttcttg atgtaaagtt agccctggac atggaaatca gtgcttacag 180

```



```

gaaactctta gaaggcgaag aagagaggtt gaagctgtct ccaagccctt cttcccgtgt 240
gacagtatcc cgagcatcct caagtcgtag tgtaccgtac aactagagga aagcggaaga 300
gggttgatgt ggaagaatca gaggcgaagt agtagtgta gcatctctca ttccgcctca 360
accactggaa atgtttgcat cgaagaaatt gatgttgatg ggaaatttat cccgcttgaa 420
gaacacttct gaacaggatc aaccaatggg aaggcttggg agatgatcag aaaaattgga 480
gacacatcag tcagttataa atatacctca a 511

```

&lt;210&gt; 136

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 136

```

catgggtttc accaggttgg ccaggctgct cttgaactsc tgacctcagg tgatccaccc 60
gcctcggcct cccaaagtgc tgggattaca ggcgtgagcc accacgcccg gccccaaaag 120
ctgtttcttt tgtcttttagc gtaaaagtct cctgccatgc agtatctaca taactgacgt 180
gactgccagc aagctcagtc actccgtggg tttttctct ttccagttct tctctctctc 240
ttcaagttct gcctcagtg aagctgcagg tccccagtta agtgatcagg tgagggttct 300
ttgaacctgg ttctatcagt cgaattaatc cttcatgatg g 341

```

&lt;210&gt; 137

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```

gatgtgttgg accctctgtg tcaaaaaaaaa cctcacaaag aatcccctgc tcattacaga 60
agaagatgca tttaaaatat gggttatttt caacttttta tctgaggaca agtatccatt 120
aattattgtg tcagaagaga ttgaatacct gcttaagaag cttacagaag ctatgggagg 180
aggttggcag caagaacaat ttgaacatta taaaatcaac tttgatgaca gtaaaaatgg 240
cctttctgca tgggaactta ttgagcttat tggaaatgga cagtttagca aaggcatgga 300
ccggcagact gtgtctatgg caattaatga agtctttaat gaacttatat tagatgtgtt 360
aaagcagggt tacatgatga aaaagggcca cagacggaaa aactggactg aaagatggtt 420
tgtactaaaa cccaacataa tttcttacta tgtagtgag gatctgaagg ataagaaagg 480
agacattctc ttggatgaaa attgctgtgt agaagtcctt gcctgacaaa agatggaaag 540
aatgccttt t 551

```

&lt;210&gt; 138

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 490

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 138

```

gactggttct ttatttcaaa aagacacttg tcaatattca gtrtcaaaac agttgacta 60
ttgatttctc tttctcccaa tcggccccaa agagaccaca taaaaggaga gtacatttta 120
agccaataag ctgcaggatg tacacctaac agacctcta gaaaccttac cagaaaatgg 180
ggactgggta gggaaggaaa cttaaaagat caacaaactg ccagcccacg gactgcagag 240
gctgtcacag ccagatgggg tggccagggt gccacaaacc caaagcaaag tttcaaaata 300
atataaaatt taaaaagttt tgtacataag ctattcaaga tttctccagc actgactgat 360
acaaagcaca attgagatgg cacttctaga gacagcagct tcaaaccag aaaagggtga 420
tgagatgaag tttcacatgg ctaaatcagt ggcaaaaaca cagtcttctt tctttctttc 480
tttcaaggan gcaggaaagc aattaagtggt tcaccttaac ataaggggga c 531

```

<210> 139  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 517  
 <223> n = A,T,C or G

<400> 139  
 tgggtgggca ccatggctgg gatcaccacc atcgaggcgg tgaagcgcaa gatccaggtt 60  
 ctgcagcagc aggagatga tgcagaggag cgagctgagc gcctccagcg agaagttgag 120  
 ggagaaaggc gggcccggga acaggctgag gctgagggtg cctccttgaa ccgtaggagc 180  
 cagctgggtg aagaagagct ggaccgtgct caggagcgcc tggccactgc cctgcaaaag 240  
 ctggaagaag ctgaaaaaag tgcctgatgag agtgagagag gtatgaaggt tattgaaaac 300  
 cgggccttaa aagatgaaga aaagatggaa ctccaggaaa tccaactcaa agaagctaag 360  
 cacattgcag aagaggcaga taggaagtat gaagaggtgg ctcgtaagtt ggtgatcatt 420  
 gaaggagact tggaaccgca cagaaggaac gagcttgagc ttggcaaaaag tcccgttgcc 480  
 cagagatggg atgaaccaga ttagactgat ggaccanaac c 521

<210> 140  
 <211> 571  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 7  
 <223> n = A,T,C or G

<400> 140  
 aggggcnegc ggtgcgtggg ccaactgggtg accgacttag cctggccaga ctctcagcac 60  
 ctggaagcgc cccgagagtg acagcgtgag gctgggaggg aggacttgcc ttgagcttgt 120  
 taaactctgc tctgagcctc cttgtcgccg gcatttagat ggctcccgcg aagaaggggtg 180  
 gcgagaagaa aaaggccgct tctgccatca acgaagtggg aaccgcagaa tacaccatca 240  
 acattcacaa gcgcattccat ggagtgggct tcaagaagcg tgcacctcgg gactcaaaag 300  
 agattcgga atttgccatg aaggagatgg gaactccaga tgtgcgcatt gacaccaggc 360  
 tcaacaaagc tgtctgggcc aaaggaataa ggaatgtgcc ataccgaatc cgggtgtgcgg 420  
 ctgtccagaa aacgtaataa ggatgaagat tcaccaaata agctatatac tttggttacc 480  
 tatgtacctg ttaccacttt caaaaatcta cagacagtca atgtggatga gaactaatcg 540  
 ctgatcgtca gatcaataa agttataaaa t 571

<210> 141  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 tcgggagcca cacttgcccc tcttctctc caaagsgcca gaacctcctt ctctttggag 60  
 aatggggagg cctcttggag acacagaggg tttcaccttg gatgacctct agagaaattg 120  
 cccaagaagc ccaccttctg gtcccaacct gcagacccca cagcagtcag ttggtcaggc 180  
 cctgctgtag aaggctcactt ggctccattg cctgcttcca accaatgggc aggagagaag 240  
 gcctttattt ctgcgccacc cattctcctt gtaccagcac ctccgttttc agtcagtgtt 300  
 gtccagcaac ggtaccgttt acacagtcac ctccagacaca ccatttcacc tcccttgcca 360  
 agctgttagc cttagagtga ttgcagtga cactgtttac acaccgtgaa tccattccca 420  
 tcagtccatt ccagttggca ccagcctgaa ccatttggtg cctgggtgta actggagtcc 480  
 tgtttacaag gtggagtggg ggcttgctga cttctcttca tttgagggca c 531

<210> 142  
<211> 491  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 410  
<223> n = A,T,C or G

<400> 142  
acctagacag aaggtgggtg agggaggact ggtaggaggc tgaggcaatt ccttggtagt 60  
ttgtcctgaa accctactgg agaagtcagc atgaggcacc tactgagaga agtgcccaga 120  
aactgctgac tgcctctggt aagagttaac agtaaagagg tagaagtgtg tttctgaatc 180  
agagtggaag cgtctcaagg gtcccacagt ggaggtccct gagctacctc ccttccgtga 240  
gtgggaagag tgaagcccat gaagaactga gatgaagcaa ggatgggggt cctgggctcc 300  
aggcaagggc tgtgctctct gcagcagggg gcccacagag tcagaagaaa agaactaatc 360  
atttgttgca agaaaccttg cccggatact agcggaaaac tggaggcggn ggtgggggca 420  
caggaaagtg gaagtgattt gatggagagc agagaagcct atgcacagtg gccgagtcca 480  
cttgtaaagt g 491

<210> 143  
<211> 515  
<212> DNA  
<213> Homo sapiens

<400> 143  
ttcaagcaat tgtaacaagt atatgtagat tagagtgagc aaaatcatat acaattttca 60  
tttccagttg ctattttcca aattgtttctg taatgtcgtt aaaattactt aaaaattaac 120  
aaagccaaaa attatattta tgacaagaaa gccatcccta cattaatctt acttttccac 180  
tcaccggccc atctccttcc tctttttcct aactatgcca ttaaaactgt tctactgggc 240  
cgggcggtgt gctcatgcct gtaatcccag cattttggga ggccaaggca ggcggatcat 300  
gaggtcaaga gattgagacc atcctggcca acatggtgaa accccgcctc gactaagaat 360  
acaaaaatta gctgggcatg gtggcgcatg cctgtagtct cagctactcg ggaggctgag 420  
gcagaagaat cgcttgaacc cgggaggcag aggatgcagt gagccccgat cgcgccactg 480  
cactctagcc tgggcgacag actgagactc tgctc 515

<210> 144  
<211> 340  
<212> DNA  
<213> Homo sapiens

<400> 144  
tgtgccagtc tacaggccta tcagcagcga ctcttccagc aacagatggg gtccccctgtt 60  
cagcccaacc ccatgagccc ccagcagcat atgtctccaa atcaggccca gtccccacac 120  
ctacaaggcc agcagatccc taattctctc tccaatcaag tgcgctctcc ccagcctgtc 180  
ccttctccac ggccacagtc ccagccccc cactccagtc cttccccaaag gatgcagcct 240  
cagccttctc cacaccagct ttccccacag acaagttccc cacatcctgg actggtagtt 300  
gcccaggcca accccatgga acaagggcat tttgccagcc 340

<210> 145  
<211> 630  
<212> DNA  
<213> Homo sapiens

<400> 145  
tgtaaaaact tgtttttaat tttgtataaa ataaaggtgg tccatgccca cgggggctgt 60

```

aggaaatcca agcagaccag ctgggggtggg gggatgtagc ctacctcggg ggactgtctg 120
tcctcaaaac gggctgagaa ggcccgtcag gggcccaggt cccacagaga ggcctgggat 180
actcccccac cccgaggggc agactgggca gtggggagcc cccatcgtgc cccagagggtg 240
gccacaggct gaaggagggg cctgaggcac cgcagcctgc aacccccagg gctgcagtcc 300
actaactttt tacagaataa aaggaacatg gggatgggga aaaaagcacc aggtcaggca 360
gggcccaggg gcccagatc ccaggagggc caggactcag gatgccagca ccaccctagc 420
agctcccaca gtccttgga caggaggccg ccacggattg gcacaggccg ctgctggcca 480
tcacgccaca ttggagaac ttgtcccagc agaggtcagc tcggaggagc tcctcgtggg 540
cacacactgt acgaacacag atctccttgt taatgacgta cacacggcgg aggtcgcggg 600
gacagggcac gggaggtctc agccccactt
630

```

&lt;210&gt; 146

&lt;211&gt; 521

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 146

```

atggctgctg gatttaggtg gtaatagggg ctgtgggcca taaatctgaa gccttgagaa 60
ccttgggtct ggagagccat gaagaggga gaaaaagagg gcaagtcctg aacctaacca 120
atgacctgat ggattgctcg accaagacac agaagtgaag tctgtgtctg tgcacttccc 180
acagactgga gtttttggtg ctgaatagag ccagttgcta aaaaattggg ggtttggtga 240
agaaatctga ttgtgtgtg tattcaatgt gtgattttaa aaataaacag caacaacaat 300
aaaaaccctg actggctggt tttccctgt attccttaca actattttt gaccctctga 360
aaattattat acttcaccta aatggaagac tgctgtgtt gtggaaattt tgtaattttt 420
taattattt tattctctct cttttttatt ttgctgcag aatccgttga gagactaata 480
aggcttaata ttaattgat ttgtttaata tgtatataa t
521

```

&lt;210&gt; 147

&lt;211&gt; 562

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 147

```

ggcatgcgag cgcactcggc ggacgcaagg gcggcgggga gcacacggag cactgcaggc 60
gccgggttgg gacagcgtct tcgctgctgc tggatagtcg tgttttcggg gatcgaggat 120
actcaccaga aaccgaaaat gccgaaacca atcaatgtcc gagttaccac catggatgca 180
gagctggagt ttgcaatcca gccaaataca actggaaaac agctttttga tcagggtgga 240
aagactatcg gcctccggga agtgtggtac tttggcctcc actatgtgga taataaagga 300
tttctacct ggctgaagct ggataagaag gtgtctgcc aggaggtcag gaaggagaat 360
ccccccagt tcaagttccg ggccaaagtt ctacctgaa gatgtggctg aggagctcat 420
ccaggacatc acccagaaac ttttcttcct tcaagtgaag gaaggaatcc ttagcgatga 480
gatctactgc ccccttggar actgccgtgc tcttgggggc ctacgcttgt gcatgccaaag 540
tttggggact accaccaaga ag
562

```

&lt;210&gt; 148

&lt;211&gt; 820

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

```

gaaggagtcg ggatactcag cattgatgca cccaatttc aaagcggcat tcttcggcag 60
gtctctggga caatctctag ggtcactacc tggaaactcg ttaggttaca actgaatgct 120
gaaaggaaag aacacctgca gaaccggaca gaaattcacc ccggcgatca gctgattgat 180
ctcgggtcgac cagaagtcag ggctaaagat gacgaggacg ttgtcaattc cctgggcttt 240
tcgaagttag tccagcagca gtctgaggta ttcgggccgg ttatgcacct ggaccaccag 300
caccagctcc cggggggccc aggtgccagc cttatctaca ttcctcaggg tctgatcaaa 360
gttcagctgg tacaccaggg accggtaccg cagcgtcagg ttgtccgctc gggctggggg 420
accgccggga ccagggaagc cgccgacacg ttggagacc tgccgatgcc cacagccaca 480

```

```

gaggggtggt cccaccgcg gccgccgga cccgcgcgg gttcggcgtc cagcaacggt 540
ggggcgaggg cctcgttctt cctttgtcgc ccattgctgc tccagaggac gaagccgcag 600
gcggccacca cgagcgtcag gattagcacc ttccgtttgt agatgcggaa cctcatggtc 660
tccagggccg ggagcgcagc tacagctcga gcgtcggcgc cgccgctagg agccgcggct 720
cggcttcgtc tccgtcctct ccattcagca ccacgggtcc cggaanaagc tcagccscgg 780
tcccaaccgc accctagctt cgttacctgc gcctcgttg 820

```

<210> 149  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

```

<400> 149
cagattttta tttgcagtcg tcaactgggc cgtttcttgc tgcttatttg tctgctagcc 60
tgctcttcca gctgcatggc caggcgcaag gccttgatga catctcgag ggctgagaaa 120
tgcttggtt gctgggccag agcagattcc gctttgttca caaaggctctc caggctcatag 180
tctggctgct cggtcacctc agagagctca agccagtctg gtccttgctg tatgatctcc 240
ttgagctctt ccatagcctt ctctccagc tccctgatct gagtcatggc ttcgttaaag 300
ctggacatct gggaagacag ttctcctct tcttggtata aattgcctgg aatcagcgc 360
ccgttagagc aggttccat ctcttctgtt tccatttgaa tcaactgctc tccactgggc 420
ccactgtggg ggctcagctc cttgacctg ctgcatact taagggtgtt taaaggatat 480
tcacaggagc ttatgcctgg t 501

```

<210> 150  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 457, 479  
 <223> n = A,T,C or G

```

<400> 150
ctcctcttgg tacatgaacc caagttgaaa gtggacttaa caaagtatct ggagaaccaa 60
gcattctgct ttgacttttg atttgatgaa acagcttcga atgaagttgt ctacaggttc 120
acagcaaggc cactggtaca gacaatcttt gaaggtggaa aagcaacttg ttttgcatat 180
ggccagacag gaagtggcaa gacacatact atgggcggag acctctctgg gaaagcccag 240
aatgcaccca aagggatcta tgccatggcc ttccgggacg tcttcttctg aagaatcaac 300
cctgctaccg gaagttgggc ctggaagtct atgtgacatt cttcgagatc tacaatggga 360
agctgtttga cctgctcaac aagaaggcca agcttgccgc tgctggaaga cggcaagcaa 420
caggtgcaag tgggtggggc ttgcaggaac atctggntaa ctctgcttga tgatggcant 480
caagatgatc gacatgggca ggcctgcag a 511

```

<210> 151  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

```

<400> 151
tccgaattc aagcgacaaa ttggawagt aaatggaaga tgcctatcat gaacatcagg 60
caaatctttt gcgccaagat ctgatgagac gacaggaaga attaagacgc atggaagaa 120
ttcacaatca agaaatgcag aaacgtaaag aaatgcaatt gaggcaagag gaggaacgac 180
gtagaagaga ggaagagatg atgattcgtc aacgtgagat ggaagaacaa atgaggcgcc 240
aaagagagga aagttacagc cgaatgggct acatggatcc acgggaaaga gacatgcgaa 300
tgggtggcgg aggagcaatg aacatgggag atccctatgg ttccaggaggc cagaaatttc 360
cacctctagg aggtggtggt ggcataggtt atgaagctaa tcctggcggt ccaccagcaa 420
ccatgagtgg ttccatgatg ggaagtgaac tgcgtactga gcgctttggg cagggaggtg 480

```

cggggcctgt ggggtggacag ggtcctagag gaatggggcc tggaaactcca gcaggatatg 540  
gtagagggag agaagagtac gaaggc 566

<210> 152  
<211> 518  
<212> DNA  
<213> Homo sapiens

<400> 152  
ttcgtgaaga ccctgactgg taagaccatc actctcgaag tggagcccga gtgacaccat 60  
tgagaatgtc aaggcaaaga tccaagacaa ggaaggcatc cctcctgacc agcakagggt 120  
gatctttgct gggaacacagc tggaaagtgg acgcaccctg tctgactaca acatccagaa 180  
agagtccacc ctgcacctgg tgctccgtct cagagggtgg atgcaaactc tctgtgaagac 240  
cctgactggg aagaccatca ccctcgaggt ggagcccagt gacaccatcg agaatgtcaa 300  
ggcaaagatc caagataagg aaggcatccc tcttgatcag cagagggtga tctttgctgg 360  
gaaacagctg gaagatggac gcaccctgtc tgactacaac atccagaaag agtccactct 420  
gcacttggtc ctgcgcttga gggggggtgt ctaagtctcc ccttttaagg tttcaacaaa 480  
tttcattgca ctttcctttc aataaagttg ttgcattc 518

<210> 153  
<211> 542  
<212> DNA  
<213> Homo sapiens

<400> 153  
gcgcgggtgc gtgggccact gggtgaccga cttagcctgg ccagactctc agcacctgga 60  
agcgcgccga gagtgcacagc gtgaggctgg gagggaggac ttggcttgag cttgttaaag 120  
tctgctctga gcctccttgt cgcctgcatt tagatggctc ccgcaaagaa ggggtggcgag 180  
aagaaaaagg gccgttctgc catcaacgaa gtggttaacc gagaaatac catcaacatt 240  
cacaagcgca tccatggagt gggcttcaag aagcgtgcac ctggggcact caaagagatt 300  
cggaattttg ccatgaagga gatgggaact ccagatgtgc gcattgacac caggctcaac 360  
aaagctgtct gggccaaagg aataaggaat gtgccatacc gaatccgtgt gcggctgtcc 420  
agaaaacgta atgaggatga agattcacca aataagctat atactttggt tacctatgta 480  
cctgttacca ctttcaaaaa tctacagaca gtcaatgtgg atgagaacta atcgctgac 540  
gt 542

<210> 154  
<211> 411  
<212> DNA  
<213> Homo sapiens

<400> 154  
aattctttat ttaaatacaac aaactcatct tctcaagcc ccagaccatg gtaggcagcc 60  
ctccctctcc atccctcac cccaccctt agccacagtg aagggaatgg aaaatgagaa 120  
gccacgaggg cccctgccag ggaaggctgc ccagatgtg tggtagcac agtcagtga 180  
gctgtggctg gggcagcagc tgccacaggc tctccctat aaattaagtt cctgcagcca 240  
cagctgtggg agaagcatac ttgtagaagc aaggccagtc cagcatcaga aggcagaggg 300  
agcatcagtg actcccagcc atggaatgaa cggaggacac agagctcaga gacagaacag 360  
gccaggggga agaaggagag acagaatagg ccaggggcatg gcggtgaggg a 411

<210> 155  
<211> 421  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 173

<223> n = A, T, C or G

<400> 155

```

tgatgaatct ggggtgggctg gcagtagccc gagatgatgg gctcttctct ggggatccca 60
actggttccc taagaaatcc aaggagaatc ctcggaactt ctcggataac cagctgcaag 120
agggcaagaa cgtgatcggg ttacagatgg gcaccaaccg cggggcgctc cangcaggca 180
tgactggcta cgggatgcca cgccagatcc tctgatccca ccccaggcct tgcccctgcc 240
ctcccacgaa tggttaatat atatgtagat atatatttta gcagtacat tcccagagag 300
ccccagagct ctcaagctcc tttctgtcag ggtggggggt tcaagcctgt cctgtcacct 360
ctgaagtgcc tgctggcatc ctctccccc tgcttactaa tacattccct tcccatagc 420
c 421

```

<210> 156

<211> 670

<212> DNA

<213> Homo sapiens

<400> 156

```

agcggagctc cttcccctgg tggctacaac ccacacacgc caggctcagg catcgagcag 60
aactccagcg actgggtaac cactgacatt caggtgaagg tgcgggacac ctacctggat 120
acacaggtgg tgggacagac aggtgtcatc cgcagtgtca cggggggcat gtgctctgtg 180
tacctgaagg acagtgaagaa ggtgtgcagc atttccagtg agcacctgga gcctatcacc 240
tccaccaaga acaacaaggt gaaagtgatc ctgggcgagg atcgggaagc cacgggcgtc 300
ctactgagca ttgatgggtga ggatggcatt gtccgtatgg accttgatga gcagctcaag 360
atcctcaacc tccgcttcct ggggaagctc ctggaagcct gaagcaggca gggccggtgg 420
acttcgtcgg atgaagagtg atcctccttc cttccctggc ccttggctgt gacacaagat 480
cctcctgcag ggctaggcgg attgttcttg atttctttt gtttttctt ttaggtttcc 540
atcttttccc tccctgggtgc tcattggaat ctgagtagag tctgggggag ggtccccacc 600
ttcctgtacc tcctccccc agcttgcttt tgtgtaccg tctttcaata aaaagaagct 660
gtttggtcta 670

```

<210> 157

<211> 421

<212> DNA

<213> Homo sapiens

<400> 157

```

ggttcacagc actgctgctt gtgtgttgcc ggccaggaat tccaggctca caaggctatc 60
ttagcagctc gttctccggg ttttagtgcc atgtttgaac atgaaatgga ggagagcaaa 120
aagaatcgag ttgaaatcaa tgatgtggag cctgaagttt ttaaggaaat gatgtgcttc 180
atttacacgg ggaaggctcc aaacctcgac aaaatggctg atgatttgct ggcagctgct 240
gacaagtatg ccctggagcg cttaaagggtc atgtgtgagg atgccctctg cagtaacctg 300
tccgtggaga acgctgcaga aattctcatc ctggccgacc tccacagtcg agatcagttg 360
aaaactcagg cagtggattt catcaactat catgcttcgg atgtcttgga gacctcttgg 420
g 421

```

<210> 158

<211> 321

<212> DNA

<213> Homo sapiens

<400> 158

```

tcgtagccat ttttctgctt ctttggagaa tgacgccaca ctgactgctc attgtcgttg 60
gttccatgcc aattgggtgaa atagaacctc atccggtagt ggagccggag ggacatcttg 120
tcatcaacgg tgatgggtgcg atttggagca taccagagct tgggtgtctc gccatacagg 180
gcaaagaggt tgtgacaaaag aggagagata cggcatgcct gtgcagccct gatgcacagt 240
tcctctgctg tgtactctcc actgcccagc cggagggggct ccctgtccga cagatagaag 300
atcaattcca cccctggctt g 321

```

<210> 159  
 <211> 596  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
 tggcacactg ctcttaagaa actatgawga tctgagattt ttttgtgtat gtttttgact 60  
 cttttgagtg gtaatcatat gtgtctttat agatgtacat acctccttgc acaaattggag 120  
 ggggaattcat tttcatcact gggagtggtcc ttagtgtata aaaaccatgc tggatatatgg 180  
 cttcaagttg taaaaatgaa agtgacttta aaagaaaata ggggatgggc caggatctcc 240  
 actgataaga ctgtttttta gtaacttaag gacctttggg tctacaagta tatgtgaaaa 300  
 aaatgagact tactgggtga ggaaattcat tgtttaaaga tggtcgtgtg tgtgtgtgtg 360  
 tgtgtgtgtg ttgtgtgtg ttttgtttt taaggagggg aatttattat ttaccgttgc 420  
 ttgaaattac tgggttaaata tatgtytgat aatgatttgc tytttgvma ctaaaattag 480  
 gvctgtataa gtwtctaratg cmtccctggg kgttgatytt ccmagatatt gatgatamcc 540  
 cttaaaattg taaccygcct ttttcccttt gctytcatt aaagtctatt cmaaag 596

<210> 160  
 <211> 515  
 <212> DNA  
 <213> Homo sapiens

<400> 160  
 gggggtaggc tctttattag acggttattg ctgtactaca gggtcagagt gcagtgtgaa 60  
 cagtgtcaga ggcccgctt cagccaaga atgtggattt tctctcccta ttgatcacag 120  
 tgggtgggtt tcttcagaaa agccccagag gcagggacca gtgagctcca aggttagaag 180  
 tggaaactga aggttcagt cacatgctgc ttccacgctt ccaggctggg cagcaaggag 240  
 gagatgcccc tgacgtgcca ggtctccca tctgacacca gtgaagtctg gtaggacagc 300  
 agccgcacgc ctgcctctgc caggaggcca atcatggtag gcagcattgc agggtcagag 360  
 gtctgagtc ggaataggag caggggcagg tccctgcgga gaggcacttc tggcctgaag 420  
 acagctccat tgagcccctg cagtacaggy gtagtgcctt ggaccaagcc cacagcctgg 480  
 taaggggcgc ctgccagggc cagggccagg aggca 515

<210> 161  
 <211> 936  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 taatttctta gtcgtttgga atccttaagc atgcaaaagc tttgaacaga aggggttcaca 60  
 aagggaaccag ggttgtctta tggcatccag ttaagccaga gctgggaatg cctctgggtc 120  
 atccacatca ggagcagaag cacttgactt gtcggtcctg ctgccacggt ttgggcgccc 180  
 accacgcccc cgtccacctc gtcctcccct gccgccagct cctgggcggc caaggtctcc 240  
 aaaattgatc tccagctgag acgttatatc atttgctggc ttccggaaat gatggtccat 300  
 aaccgaatct tcagcatgag cctcttcact ctttgattta tgaagaacaa atcccttctt 360  
 cactgcccc tcagcacctt catttggttt tcggatatta aattctactt ttgcccggtc 420  
 cttattttga atagccttcc actcatccaa agtcatctct tttggaccct cctcttttac 480  
 ctcttcaact tcatttcact tattttcagt gtctgccact ggatgatgtt cttcaccttc 540  
 aggtgtttcc tcagtcacat ttgattgac caagtcagtt aattcgtctt tgacagttcc 600  
 ccagttgtga gatccgctac ctccacgttt gtcctcgtgc ttcaggccag atctatcact 660  
 tccactatgc ctatcaaatt cacgtttgcc acgagaatca aatccatctc ctcgccccat 720  
 tccacgtcca cgccccctc gacctcttcc aagaccacca cgacctcgaa taggtcggtc 780  
 aataatcggc ctatcaactg aaaattcgcc tccttcaccc ttttcttcaa gtggcttttc 840  
 gaatcttcgt tcacgaggtg gtcgccttcc tggctcttca tcaattattt tcccttcacc 900  
 ctgaagttgt tgatcaggtc ttcttccaac tcgtgc 936

<210> 162



<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 162  
aagcggatgg acctgagtca gccgaatcct agcccccttc cttgggcctg ctgtggtgct 60  
cgacatcagt gacagacgga agcagcagac catcaaggct acgggaggcc cggggcgctt 120  
gcgaagatga agtttggctg cctctccttc cggcagcctt atgctggctt tgtcttaaat 180  
ggaatcaaga ctgtggagac gcgctggcgt cctctgctga gcagccagcg gaactgtacc 240  
atcgccgtcc acattgctca cagggactgg gaaggcgatg cctgtcgga gctgctggtg 300  
gagagactcg ggatgactcc tgctcagatt caggccttgc tcaggaaagg ggaaaagttt 360  
ggtcgaggag tgatagcggg actcgttgac attggggaaa ctttgcaatg ccccgagac 420  
ttaactcccg atgaggttgt ggaactagaa aatcaagctg cactgaccaa cctgaagcag 480  
aagtacctga ctgtgatttc aaaccccagg tggttactgg agcccatacc taggaaagga 540  
ggcaaggatg tattccaggt agacatccca gagcacctga tccctttggg gcatgaagtg 600  
tgacaagtgt gggctcctga aagggaatgtt ccragaaaac cagctaaatc atggcacctt 660  
caatttgcca tcgtgacgca gacctgtata aattagggtt aagatgaatt tccactgctt 720  
tggagagtcc caccactaa gcactgtgca tgtaaacagg ttcctttgct cagatgaagg 780  
aagtaggggg tggggctttc cttgtgtgat gcctccttag gcacacaggc aatgtctcaa 840  
gtactttgac cttagggtag aaggcaaagc tgccagtaaa tgtctcagca ttgctgctaa 900  
ttttggtcct gctagtttct ggattgtaca aataaatgtg ttgtagatga 950

<210> 163  
<211> 475  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 301, 317, 331, 458, 464, 470  
<223> n = A,T,C or G

<400> 163  
tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagttgt 60  
tctccggctg cccattgctc tcccactcca cggcgatgtc gctgggatag aagcctttga 120  
ccaggcaggt caggctgacc tggttcttgg tcatctcctc ccgggatggg ggcagggtgt 180  
acacctgtgg ttctcggggc tgccctttgg ctttggagat ggttttctcg atgggggctg 240  
ggagggcttt gttggagacc ttgcaattgt actccttgcc attcaaccag tcctggtgca 300  
ngacggtgag gacgctnacc acacggtacg ngctggtgta ctgctcctcc cgcggctttg 360  
tcttggcatt atgcacctcc acgccgtcca cgtaccaatt gaacttgacc tcagggtctt 420  
cgtggctcac gtccaccacc acgcatgtaa cctcaaanct cggncgcgan cacgc 475

<210> 164  
<211> 476  
<212> DNA  
<213> Homo sapiens

<400> 164  
agcgtggtcg cggccgaggt ctgaggttac atgcgtggtg gtggacgtga gccacgaaga 60  
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120  
gccgcgggag gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca 180  
ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc 240  
ccccatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac 300  
cctgccccca tccggggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa 360  
aggcttctat cccagcgaca tcgcccgtgg agtgggagag caatgggcag ccggagaaca 420  
actacaagac cacgcctccc gtgctggact ccgacacctg ccgggcggcc gctcga 476

<210> 165

<211> 256  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 10, 37, 249  
<223> n = A,T,C or G

<400> 165  
agcgtggttn cggccgaggt cccaaccaag gctgcancct ggatgccatc aaagtcttct 60  
gcaacatgga gactggtgag acctgcgtgt accccactca gcccagtgtg gcccagaaga 120  
actggtacat cagcaagaac cccaaggaca agaggcatgt ctgggttcggc gagagcatga 180  
ccgatggatt ccagttcgag tatggcggcc agggctccga ccctgccgat gtggacctgc 240  
ccgggcggnc gctcga 256

<210> 166  
<211> 332  
<212> DNA  
<213> Homo sapiens

<400> 166  
agcgtggtcg cggccgaggt caagaacccc gcccgcacct gccgtgacct caagatgtgc 60  
cactctgact ggaagagtgg agagtactgg attgacccca accaaggctg caacctggat 120  
gccatcaaag tcttctgcaa catggagact ggtgagacct gcgtgtacct cactcagccc 180  
agtgtggccc agaagaactg gtacatcagc aagaacccca aggacaagag gcatgtctgg 240  
ttcggcgaga gcatgaccga tggattccag ttcgagtatg gcggccaggg ctccgaccct 300  
gccgatgtgg acctgcccgg gcggccgctc ga 332

<210> 167  
<211> 332  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 77, 109, 136, 184, 198  
<223> n = A,T,C or G

<400> 167  
tcgagcggtc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60  
aactggaatc catcggnat gctctcgccg aaccagacat gcctcttgnc cttgggggttc 120  
ttgctgatgt accagntctt ctggggccaca ctgggctgag tggggtacac gcagggtctca 180  
ccantctcca tggtgcanaa gactttgatg gcatccagggt tgcagccttg gttgggggtca 240  
atccagtact ctccactctt ccagacagag tggcacatct tgaggtcacg gcagggtgcgg 300  
gcgggggttct tgacctcggt cgcgaccacg ct 332

<210> 168  
<211> 276  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 72, 84  
<223> n = A,T,C or G

<400> 168

```

tcgagcggcc gcccgggcag gtcctcctca gagcggtagc tgttcttatt gccccggcag 60
cctccataga tnaagttatt gcangagttc ctctccacgt caaagtacca gcgtgggaag 120
gatgcacggc aaggcccagt gactgcgttg gcggtgcagt attcttcata gttgaacata 180
tcgctggagt ggacttcaga atcctgcctt ctgggagcac ttgggacaga ggaatccgct 240
gcattcctgc tggtagacct cggccgcgac cacgct 276

```

&lt;210&gt; 169

&lt;211&gt; 276

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

```

agcgtggtcg cggccgaggt ccaccagcag gaatgcagcg gattcctctg tcccaagtgc 60
tcccagaagg caggattctg aagaccactc cagcgatatg ttcaactatg aagaatactg 120
caccgccaac gcagtcactg ggccttgccg tgcacccctc ccacgctggt actttgacgt 180
ggagaggaac tcctgcaata acttcaccta tggaggctgc cggggcaata agaacagcta 240
ccgctctgag gaggacctgc ccgggcggcc gctcga 276

```

&lt;210&gt; 170

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 294

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 170

```

tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgct cttgggggtc 120
ttgctgatgt accagttctt ctggggccaca ctgggctgag tggggtacac gcaggctctca 180
ccagtctcca tgttcagaa gactttgatg gcattcaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagccagaa tggcacatct tgaggtcacg gcangtgcgg 300
gcgggggtct tgacctcggc cgcgaccagc ct 332

```

&lt;210&gt; 171

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 171

```

agcgtggtcg cggccgaggt caagaaaccc cggccgcacc tgccgtgacc tcaagatgtg 60
ccactctggc tggaagagtg gagagtactg gattgacccc aaccaaggct gcaacctgga 120
tgccatcaaa gtcttctgca acatggagac tggtagagacc tgcgtgtacc ccactcagcc 180
cagtgtggcc cagaagaact ggtacatcag caagaacccc aaggacaaga ggcattgtctg 240
gctcggcgag agcatgaccg atggattcca gttcgagtat ggcggccagg gctccgaccc 300
tgccgatgtg gacctgcccg ggcggccgct cga 333

```

&lt;210&gt; 172

&lt;211&gt; 527

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 46, 125, 140, 148, 220, 229, 291, 388, 456

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 172

```

agcgtggtcg cggccgaggt cctgtcagag tggcactggt agaagntcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctgnaatgg ggcccatgan atggttgntc gagagagagc ttcttgcct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgn gggcggtgng gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caacactggg ttgctgacca naagtgccag 300
gaagctgaat accatttcca gtgtcatacc cagggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctgntc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctgtct ttttccttcc aatcangggc tcgctcttct gaattattctt 480
cagggcaatg acataaattg tatattcggg tcccgggtcc aggccag 527

```

&lt;210&gt; 173

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 444, 453, 517, 540, 546, 551, 573, 593

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 173

```

tcgagcgggc gcccgggcag gtccaccaca cccaattcct tgctggtatc atggcagccg 60
ccacgtgcc a gattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtc ctcgccccc cctggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240
attggaagga aaaagacaga cgagcttccc caactggtta cccttccaca cccaatctt 300
catggaccag agatcttgga tgttccttcc acagttcaaa agacccttt cgtcaccac 360
cctgggtatg acactggaaa tggattcag cttcctggca cttctggtca gcaaccagt 420
gttgggcaac aaatgatctt tgangaacat ggnnttaggc ggaccacacc ggccacaacc 480
ggcaccacca taaggcatag gccaaagaac taccgncga atgtaggaca agaagctctn 540
tctcanacaa ncatctcatg ggccccattc cangacactt ctgagtacat canttcatgg 600
catcctggtg gcactgataa aaacccttac agtta 635

```

&lt;210&gt; 174

&lt;211&gt; 572

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 457, 511, 520, 552, 568

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 174

```

agcgtggtcg cggcgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgcct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgt gggcggtgtg gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caacactggg ttgctgacca gaagtgccag 300
gaagctgaat accatttcca gtgtcatacc cagggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctggtc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctgtct ttttccttcc caatcanggg ctgctcttcc tgattattctt 480
tcagggcaat gacataaatt gtatattcgg ntcccgggtg cagccaataa taataaccct 540
ctgtgacacc anggcggggc cgaagganct ct 572

```

&lt;210&gt; 175

<211> 372  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 247  
<223> n = A,T,C or G

<400> 175  
agcgtggtcg cggccgaggt cctcaccaga ggtaccacct acaacatcat agtggaggca 60  
ctgaaagacc agcagaggca taaggttcgg gaagaggttg ttaccgtggg caactctgtc 120  
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180  
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240  
tgcttangct ttggaagtgg tcatttcaga tgtgattcat ctagatggtg ccatgacaat 300  
ggtgtgaact acaagattgg agagaagtgg gaccgtcagg gagaaaatgg acctgcccgg 360  
gcggccgctc ga 372

<210> 176  
<211> 372  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 251  
<223> n = A,T,C or G

<400> 176  
tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60  
gtagttcaca ccattgtcat gccaccatct agatgaatca catctgaaat gaccacttcc 120  
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcggt cccactcatc 180  
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatccg taggttggtt 240  
caagccttcg ntgacagagt tgcccacggt aacaacctct tcccgaacct tatgcctctg 300  
ctgggtctttc agtgcctcca ctatgatgtt gtaggtggta cctctggtga ggacctcggc 360  
cgcgaccacg ct 372

<210> 177  
<211> 269  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 94, 225  
<223> n = A,T,C or G

<400> 177  
agcgtggccg cggccgaggt ccattggctg gaacggcatc aacttggag ccagtgatcg 60  
tctcagcctt ggttctccag ctaatggtga tggnggtctc agtagcatct gtcacacgag 120  
cccttcttgg tgggctgaca ttctccagag tggtgacaac accctgagct ggtctgcttg 180  
tcaaagtgtc ctttaagagca tagacactca cttcatattt ggcnccacc ataagtcctg 240  
atacaaccac ggaatgacct gtcaggaac 269

<210> 178  
<211> 529  
<212> DNA  
<213> Homo sapiens

```

<400> 178
tcgagcggcc gcccgggcag gtcctcagac cgggttctga gtacacagtc agtgtggttg 60
ccttgcacga tgatatggag agccagcccc tgattggaac ccagtccaca gctattcctg 120
caccaactga cctgaagttc actcaggtca caccacaag cctgagcgcc cagtggacac 180
cacccaatgt tcagctcact ggatatcgag tgcgggtgac cccaaggag aagaccggac 240
caatgaaaga aatcaacctt gtcctgaca gtcctccgt ggttgatca ggacttatgg 300
cggccaccaa atatgaagtg agtgtctatg ctcttaagga cactttgaca agcagaccag 360
ctcaggtgtg tgcaccact ctggagaatg tcagcccacc aagaagggt cgtgtgacag 420
atgctactga gaccaccatc accattagct ggagaaccaa gactgagacg atcactggct 480
tccaagttga tgccgttcca gccaatggac ctgcggccgc accacgctt 529

```

```

<210> 179
<211> 454
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 64
<223> n = A,T,C or G

```

```

<400> 179
agcgtggtcg cggccgaggt ctggccgaac tgccagtgtg cagggaagat gtacatgtta 60
tagntcttct cgaagtcccg ggccagcagc tccacgggtt ggtctcctgc ctccaggcgc 120
ttctcattct catggatctt cttcaccgcg agcttctgct tctcagtcag aagggtgttg 180
tcctcatccc tctcatacag ggtgaccagg acgttcttga gccagtcccg catgctcagg 240
gggaattcgg tcagctcaga gtccaggcaa ggggggatgt atttgcaagg cccgatgtag 300
tccaagtgga gcttggtggc cttcttgggt cctccaagg tgcactttgt ggcaaagaag 360
tggcaggaag agtcgaaggt cttgttgtca ttgctgcaca cttctcaaa ctgcctaag 420
ggggtgggc agacctgcc gggcgccgc tcga 454

```

```

<210> 180
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 55, 299, 317, 332, 342, 348
<223> n = A,T,C or G

```

```

<400> 180
tcgagcggcc gcccgggcag gtctgcccag ccccatgttg cgagtttgag aaggngtgca 60
gcaatgacaa caagaccttc gactcttctt gccacttctt tgccacaaag tgcaccctgg 120
agggcaccaa gaagggccac aagctccacc tggactacat cgggccttgc aaatacatcc 180
ccccttgctt ggactctgag ctgaccgaat tccccctgcg catgcgggac tggctcaaga 240
acgtcctggt caccctgtat gagagggatg aggacaacaa cttctgact gagaagcana 300
agctgctggg gaagaanatc catgagaatg anaagcgct gnaggcanga gaccaccccg 360
tggagctgct ggcccgggac ttcgagaaga actataacat gtacatcttc cctgtacact 420
ggcagttcgg ccagacctcg gccgcgacca cgct 454

```

```

<210> 181
<211> 102
<212> DNA
<213> Homo sapiens

```

```

<220>

```

<221> misc feature  
 <222> 8, 47, 60, 67  
 <223> n = A,T,C or G

<400> 181  
 agcgtgnttg cggacgacgc ccacaaagcc attgtatgta gttttanttc agctgcaaan 60  
 aataccncca gcatccacct tactaaccag catatgcaga ca 102

<210> 182  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc feature  
 <222> 169, 195, 253, 314  
 <223> n = A,T,C or G

<400> 182  
 tcgagcggtc gcccgggcag gtctgggcgg atagcaccgg gcatattttg gaatggatga 60  
 ggtctggcac cctgagcagc ccagcgagga cttggtctta gttgagcaat ttggctagga 120  
 ggatagtatg cagcacgggt ctgagtctgt gggatagctg ccatgaagna acctgaagga 180  
 ggcgctggct ggtanggggt gattacaggg ctgggaacag ctctacact tgccattctc 240  
 tgcataatact ggntagttag gcgagcctgg cgctcttctt tgcgctgagc taaagctaca 300  
 tacaatggct ttgnggacct cggccgcgac cagcgtt 337

<210> 183  
 <211> 374  
 <212> DNA  
 <213> Homo sapiens

<400> 183  
 tcgagcggcc gcccgggcag gtccattttc tcctgacgg tcccacttct ctccaatctt 60  
 gtagttcaca ccattgtcat gacaccatct agatgaatca catctgaaat gaccacttcc 120  
 aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt occactcatc 180  
 tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240  
 caagccttcg ttgacagaag ttgccacgg taacaacctc ttcccgaacc ttatgcctct 300  
 gctggtcttt caagtgcctc cactatgatg ttgtagggtg cacctctggt gaggacctcg 360  
 gccgcgacca cgct 374

<210> 184  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc feature  
 <222> 30, 174, 248, 285, 306, 332, 345, 368  
 <223> n = A,T,C or G

<400> 184  
 agcgtgggtt gcggccgagg tcctcaccan aggtgccacc tacaacatca tagtgagggc 60  
 actgaaagac cagcagaggc ataaggttcg ggaagagggt gttaccgtgg gcaactctgt 120  
 caacgaaggc ttgaaccaac ctacggatga ctctgtcttt gacccttaca cagnttccca 180  
 ttatgccgtt ggagatgagt gggaacgaat gtctgaatca ggctttaaac tggttggtcca 240  
 gtgcttange tttggaagtg gtcatttcag atgtgattca tctanatggt gtcattgaaa 300  
 tgggtngaac tacaagattg gagagaagtg gnaccgtcag ggganaaaat ggacctgccc 360  
 gggcggcncg ctca 375

<210> 185  
 <211> 148  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 28, 36, 86  
 <223> n = A,T,C or G

<400> 185  
 agcgtggtcg cggccgaggt ctggcttctc gctcangtga ttatcctgaa ccatccaggc 60  
 caaataagcg ccggctatgc ccctgnattg gattgccaca cggctcacat tgcattgcaag 120  
 ttgctgagc tgaaggaaaa gattgac 148

<210> 186  
 <211> 397  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 78  
 <223> n = A,T,C or G

<400> 186  
 tcgagcggcc gcccgggcag gtccaattga aacaaacagt tctgagaccg ttcttccacc 60  
 actgattaag agtggggngg cgggtattag ggataatatt catttagcct tctgagcttt 120  
 ctgggcagac ttggtgacct tgccagctcc agcagccttc tgggtccactg ctttgatgac 180  
 acccaccgca actgtctgtc tcatacacg aacagcaaag cgacccaaag gtggatagtc 240  
 tgagaagctc tcaacacaca tgggcttgcc aggaaccata tcaacaatgg gcagcatcac 300  
 cagacttcaa gaatttaagg gccatcttcc agctttttac cagaacggcg atcaatcttt 360  
 tccttcagct cagcaactt gcatgcaatg tgagccg 397

<210> 187  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 145, 286, 363, 365, 425, 433, 452, 462, 471, 512, 514, 534,  
 536, 540, 565, 583  
 <223> n = A,T,C or G

<400> 187  
 tcgagcggcc gcccgggcag gtccagaggg ctgtgctgaa gtttgctgct gccactggag 60  
 ccactccaat tgctggccgc ttactcctg gaaccttcac taaccagatc caggcagcct 120  
 tccgggagcc acggcttctt gtggtactg accccagggc tgaccaccag cctctcacgg 180  
 aggcattcta tgtaacctta cctaccattg cgctgtgtaa cacagattct cctctgcgct 240  
 atgtggacat tgccatccca tgcaacaaca agggagctca ctcagngggg tttgatgtgg 300  
 tggatgctgg ctcggaagt tctgctgcatg cgtggcacca tttcccgta acacccatgg 360  
 gangncatgc ctgatctgga cttctacaga gatcctgaag agattgaaaa agaagaacag 420  
 gctgnttgct ganaaagcaa gtgaccaagg angaaatttc angggtgaaa nggactgctc 480  
 ccgctcctga attcactgct actcaacctg angntgcaga ctggtcttga aggnagnacan 540  
 gggccctctg ggcctattta agcancttcg gtcgcgaaca cgnt 584



<210> 188  
<211> 579  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 7, 136, 486  
<223> n = A,T,C or G

<400> 188  
agcgtgngtc gcggccgagg tgctgaatag gcacagaggg cacctgtaca ccttcagacc 60  
agtctgcaac ctcaggctga gtagcagtga actcaggagc gggagcagtc cattcaccct 120  
gaaattcctc cttgncact gccttctcag cagcagcctg ctcttctttt tcaatctctt 180  
caggatctct gtagaagtac agatcaggca tgacctcca tgggtgttca cgggaaatgg 240  
tgccacgcat gcgcagaact tcccagcca gcattccacca catcaaacc actgagttag 300  
ctcccttggt gttgcatggg atgggcaatg tccacatagc gcagaggaga atctgtgtta 360  
cacagcgcaa tggtaggtag gttaacataa gatgcctccg cgagaagctg gtggtcagcc 420  
ctggggtcaa gtaaccacaa gaagccgtgg ctcccgaag gctgcctgga tctggttagt 480  
gaaggntcca ggagtgaagc ggccaacaat tggagtggct tcagtggcaa gcagcaaaact 540  
tcagcacaag ccctctggac ctgcccggcg gccgtcga 579

<210> 189  
<211> 374  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 41, 280, 314, 330, 350, 353  
<223> n = A,T,C or G

<400> 189  
tcgagcggcc gcccgggcag gtccattttc tccctgacgg ncccacttct ctccaatctt 60  
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120  
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcacc 180  
tccaaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatccg taggttggtt 240  
caagccttcg ttgacagagt tgcccacggt aacaacctcn tcccgaacc ttatgcctct 300  
gctgggcttt cagngcctcc actatgatgn tgtagggggg cacctctggn gangacctcg 360  
gccgcgacca cgct 374

<210> 190  
<211> 373  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 247, 304, 306, 332, 337  
<223> n = A,T,C or G

<400> 190  
agcgtgggtcg cggccgaggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60  
ctgaaagacc agcagaggca taaggctcgg gaagaggttg ttaccgtggg caactctgtc 120  
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg accctacac agtttcccat 180  
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240  
tgcttangct ttggaagtgg gtcatttcag atgtgattca tctagatggt gccatgacaa 300  
tggngngaac tacaagattg gagagaagtg gnaccgncag ggagaaaatg gacctgcccg 360

ggcggccgct cga

373

&lt;210&gt; 191

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 218, 299, 306, 326, 333, 337, 341

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 191

```

agcgtggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctctgtcct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggntg caaccttggt tggggtaaat 240
ccagtactct ccactcttcc agccagagtg gcacatcttg aggtcacggc aggtgcggnc 300
gggggntttt gcgggtgccc tctggncttc ggntgtntct natctgctgg ctca 354

```

&lt;210&gt; 192

&lt;211&gt; 587

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 276

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 192

```

tcgagcggcc gcccgggcag gtctcgcggt cgcactggtg atgctgggtcc tgttgggtccc 60
cccggccctc ctggacctcc tggcccccct ggtcctccca gcgctgggtt cgacttcagc 120
ttctgcccc agccacctca agagaaggct cagcatggtg gccgctacta cggggctgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagcctgagc 240
cagcagatcg agaacatccg gagcccgagag ggcagncgca agaaccgcc cgcacctgc 300
cgtgacctca agatgtgcca ctctgactgg aagagtggag agtactggat tgacccaac 360
caagctgcaa cctggatgcc atcaaaagtct tctgcaacat ggagactggt gagacctgac 420
tgtaccccaac tcagcccagt gtggcccaaa agaactggta catcagcaag aacccaagg 480
acaagaagca tgtctgggtc ggcgagaaca tgaccgatgg attccagttc gagtatggcg 540
ggcagggtc cgacctgcc gatggggacc ttggccgcga acacgct 587

```

&lt;210&gt; 193

&lt;211&gt; 98

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 8, 9, 33, 58, 71, 90

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 193

```

agcgtggng cggccgaggt ataaatatcc agnccatata ctccctccac acgctganag 60
atgaagctgt ncaaagatct cagggtggan aaaacat 98

```

&lt;210&gt; 194

&lt;211&gt; 240

<212> DNA

<213> Homo sapiens

<400> 194

```
tcgagcgggc gcccgggcag gtccttcaga cttggactgt gtcacactgc caggcttcca 60
gggtccaac ttgcagacgg cctgttgtgg gacagtctct gtaatcgcca aagcaaccat 120
ggaagacctg ggggaaaaca ccatggtttt atccaccctg agatctttga acaacttcat 180
ctctcagcgt gcggaggagg gctctggact ggatatttct acctcggccg cgaccacgct 240
```

<210> 195

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 22, 37, 39, 105, 268, 276, 302, 323, 331, 335, 347, 351, 371, 378

<223> n = A,T,C or G

<400> 195

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cgagcgggag accgggcagg tncagactcc aatccanana accatcaagc cagatgtcag 60
aagtacacc atcacagggt tacaaccagg cactgactac aaganctacc tgcacacctt 120
gaatgacaat gtcggagct cccctgtggt catcgacgcc tccactgcca ttgatgcacc 180
atccaacctg cgtttcctgg ccaccacacc caattccttg ctgggtatcat ggcagccgcc 240
acgtgccagg attaccggta catcatcnag tatganaagc ctgggcctcc tcccagagaa 300
gnggtccctc ggccccgccc tgntgtccca naggntacta ttactgngcc ngcaaccggc 360
aaccgatatc nattttgnca ttggccttca acaataatta 400
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<210> 196

<211> 494

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 19, 83, 168, 252, 271, 292, 430

<223> n = A,T,C or G

<400> 196

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aactgtaagg gttcttcac agngccaaca ggatgacatg aaatgatgta ctcagaagtg 120
tcctggaatg gggcccatga gatgggtgtc tgagagagag cttcttgncc tgtctttttc 180
cttccaatca ggggctcgct cttctgatta ttcttcaggg caatgacata aattgtatat 240
tcgggtcccg gntccaggcc agtaatagta ncctctgtga caccagggcg gngccgaggg 300
accacttctc tgggaggaga cccaggcttc tcatacttga tgatgtaacc ggtaatcctg 360
gcacgtggcg gctgccatga taccagcaag gaattggggg gtgggtggcca ggaaacgcag 420
gttggatggn gcatcaatgg cagtggaggc cgtcgatgac cacaggggga gctccgacat 480
tgtcattcaa ggtg 494
```

<210> 197

<211> 118

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 8, 71, 96

<223> n = A,T,C or G

<400> 197

agcgtggnccg cggccgaggt gcagcgcggg ctgtgccacc ttctgctctc tgcccaacga 60  
taaggagggt ncctgcccc aggagaacat taactntccc cagctcgcc tctgccgg 118

<210> 198

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 41, 53, 98, 195, 350

<223> n = A,T,C or G

<400> 198

tcgagcggcc gcccgggcag gttttttttg ctgaaagtgg ntactttatt ggntgggaaa 60  
gggagaagct gtggtcagcc caagagggaa tacagagncc cgaaaaaggg gagggcaggt 120  
gggctggaac cagacgcagg gccaggcaga aactttctct cctcactgct cagcctggtg 180  
gtggctggag ctcanaaatt gggagtgaac caggacacct tcccacagcc attgcggcgg 240  
catttcatct ggccaggaca ctggctgtcc acctggcact ggtcccagaca gaagcccag 300  
ctggggaaag ttaatgttca cctgggggca ggaaccctcc ttatcattgn gcagagagca 360  
gaaggtggca cagcccgcgc tgcacctcgg ccgcgaccac gct 403

<210> 199

<211> 167

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 92, 107

<223> n = A,T,C or G

<400> 199

tcgagcggcc gcccgggcag gtccaccata agtcctgata caaccacgga tgagctgtca 60  
ggagcaaggt tgatttcttt cattggtccg gnetttctct tgggggncac ccgcactcga 120  
tatccagtga gctgaacatt gggtaggcgc cactgggcgc tcaggct 167

<210> 200

<211> 252

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 210, 226, 227, 230, 236

<223> n = A,T,C or G

<400> 200

tcgagcgggt cgccccggca ggtccaccac acccaattcc ttgctggtat catggcagcc 60  
gccacgtgcc aggattaccg gctacatcat caagtatgag aagcctgggt ctctcccag 120  
agaagcggtc cctcgcccc gccctggtgt cacagaggct actattactg gcctggaacc 180  
gggaaccgaa tatacaattt atgtcattgn cctgaagaat aatcannaan agcgancccc 240  
tgattggaag ga 252

<210> 201  
<211> 91  
<212> DNA  
<213> Homo sapiens

<400> 201  
agcgtgggtcg cggccgaggt tgtacaagct tttttttttt tttttttttt tttttttttt 60  
tttttttttt tttttttttt tttttttttt t 91

<210> 202  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 9, 354  
<223> n = A,T,C or G

<400> 202  
tcgagcggnc gcccgggcag gtctgccaac accaagattg gccccgccg catccacaca 60  
gtccgtgtgc ggggaggtaa caagaaatac cgtgccctga ggttggacgt ggggaatttc 120  
tcctggggct cagagtgttg tactcgtaaa acaaggatca tcgatgttgt ctacaatgca 180  
tctaataacg agctggttcg taccaagacc ctggtgaaga attgcatcgt gctcatcgac 240  
agcacaccgt accgacagtg gtacgagtcc cactatgcgc tgcccctggg ccgcaagaag 300  
ggagccaagc tgactcctga ggaagaagag attttaaaaca aaaaacgatc taanaaaaaa 360  
aaaacaat 368

<210> 203  
<211> 340  
<212> DNA  
<213> Homo sapiens

<400> 203  
agcgtgggtcg cggccgaggt gaaatggtat tcagcttcct ggcacttctg gtcagcaacc 60  
cagtgttggg caacaaatga tctttgagga acatggtttt aggcggacca caccgcccac 120  
aacggccacc ccataaggc ataggccaag accatacccg ccgaatgtag gacaagaagc 180  
tctctctcag acaaccatct catgggcccc attccaggac acttctgagt acatcatttc 240  
atgtcatcct gttggcactg atgaagaacc cttacagtgc agggttcctg gaactttctac 300  
cagtgccact ctgacaggac ctgcccgggc ggccgctcga 340

<210> 204  
<211> 341  
<212> DNA  
<213> Homo sapiens

<400> 204  
tcgagcggcc gcccgggcag gtccgtgcag agtggcactg gtagaagttc caggaaccct 60  
gaactgtaag ggttcttcat cagtgccaac aggatgacat gaaatgatgt actcagaagt 120  
gtcctggaat ggggcccatg agatggttgt ctgagagaga gcttcttgtc ctacattcgg 180  
cgggtatggg cttggcctat gccttatggg ggtggccggt gtgggcggtg tgggtccgct 240  
aaaaccatgt tcctcaaaga tcatttgttg cccaacactg ggttgctgac cagaagtgcc 300  
aggaagctga ataccatttc acctcgcccg cgaccacgct a 341

<210> 205  
<211> 770  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 529, 591, 623, 626, 629, 630, 656, 702, 709, 712, 717, 743, 746, 749, 759, 762, 766

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 205

```

tcgagcggcc gcccgggcag gtctcccttc ttgcggccca ggggcagcgc atagtgggac 60
tcgtaccact gtcggtacgg tgtgctgtcg atgagcacga tgcaattctt caccagggtc 120
ttggtacgaa ccagctcggt attagatgca ttgtagacaa catcgatgat ccttgtttta 180
cgagtacaac actctgagcc ccaggagaaa ttccccacgt ccaacctcag ggcacggtat 240
ttcttgttac ctccccgcac acggactgtg tggatgcggc gggggccaag ctgactcctg 300
aggaagaaga gattttaaac aaaaaacgat ctaaaaaaat tcagaagaaa tatgatgaaa 360
ggaaaaagaa tgccaaaatc agcagtctcc tggaggagca gttccagcag ggcaagcttc 420
ttgctgcat cgcttcaagg ccgggacagt gtgaccgagc agatggctat gtgctagagg 480
gcaagaagat ggagttctat cttaaagaaa tcaggggcca gaatggtgng tcttcaacta 540
atccaaaggg gagtttcaga ccagtgcaat cagcaaaaac attgatactg ntggccaaat 600
ttattggtgc agggcttgca cantangann ggctgggtct tggggcttgg attggnacaa 660
gctttggcag ctttttcttt ggttttgcca aaaacctttt gntgaagang anacctnggg 720
cggaccctt aaccgattcc acnccnggng gcgttctang gncccncttg 770

```

&lt;210&gt; 206

&lt;211&gt; 810

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 574, 621, 625, 636, 668, 673, 704, 728, 743, 767, 772, 786, 789, 807, 809, 810

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 206

```

agcgtggtcg cggccgaggt ctgctgcttc agcgaagggt ttctggcata accaatgata 60
aggctgccaa agactgttcc aataccagca ccagaaccag ccactcctac tggtgcagca 120
cctgcaccaa taaatttggc agcagtatca atgtctctgc tgattgcact ggtctgaaac 180
tccctttgga ttagctgaga cacaccattc tgggccctga ttttcctaag atagaactcc 240
aactctttgc cctctagcac atagccatct gctcggtcac actgtcccgg ccttgaagcg 300
atgcacgcaa gaagcttgcc ctgctggaac tgctcctcca ggagactgct gatttttgca 360
ttctttttcc tttcatcata tttcttctga attttttag atcgtttttt gtttaaaatc 420
tcttcttctc caggagtcag cttggccccc gccgcatcca cacagtccgt gtgcggggag 480
gtaacaagaa ataccgtgcc ctgaggttgg acgtggggaa tttctcctgg ggctcagagt 540
ggtgtactcg taaaacaagg atcatcgatg gtgnetacaa tgcatactaat aacgagctgg 600
gtcggacca aagaacctgg ngaanaaatg gatcgnetca tcgacaggac accgtaccgg 660
acaggggnac gantccact atgcgcttgc ccctggggcg caanaaagga aaactgcccg 720
ggcggccntc gaaagcccaa ttntggaaaa aatccatcac actggngngc cngtcgagca 780
tgcatntana ggggcccatt cccctnann

```

&lt;210&gt; 207

&lt;211&gt; 257

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

tcgagcggcc gcccgggcag gtccccaacc aaggctgcaa cctggatgcc atcaaagtct 60
tctgcaacat ggagactggg gagacctgcg tgtacccac tcagcccagt gtggcccaga 120
agaactggtg catcagcaag aaccccaagg acaagaggca tgtctggttc ggcgagagca 180

```

tgaccgatgg attccagttc gaggatggcg gccagggctc cgaccctgcc gatgtggacc 240  
tcggccgcga ccacgct 257

<210> 208  
<211> 257  
<212> DNA  
<213> Homo sapiens

<400> 208  
agcgtgggtc cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60  
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120  
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180  
agtctccatg ttgcagaaga ctttgatggc atccaggttg cagccttggg tggggacctg 240  
cccgggcggc cgctcga 257

<210> 209  
<211> 747  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 453, 538, 540, 542, 546, 554, 556, 598, 659, 670, 679, 689,  
693, 711, 723, 724, 731, 747  
<223> n = A,T,C or G

<400> 209  
tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctgggtatc atggcagccg 60  
ccacgtgcca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120  
gaagtgggtc ctcggccccc ccctgggtgc acagaggcta ctattactgg cctggaaccg 180  
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240  
attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300  
catggaccag agatcttggg tgttccttcc acagttcaaa agaccctttt cgtcaccac 360  
cctgggtatg aacttggaaa tggattcag ctctctggca cttctggtca gcaaccacg 420  
gttgggcaac aatgatctt tgaggacat ggntttaggc ggaccacacc gccacaacg 480  
gccaccccc taaggcatag gccaaagacca taccgcccga atgtaggaca agaagctntn 540  
tntcanacac catnntatgg gcccattcc aggacacttc tgagtacatc atttatgnca 600  
tctgtggcac ttgatgaaaa cccttacagt tcagggttct ggaactttta ccaggcctnt 660  
tacaggactn ggccggacnc cttaagccna ttncaccctg gggcggttcta nggtcccact 720  
cgnnactgg ngaaaatggc tactgtn 747

<210> 210  
<211> 872  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 165, 174, 181, 256, 260, 269, 271, 277, 286, 289, 294, 298,  
300, 301, 303, 308, 311, 321, 325, 328, 329, 333, 338, 342,  
346, 349, 351, 357, 359, 364, 366, 379, 385, 395, 396, 397,  
407, 408, 410, 414, 415, 429, 431, 434, 435, 440, 443  
<223> n = A,T,C or G

<221> misc\_feature  
<222> 444, 446, 447, 448, 449, 450, 451, 464, 470, 472, 475, 479,  
483, 484, 485, 488, 494, 496, 497, 504, 508, 509, 511, 513,  
517, 522, 524, 526, 532, 533, 542, 543, 553, 559, 566, 567,

571, 572, 578, 582, 588, 591, 594, 595, 596, 600, 606

<223> n = A,T,C or G

<221> misc\_feature

<222> 612, 614, 617, 618, 629, 630, 631, 652, 654, 655, 661, 663,  
664, 666, 671, 673, 678, 679, 681, 688, 690, 691, 698, 706,  
707, 708, 714, 719, 721, 723, 726, 741, 751, 761, 762, 769,  
770, 778, 779, 781, 782, 785, 791, 802, 807, 808, 812

<223> n = A,T,C or G

<221> misc\_feature

<222> 815, 820, 827, 828, 838, 841, 844, 851, 857, 864, 866, 869,  
872

<223> n = A,T,C or G

<400> 210

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agcgtggtcg cggccgaggt ccactagagg tctgtgtgcc attgccagc cagagtctct 60
gcgttacaaa ctcctaggag ggcttgcgtg gcggagggcc tgctatggtg tgctgcggtt 120
catcatggag agtggggcca aaggctgcga ggttgtggtg tctgngaaac tccnaggaca 180
ngagggctaa attccatgaa gtttgtggat ggctgatga tccacaatcg gagaccctgt 240
taactactac cgtctnaccn cctgctgtnc nccccnttt ctgetnaana catngggntn 300
ntncttgnc ntccttgggt ngaanatnna atngcctncc cnttctanc nctactngnt 360
ccananttgg cctttaaana atcnccttg ccttnnncac tgttcanntn tttntcgt 420
aaccctatna ntttnattan atnntnnnn nctcaccgcc ctctcattn anccnatang 480
ctnnnaantc cttannncct cccnccnnt ncnctcntac tnantncttc tnnccatta 540
cnnagctctt tcntttaana taatgnngcc nngctctnca tntctacnat ntgnnaatn 600
ccccncccc cnancgnntt ttgacctnn naacctcctt tctcttccc tncnnaaatt 660
ncnnanttcc ncnttcnnc ntttcggntn ntcccatnct ttccannnct tcantctanc 720
ncnctncaac ttattttcct ntcacccctt nttctttaca nccccctnn tctactcnc 780
nnttncatta natttgaac tncacnnc anttnccn ctctacnntt ttattttncg 840
ntcnctctac ntaatanttt aatnanttnt cn 872
```

<210> 211

<211> 517

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 462, 464, 506

<223> n = A,T,C or G

<400> 211

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tcgagcggcc gcccgggcag gtctgccaa gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggctctg gcttcccacc cttctgttct gagatggggg tgggtggcag 120
tatctcatct ttgggttcca caatgctcac gtggtcaggc aggggcttct tagggccaat 180
cttaccagtt ggggtcccagg gcagcatgat cttcaccttg atgccagca caccctgtct 240
gagcaacacg tggcgacaa gcagtgtcaa cgtagtaagt taacagggtc tccgctgtgg 300
atcatcaggc catccacaaa cttcatggat ttagccctct gtctcggag tttcccagac 360
accacaacct cgcagccttt ggccccactc tccatgatga accgcagcac accatagcag 420
gccctccgca caagcaagcc ctctaaagaa tttgtaacgc ananactctg ctggcaatgg 480
cacacaaacc tctagtggac ctcgngcgcg accacgc 517
```

<210> 212

<211> 695

<212> DNA

<213> Homo sapiens



&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 432, 476, 522, 547, 621, 624, 647, 679

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 212

```

tcgagcggcc gcccgggcag gtctgggtcca ggatagcctg cgagtcctcc tactgctact 60
ccagacttga catcatatga atcatactgg ggagaatagt tctgaggacc agtagggcat 120
gattcacaga ttccaggggg gccaggagaa ccaggggacc ctgggtgtcc tggaatacca 180
gggtcaccat ttctcccagg aataccagga gggcctggat ctcccttggg gccttgaggt 240
ccttgaccat taggagggcg agtaggagca gttggaggct gtgggcaaac tgcacaacat 300
tctccaaatg gaatttctgg gttggggcag tctaattctt gatccgtcac atattatgtc 360
atcgacagaga acggatcctg agtcacagac acatatttgg catgggttctg gcttccagac 420
atctctatcc gncataggac tgaccaagat gggaacatcc tccttcaaca agcttnctgt 480
tgtgccaaaa ataatagtgg gatgaagcag accgagaagt anccagctcc cctttttgca 540
caaagcntca tcatgtctaa atatcagaca tgagacttct ttgggcaaaa aaggagaaaa 600
agaaaaagca gttcaaagta nccnccatca agttgggtcc ttgcccnttc agcaccggg 660
ccccgttata aaacacctng ggccggaccc ccctt 695

```

&lt;210&gt; 213

&lt;211&gt; 804

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 552, 555, 592, 624, 629, 633, 658, 695, 697, 698, 700, 702, 745, 753, 755, 762, 773, 786, 788, 793, 795

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 213

```

agcgtgggtcg cggccgaggt gttttatgac gggcccgggtg ctgaagggca gggaacaact 60
tgatgggtgct actttgaact gcttttcttt tctccttttt gcacaaagag tctcatgtct 120
gatatttaga catgatgagc tttgtgcaaa aggggagctg gctacttctc gctctgcttc 180
atcccaactat tattttggca caacaggaag ctggtgaagg aggatgttcc catcttggtc 240
agtcctatgc ggatagagat gtctggaagc cagaacctatg ccaaatatgt gtctgtgact 300
caggatccgt tctctgcgat gacataatat gtgacgatca agaattagac tgccccaacc 360
cagaaattcc atttgagaa tggtgtgcag tttgccaca gcctccaact gctcctactc 420
gccctcctaa tggtaagga cctcaaggcc ccaagggaga tccaggccct cctggtatte 480
ctgggagaaa tggtgaccct ggtattccag gacaaccagg gtccctgggt tctcctggcc 540
cccctggaat cngngaatc atgccctact ggtcctcaaa ctattctccc anatgattca 600
tatgatgtca agtctgggat agcnagtang ganggactcg caggctattc tggaccanac 660
ctgccggggg ggcgttcgaa agcccgaatc tgcananntn cnttcacact ggccggcgtc 720
gagctgcttt aaaagggccca ttcnccttt agnngngggg antacaatta ctnggcggcg 780
ttttanancg cngnctggg aaat 804

```

&lt;210&gt; 214

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 452, 509, 585

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 214

```

agcgtgggtcg cggccgaggt ccacatcggc agggctcgag ccctggccgc cataactcgaa 60

```

```

ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgcct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtaacacg aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggttg cagccttggt tgggggtcaat 240
ccagtactct ccactcttcc agtcagagtg gcacatcttg aggtcacggc aggtgcgggc 300
gggggttcttg cggtgccct ctgggtccg gatgttctcg atctgctggc tcaggctctt 360
gagggtggtg tccacctoga ggtcacggc acgaaccaca ttggcatcat cagcccggta 420
gtagcgcca ccatcgtgag ccttctcttg angtggctgg ggcaggaaact gaagtcgaaa 480
ccagcgctgg gaggaccagg gggaccaana ggtccaggaa gggcccggg gggaccaaca 540
ggaccagcat caccaagtgc gaccgcgag aacctgcccg gccgnccgct cgaa 594

```

<210> 215

<211> 590

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 8, 9

<223> n = A,T,C or G

<400> 215

```

tcgagcggnnc gcccgggcag gtctcgcggt cgcactggtg atgctggtcc tgttgggtccc 60
cccgccctc ctggacctcc tggteccct ggtcctccca gcgtggttt cgacttcage 120
ttctgcccc agccacctca agagaaggct cagcatggtg gccgtacta ccgggtgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagcctgagc 240
cagcagatcg agaacatccg gagcccagag ggcagccgca agaaccgcc ccgcacctgc 300
cgtgacctca agatgtgcc ctctgactgg aagagtggag agtactggat tgaccccaac 360
caaggctgca acctggatgc catcaaagtc ttctgcaaca tggagactgg tgagacctgc 420
gtgtaccca ctcagcccag tgtggcccag aagaactggt acatcagcaa gaacccaag 480
gacaagaggc atgtctggtt cggcgagagc atgaccgatg gattccagtt cgagtatggc 540
ggccagggt cccacctgc cgatgtggac ctccggccgc gaccacctt 590

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<210> 216

<211> 801

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 2, 22, 25, 26, 328, 373, 385, 440, 473, 534, 571, 572, 573, 582, 587, 589, 593, 600, 605, 617, 633, 642, 653, 672, 681, 685, 696, 699, 709, 715, 717, 726, 731, 739, 742, 745, 758, 769, 772, 778, 780, 788, 789, 791, 793, 796

<223> n = A,T,C or G

<400> 216

```

tngagcggcc gcccgggcag gntgnnaacg ctggctctgc tggctctcct ggcaaggctg 60
gtgaagatgg tcacctgga aaaccggac gacctggtga gagaggagt gttggaccac 120
aggggtctcg tggttccct ggaactcctg gacttcctgg cttcaaaggc attaggggac 180
acaatggtct ggatggattg aagggacagc ccggtgctcc tgggtgtaag ggtgaacctg 240
gtgcccctgg tgaaaatgga actccaggtc aaacaggagc ccgtgggctt cctggtgaga 300
gaggaccgtg ttggtgcccc tggccanac ctcgccgcg accacgctaa gccgaattt 360
ccagcacact gnggcccgtt actantggat ccgagctcgg taccaagctt ggcgtaatca 420
tggatcatagc tgttctctgn gtgaaattgt tatccgctca caatttcaca cancatacga 480
agccggaaag cataaagtgt aaagccttg ggtgctaag agtgagctaa ctncattaa 540
attgcgttgc gctcactgcc cgctttcca nnngggaaac cntggcntng cngcttgn 600
ttaantgaaa tccgcnacc cccgggaaa agncggttt cngtattggg gcnccttttc 660
ccttctctcg gnttacttga nttantgggc tttgncgnt tcgggttng gcgancnggt 720

```

tcaacntcac nccaaaggng gnaanacggt tttcccanaa tccgggggnt ancccaangn 780  
 aaaacatnng ncnaangggc t 801

<210> 217  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 10, 157, 170  
 <223> n = A,T,C or G

<400> 217  
 agcgtgggtn gcggccgagg tctgggccag gggcaccaac acgtcctctc tcaccaggaa 60  
 gccacagggc tctgtttga cctggagttc cattttcacc aggggcacca ggttcaccct 120  
 tcacaccagg agcaccgggc tgtcccttca atccatncag accattgtgn ccctaatagc 180  
 ctttgaagcc aggaagtcca ggagttccag ggaaaccacc gagcaccctg tggccaaca 240  
 actcctctct caccagggtcg tccgggtttt ccagggtgac catcttcacc agccttgcca 300  
 ggaggaccag caggaccagc gttaccaacc tgcccgggcg gccgctcga 349

<210> 218  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

<400> 218  
 tcgagcggcc gccggggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60  
 gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120  
 aaagcctaag cactggcaca acagttaaaa gcctgattca gacattcgtt cccactcacc 180  
 tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatccg taggttggtt 240  
 caagccttcg ttgacagagt tgcccacggg aacaacctct tcccgaacct tatgcctctg 300  
 ctggtctttc agtgcctcca ctatgatgtt gtaggtggca cctctggtga ggacctcgcc 360  
 cgcgaccacg ct 372

<210> 219  
 <211> 374  
 <212> DNA  
 <213> Homo sapiens

<400> 219  
 agcgtgggtcg cggccgaggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60  
 ctgaaagacc agcagaggca taagggtcgg gaagaggttg ttaccgtggg caactctgtc 120  
 aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180  
 tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaaact gttgtgccag 240  
 tgcttaggct ttggaagtgg tcatttcaag atgtgattca tctagatggt gccatgacaa 300  
 tgggtgtgaac tacaagattg gagagaagtg ggaccgtcag ggagaaaatg gacctgccc 360  
 ggccggccgc tcga 374

<210> 220  
 <211> 828  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 8, 9, 557, 571, 587, 588, 601, 642, 643, 647, 654, 664, 681,  
 688, 698, 719, 720, 725, 734, 738, 743, 744, 757, 765, 773,

778, 780, 782, 783, 793, 798, 805, 809, 822, 827

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 220

```

tcgagcggnnc gcccgggcag gtccagtagt gccttcggga ctgggttcac cccaggtct 60
gcggcagttg tcacagcgcc agccccgctg gcctccaaag catgtgcagg agcaaattgg 120
accgagatat tccttctgcc actgttctcc tacgtggtat gtcttcccat catcgtaaca 180
cgttgcctca tgagggtcac acttgaattc tccttttccg ttcccaagac atgtgcagct 240
catttggtg gctctatagt ttggggaaaag tttgttgaaa ctgtgccact gacctttact 300
tcctccttct ctactggagc tttcgtacct tccacttctg ctgttggtta aatgggtgat 360
cttctatcaa tttcattgac agtaccact tctcccaaac atccaggga atagtattt 420
cagagcgatt aggagaacca aattatgggg cagaaataag gggcttttcc acaggttttc 480
ctttggagga agatttcagt ggtgacttta aaagaatact caacagtgc ttcattccca 540
tagcaaaaga agaaacngta aatgatggaa ngcttctgga gatgccnca ttttaaggga 600
nccagaact tcaccatcta caggacctac ttcagtttac annaagncac atantctgac 660
tcanaaagga cccaagtagc nccatggnca gcactttnag ctttccctt ggggaaaann 720
ttacnttctt aaancctngg ccnngacccc cttaagncca aattntggaa aanttcctn 780
cnnctggggg gcngtctnac atgcntttna agggcccaat tncccnt 828

```

&lt;210&gt; 221

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

```

tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagttgt 60
tctccggctg ccattgtct tccactcca cggcgatgtc gctgggatag aagcctttga 120
ccaggcaggt caggctgacc tggttcttgg tcatctctc ccgggatggg ggcagggtgt 180
acacctgtgg ttctcggggc tgccctttgg ctttgagat ggttttctcg atgggggctg 240
ggagggcttt gttggagacc ttgcacttgt actccttgcc attcagccag tcttggtgca 300
ggacggtgag gacgtgacc acacggtacg tgctgttgta ctgctcctcc cgcggctttg 360
tcttggcatt atgcacctcc acgccgtcca cgtaccagtt gaacttgacc tcagggtctt 420
cgtgggtcac gtccaccacc acgcatgtaa cctcagacct cggccgcgac cacgct 476

```

&lt;210&gt; 222

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 222

```

agcgtggctg cggccgaggt ctgaggttac atgcgtgggt gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gccgcgggag gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca 180
ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc 240
ccccatcgag aaaaccatct ccaaagccaa agggcaagcc ccgagaacca cagggtgtaca 300
ccctgcccc atccccggag gagatgacca agaaccaggt cagcctgacc tgcctggtca 360
aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca 420
actacaagac cagcctccc gtgctggact ccgacacctg cccgggcggc cgctcga 477

```

&lt;210&gt; 223

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 223

```

tcgagcggcc gcccgggcag gttgaatggc tctcgtgta ccaccccggt gctgggtggtg 60
ggtacagagc tccgatgggt gaaaccattg acatagagac tgtccctgtc cagggtgtag 120
gggcccagct cagtgtatgcc gtgggtcagc tggctcagct tccagtacag ccgtctctg 180

```

```
tccagtccag ggcttttggg gtcaggacga tgggtgcaga cagcatccac tctggtgget 240
gccccatcct tctcaggcct gagcaaggtc agtctgcaac cagagtacag agagctgaca 300
ctggtgttct tgaacaaggg cataagcaga ccctgaagga cacctcggcc gcgaccacgc 360
t 361
```

```
<210> 224
<211> 361
<212> DNA
<213> Homo sapiens
```

```
<400> 224
agcgtggtcg cgcccgagggt gtccttcagg gtctgcttat gcccttggtc aagaacacca 60
gtgtcagctc tctgtactct ggttgacagac tgaccttgct caggcctgag aaggatgggg 120
cagccaccag agtggatgct gtctgcaccc atcgctcctga ccccaaaagc cctggactgg 180
acagagagcg gctgtactgg aagctgagcc agctgaccca cggcatcact gagctggggc 240
cctacaccct ggacagggac agtctctatg tcaatggttt caccatcgg agctctgtac 300
ccaccaccag caccgggggtg gtcagcgagg agccattcaa cctgcccggg cgccgctcg 360
a 361
```

```
<210> 225
<211> 766
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> 574, 610, 631, 643, 657, 660, 666, 688, 712, 735, 747
<223> n = A,T,C or G
```

```
<400> 225
agcgtggtcg cgcccgagggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgcct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgt gggcggtgtg gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caacactggg ttgctgacca gaagtgccag 300
gaagctgaat accatttcca gtgtcatacc cagggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctggtc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctctgtc ttttccctc caatcagggg ctgctcttc tgattattct 480
tcagggcaat gacataaatt gtatattcgg tcccggttcc aggccagtaa tagtagcctc 540
tgtgacacca gggcgggggc gagggaccct tctnttggaa gagaccagct tctcatactt 600
gatgatgagn ccgtaatcc tggcacgtgg nggttgcatt atnccaccaa ggaaatnggn 660
ggggngggac ctgcccggcg gccgttcnaa agcccaattc cacacacttg gnggccgtac 720
tatggatccc actcngtcca acttggngga atatggcata actttt 766
```

```
<210> 226
<211> 364
<212> DNA
<213> Homo sapiens
```

```
<400> 226
tcgagcggcc gcccgggcag gtccttgacc ttttcagcaa gtgggaagggt gtaatccgtc 60
tccacagaca aggccaggac tcgtttgtac ccgttgatga tagaatgggg tactgatgca 120
acagtgggt agccaatctg cagacagaca ctggcaacat tgcggacacc ctccaggaag 180
cgagaatgca gagtttctc tgtgatatca agcacttcag ggtttagat gctgccattg 240
tcgaacacct gctggatgac cagcccaaag gagaaggggg agatgttgag catgttcagc 300
agcgtggctt cgctggctcc cactttgtct ccagtcttga tcagacctcg gccgcgacca 360
cgct 364
```

<210> 227  
<211> 275  
<212> DNA  
<213> Homo sapiens

<400> 227  
agcgtggtcg cggccgaggt ctgtcctaca gtcctcagga ctctactccc tcagcagcgt 60  
ggtgaccgtg ccctccagca acttcggcac ccagacctac acctgcaacg tagatcacia 120  
gcccagcaac accaaggttg acaagagagt tgagcccaaa tcttgtgaca aaactcacac 180  
atgcccaccg tggccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccg 240  
catccccctt ccaaacctgc ccgggcggcc gctcg 275

<210> 228  
<211> 275  
<212> DNA  
<213> Homo sapiens

<400> 228  
cgagcgggcg cccgggcagg tttggaaggg ggatgcgggg gaagaggaag actgacggtc 60  
ccccaggag ttcagggtgct gggcacgggt ggcatgtgtg agttttgtca caagatttgg 120  
gtcaactct cttgtccacc ttgggtgttg tgggcttgtg atctacgttg caggtgtagg 180  
tctgggtgcc gaagttgctg gagggcacgg tcaccacgct gctgaggagg tagagtcctg 240  
aggactgtag gacagacctc ggccgcgacc acgct 275

<210> 229  
<211> 40  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 1, 4, 5, 13, 15, 17, 29  
<223> n = A,T,C or G

<400> 229  
nggnnggtcc ggnngncag gaccactcnt cttcgaaata 40

<210> 230  
<211> 208  
<212> DNA  
<213> Homo sapiens

<400> 230  
agcgtggtcg cggccgaggt cctcacttgc ctctcgaaa gcaccgatag ctgcgctctg 60  
gaagcgaga tctgttttaa agtcctgagc aatttctcgc accagacgct ggaagggaag 120  
tttgcaatc agaagttcag tggacttctg ataacgtcta atttcacgga gcgccacagt 180  
accaggacct gcccgggcgg ccgctcga 208

<210> 231  
<211> 208  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 33  
<223> n = A,T,C or G

&lt;400&gt; 231

```
tcgagcggcc gcccgggcag gtccctggtac tgnnggcgtc cgtgaaatta gacgttatca 60
gaagtccact gaacttctga ttcgcaaact tcccttccag cgtctggtgc gagaaattgc 120
tcaggacttt aaaacagatc tgcgcttcca gagcgcagct atcggtgctt tgcaggaggc 180
aagtgaggac ctcgggccgcg accacgct 208
```

&lt;210&gt; 232

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 232

```
tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgt accagttctt ctgggccaca ctgggctgag tggggtagac gcaggtctca 180
ccagtctcca tgttcagaa gactttgatg gcatccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcaggtgcgg 300
gcgggggttct tgacctcggc cgcgaccacg ct 332
```

&lt;210&gt; 233

&lt;211&gt; 415

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; 6, 15, 19, 21

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 233

```
gtgggnttga acccnttttna nctccgcttg gtaccgagct cggatccact agtaacggcc 60
gccagtgtgc tggaattcgg cttagcgtgg tcgcggccga ggtcaagaac cccgcccga 120
cctgccgtga cctcaagatg tgccactctg actggaagag tggagagtac tggattgacc 180
ccaaccaagg ctgcaacctg gatgccatca aagtcttctg caacatggag actggtgaga 240
cctgcgtgta cccactcag cccagtgtgg ccagaagaa ctggtacatc agcaagaacc 300
ccaaggacaa gaggcatgtc tggttcggcg agagcatgac cgatggattc cagttcgagt 360
atggcggccca gggctccgac cctgccgatg tggacctgcc cgggcggccg ctgca 415
```

&lt;210&gt; 234

&lt;211&gt; 776

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; 505, 550, 574, 601, 604, 608, 612, 649, 656, 657, 680, 711, 750, 776

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 234

```
agcgtgggtcg cggccgaggt ctgggatgct cctgctgtca cagtgagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgcc tgggagcaag 120
ttacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa tttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tcccaaaaat 360
ggaccaggac caacaaaaac taaaactgca ggtccagatc aaacagaaat gactattgaa 420
ggcttgcagc ccacagtgga gtatgtggtt aagtgtctat gctcagaatc caagcggaga 480
```

```

gaagtcagcc tctggttcag actgnaagta accaacattg atcgccctaaa ggactggcat 540
tcactgatgn ggatgccgat tccatcaaaa ttgnttgga aaaccacag gggcaagttt 600
ncangtcnag gnggacctac tcgagccctg aggatggaat ccttgactnt tccttncct 660
gatggggaaa aaaaaccttn aaaacttgaa ggacctgccc gggcgccgt ncaaaaccca 720
attccacccc cttgggggcy ttctatgggn ccactcgga ccaaacttg ggtaan 776

```

&lt;210&gt; 235

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 637, 684, 705, 724, 733, 756, 778, 793, 796, 804

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 235

```

tcgagcggcc gcccgggcag gtccttcag ctctgcagt tcttcttcac catcagggtgc 60
agggaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg gcatccacat cagtgaatgc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttgattc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt tttagttttt gttggtcctg gtccattttt 360
gggagtgtg gttactctgt aaccagtaac aggggaactt gaaggcagcc acttgacact 420
aatgctgttg tctgaacat cggtcacttg catctgggat ggtttgtcaa tttctgttcg 480
gtaattaatg gaaattggct tgcgtcttgc ggggcttgc tccacggcca gtgacagcat 540
acacagtgat ggtataatca actccaggtt taagccgctg atggtagctg aaactttgct 600
ccaggcacaa gtgaactcct gacagggcta tttcctnctg ttctccgtaa gtgacactgt 660
aatatctcac tgggacagca ggangcattc caaaacttcg ggcgngaccc cctaagccga 720
attntgcaat atncatcaca ctggcgggcy ctcgancatt cattaaaagg cccaatcncc 780
cctataggga gtntantaca attng 805

```

&lt;210&gt; 236

&lt;211&gt; 262

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

```

tcgagcggcc gcccgggcag gtcacttttg gtttttggtc atgttcggtt ggtcaaagat 60
aaaaactaag tttgagagat gaatgcaaag gaaaaaata tttccaaag tccatgtgaa 120
attgtctccc attttttttg cttttgaggg ggttcagttt gggttgcttg tctgtttccg 180
ggttgggggg aaagttggtt ggggtgggag gagccaggtt gggatggagg gagtttacag 240
gaagcagaca gggccaactg cg 262

```

&lt;210&gt; 237

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 237

```

agcgtggtcg cggccgaggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60
ctgaaagacc agcagaggca taagggttcg gaagaggttg ttaccgtggg caactctgtc 120
aacgaaggt tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaaact gttgtgccag 240
tgcttaggct ttggaagtgg tcatttcaga tgtgattcat ctagatggtg ccatgacaat 300
ggtgtgaact acaagatttg agagaagtgg gaccgtcagg gagaaaatgg acctgcccgg 360
gcggccgctc ga 372

```



<210> 238  
 <211> 372  
 <212> DNA  
 <213> Homo.sapiens

<400> 238  
 tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60  
 gtagttcaca ccattgtcat ggcacatct agatgaatca catctgaaat gaccacttcc 120  
 aaagcctaag cactggcaca acagttaaa gcctgattca gacattcgtt cccactcatc 180  
 tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240  
 caagccttcg ttgacagagt tgcccacggg aacaacctct tcccgaacct tatgcctctg 300  
 ctgggtctttc agtgcctcca ctatgatgtt gtaggtggca cctctggtga ggacctcggc 360  
 cgcgaccacg ct 372

<210> 239  
 <211> 720  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 478, 557, 563, 566, 620, 660, 663, 672, 673, 684, 693, 695  
 <223> n = A,T,C or G

<400> 239  
 tcgagcggcc gcccgggcag gtccaccata agtcctgata caaccacgga tgagctgtca 60  
 ggagcaagggt tgatttcttt cattgggtccg gtcttctcct tgggggtcac ccgactcga 120  
 tatccagtga gctgaacatt ggggtgtgtc cactgggcgc tcaggcttgt ggggtgtgacc 180  
 tgagtgaact tcaggtcagt tgggtgcagga atagtgttga ctgcagtctg aaccagaggc 240  
 tgactctctc cgcttggatt ctgagcatag acactaacca catactccac tgtgggctgc 300  
 aagccttcaa tagtcatttc tgtttgatct ggacctgcag ttttagtttt tgttggctct 360  
 ggtccatttt tgggagtggg ggttactctg taaccagtaa caggggaact tgaaggcagc 420  
 cacttgacac taatgctgtt gtcctgaaca tcggtcactt gcatctggga tggtttgnca 480  
 atttctgttc ggtaattaat ggaaattggc ttgctgcttg cggggctgtc tccacggcca 540  
 gtgacagcat acacagngat ggnatnatca actccaagtt taaggccctg atggtaactt 600  
 taaacttgct cccagccagn gaactccgg acaggggtatt tcttctggtt ttccgaaagn 660  
 gancctggaa tnntctcctt ggancagaag gancntccaa aacttgggcc ggaaccctt 720

<210> 240  
 <211> 691  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 564, 582, 640, 651, 666, 669, 690  
 <223> n = A,T,C or G

<400> 240  
 agcgtggctc cggccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60  
 actgtaagggt ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120  
 cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgcctt acattcggcg 180  
 ggtatggctt tggcctatgc cttatggggg tggcgttgt gggcggtgtg gtccgcctaa 240  
 aacctgttct ctcaaaagatc atttgtggcc caacactggg ttgctgacca gaagtgccag 300  
 gaagctgaat accatttcca gtgtcatacc caggggtggg gacgaaaggg gtcttttgaa 360  
 ctgtggaagg aacatccaag atctctggc catgaagatt ggggtgtgga agggttacca 420  
 gttggggaag ctctgtctgtc ttttctctc caatcagggg ctctgtcttc tgattattct 480

```

tcagggcaat gacataaatt gtatatcgg ttcccggttc cagggcagta atagtagcct 540
cttgtgacac caggcggggc ccanggacca cttctctggg angagacca gcttctcata 600
cttgatgatg taaccgggta atcctgcacg tggcggctgn catgatacca ncaaggaatt 660
gggtgngng gacctgccc gggccctcn a 691

```

```

<210> 241
<211> 808
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 680, 715, 721, 728, 735, 749, 757, 762, 772, 776, 779, 781,
792, 796, 800, 808
<223> n = A,T,C or G

```

```

<400> 241
agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagtgagata ttacaggatc 60
acttacggag aaacaggag aaatagccct gtccaggagt tcaactgtgc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa ttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tccccaaaat 360
ggaccaggac caacaaaaac taaaactgca ggtccagatc aaacagaaat gactattgaa 420
ggcttgacgc ccacagtgga gtatgtggtt agtgtctatg ctccagaatcc aagcggagag 480
agtcagcctc tgggtcagac tgcagtaacc actattcctg caccaactga cctgaagttc 540
actcaggtca caccacaag cctgagccgc cagtggacac caccaatgt tcaactcactg 600
gatatcgagt gcgggtgacc cccaaggaga agaccggac ccatgaaaga aatcaacctt 660
gtcctgaca gtcctccgn ggggtgatca ggacttatgg gggactgcc cggcnggccg 720
ntcgaaancg aattntgaaa ttctcttenc actggnggc gnttcgagct tncctntana 780
nggcccaatt cncctntagn gggtcgtn 808

```

```

<210> 242
<211> 26
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 22
<223> n = A,T,C or G

```

```

<400> 242
agcgtggtcg cggccgaggt cnagga 26

```

```

<210> 243
<211> 697
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 496, 541, 624, 662, 679, 688
<223> n = A,T,C or G

```

```

<400> 243
tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggtatc atggcagccg 60
ccacgtgcca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120

```

```

gaagtgggtcc ctcgccccg ccctgggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagccccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttcaca cccaatctt 300
catggaccag agatcttggg tgttccttcc acagttcaaa agacccttt cgtcaccac 360
cctgggtatg acactggaaa tgggtattcag ctctcctggca cttctggtca gcaaccacgt 420
gttgggcaac aaatgatctt tgaggaacat ggttttaggc ggaccacacc gccacaacg 480
ggcaccacca taaggnatag gccaaagacca taccgcgcg aatgtaggac aagaagctct 540
ntctcaacaa ccatctcatg ggccccattc caggacactt ctgagtacat catttcatgt 600
catcctgggtg ggcacttgat gaanaaccct tacagttcag ggttcctgga acttctacca 660
gngccacttc tgacagganc ttgggcgnga ccaccct 697

```

&lt;210&gt; 244

&lt;211&gt; 373

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 244

```

agcgtgggtcg cggccgaggt ccattttctc cctgacggtc ccacttctct ccaatcttgt 60
agttcacacc attgtcatgg caccatctag atgaatcaca tctgaaatga ccacttccaa 120
agcctaagca ctggcacaa agtttaaaagc ctgattcaga cattcggtcc cactcatctc 180
caacggcata atgggaaact gtgtaggggt caaagcacga gtcacccgta ggttgggtca 240
agccttcgtt gacagagttg cccacggtaa caacctctc ccgaacctta tgccctctgt 300
ggtctttcag tgcctccact atgatgttgt aggtggcacc tctggtgagg acctgcccgg 360
gcggcccgtc cga 373

```

&lt;210&gt; 245

&lt;211&gt; 307

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 245

```

agcgtgggtcg cggccgaggt gtgccccaga ccaggaattc ggcttcgacg ttggccctgt 60
ctgcttcctg taaactccct ccatccaac ctggtccct cccaccaac caactttccc 120
cccaaccgg aaacagacaa gcaaccaaa ctgaacccc tcaaaagcca aaaaaatggg 180
agacaatttc acatggactt tggaaaatat ttttttctt tgcattcatc tctcaaactt 240
agtttttatc tttgaccaac cgaacatgac caaaaacaa aagtgacctg cccgggcggc 300
cgctcga 307

```

&lt;210&gt; 246

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 246

```

tcgagcggcc gcccgggcag gtctcacca gaggtgccac ctacaacatc atagtggagg 60
cactgaaaga ccagcagagg cataaggctc gggaagaggt tgttaccgtg ggcaactctg 120
tcaacgaagg cttgaaccaa cctacggatg actcgtgctt tgaccctac acagtttccc 180
attatgccgt tggagatgag tgggaacgaa tgtctgaatc aggcctttaa ctgttgtgcc 240
agtgcctagg ctttggaagt ggtcatttca gatgtgattc atctagatgg tgccatgaca 300
atggtgtgaa ctacaagatt ggagagaagt gggaccgtca gggagaaaat ggacctcggc 360
cgcgaccacg ct 372

```

&lt;210&gt; 247

&lt;211&gt; 348

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc\_feature  
 <222> 284, 297, 299, 322, 325, 338, 342, 345  
 <223> n = A,T,C or G

<400> 247  
 tcgagcggcc gcccgggcag gtaccggggt ggtcagcgag gagccattca cactgaactt 60  
 caccatcaac aacctgcggt atgaggagaa catgcagcac cctgggtcca ggaagttcaa 120  
 caccacggag agggctcctc agggcctgct caggtccctg ttcaagagca ccagtgttg 180  
 ccctctgtac tctggctgca gactgacttt gctcagacct gagaaacatg gggcagccac 240  
 tggagtggac gccatctgca ccctccgcct tgatccact ggtinctggac tggacanana 300  
 gcggctatac ttgggagctg anccnaacct ttggcgnga cncnctt 348

<210> 248  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 125  
 <223> n = A,T,C or G

<400> 248  
 gaggactggc tcagctccca gtatagccgc tctctgtcca gtccaggacc agtgggatca 60  
 aggcggaggg tgcagatggc gtccactcca gtggctgcc catgtttctc aagtctgagc 120  
 aaagnacagtc tgcagccaga gtacagagg ccaacactgg tgctcttgaa caggacctg 180  
 agcaggccct gaaggaccct ctccgtggtg ttgaacttcc tggagccagg gtgctgcatg 240  
 ttctcctcat accgcaggtt gttgatggtg aagttcagtg tgaatggctc ctgctgacc 300  
 accc 304

<210> 249  
 <211> 400  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 308, 310, 312, 320, 331, 336, 383, 392, 396  
 <223> n = A,T,C or G

<400> 249  
 agcgtggtcg cggccgaggt ccaccacacc caattccttg ctggtatcat ggcagccgcc 60  
 acgtgccagg attaccggct acatcatcaa gtatgagaag cctgggtctc ctcccagaga 120  
 agtggctcct cggccccgcc ctggtgtcac agaggctact attactggcc tggaaaccggg 180  
 aaccgaatat acaatttatg tcattgccct gaagaataat cagaagagcg agcccctgat 240  
 tggaaaggaaa aagacagacg agcttcccca actggttaacc ctccacacc ccaatcttca 300  
 tggaccanan ancttgatn gtcctttcac nggttnaaaa aacccttttc gccccccac 360  
 cttggggatt aaccttggga aanggggatt tnacnttcc 400

<210> 250  
 <211> 400  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 338, 357, 361, 369, 388, 394  
 <223> n = A,T,C or G

<400> 250  
tcgagcggcc gcccgggcag gtcctgtcag agtggcactg gtagaagttc caggaaccct 60  
gaactgtaag ggttcttcat cagtgccaac aggatgacat gaaatgatgt actcagaagt 120  
gtcctggaat ggggcccctat agatggttgt ctgagagaga gcttcttgtc ctacattcgg 180  
cgggtatggt cttggcctat gccttatggg ggtggccggt gtgggcggtg tgggccgcct 240  
aaaaccatgt tcctcaaaga tcatttgttg cccaacactg ggttgctgac cagaagtgcc 300  
aggaagctga ataccatttc cagtgtcata cccaggngg gtgaccaaag ggggtcnttt 360  
ngacctggng aaaggaacca tccaaaanct ctgncccatg 400

<210> 251  
<211> 514  
<212> .DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 8, 107, 312, 338, 351, 352, 357, 363, 366, 373, 380, 405,  
421, 444, 508  
<223> n = A,T,C or G

<400> 251  
agcgtggncg cggccgaggt ctgaggatgt aaactcttcc caggggaagg ctgaagtgtc 60  
gaccatggtg ctactgggtc cttctgagtc agatatgtga ctgatngaa ctgaagtagg 120  
tactgtagat ggtgaagtct ggggtgccct aaatgctgca tctccagagc cttccatcat 180  
taccgtttct tcttttgcta tgggatgaga cactgttgag tattctctaa agtcaccact 240  
gaaatcttcc tccaaaggaa aacctgtgga aaagcccctt atttctgccc cataatttgg 300  
ttctccta at cncctctgaaa tcaactatctt cctggaangt ttgggaaaaa nngggcnacc 360  
tgncantgga aantggatan aaagatccca ccattttacc caacnagcag aaagtgggaa 420  
nggtaccgaa aagctccaag taanaaaaag gagggaagta aaggtcaagt gggcaccagt 480  
ttcaaacaaa actttcccca aactatanaa ccca 514

<210> 252  
<211> 501  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 20, 21, 25, 44, 343, 347, 356, 362, 387, 391, 398, 409, 428,  
430, 453, 494  
<223> n = A,T,C or G

<400> 252  
aagcggccgc ccgggcaggn ncagnagtgc cttcgggact gggntcacc ccaggtctgc 60  
ggcagttgtc acagcgccag ccccgctggc ctccaaagca tgtgcaggag caaatggcac 120  
cgagatatc cttctgccac tgttctccta cgtggtatgt cttcccatca tcgtaacacg 180  
ttgcctcatg agggtcacac ttgaattctc ctttccggt cccaagacat gtgcagctca 240  
tttggtggc tctatagttt ggggaaagt tgttgaaact gtgccactga ctttacttc 300  
ctccttctct actggagctt tccgtacctt ccacttctgc tgntggnaaa aaggngggaa 360  
cntcttatca atttcattgg acagtanccc nctttctncc caaaacatnc aagggaat 420  
attgattncn agagcggatt aaggaacaac ccnaattatg ggggccagaa ataaagggg 480  
ctttccaca ggtnttttcc t 501

<210> 253  
<211> 226  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 253

```

tcgagcggcc gcccgggcag gtctgcaggc tattgtaagt gttctgagca catatgagat 60
aacctgggccc aagctatgat gttcgatacg ttaggtgtat taaatgcact tttgactgcc 120
atctcagtgg atgacagcct tctcactgac agcagagatc ttctcactg tgccagtggg 180
caggagaaaag agcatgctgc gactggacct cggccgcgac cacgct 226

```

&lt;210&gt; 254

&lt;211&gt; 226

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 254

```

agcgtgggtcg cggccgaggt ccagtcgcag catgctcttt ctccctgcca ctggcacagt 60
gaggaagatc tctgctgtca gtgagaaggc tgtcatccac tgagatggca gtcaaaagtg 120
catttaatac acctaacgta tcgaacatca tagcttgaggc caggttatct catatgtgct 180
cagaacactt acaatagcct gcagacctgc ccgggcggcc gctcga 226

```

&lt;210&gt; 255

&lt;211&gt; 427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 327, 403

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 255

```

cgagcggccg cccgggcaggt tccagactcc aatccagaga accaccaagc cagatgtcag 60
aagctacacc atcacaggtt tacaaccagg cactgactac aagatctacc tgtacacctt 120
gaatgacaat gctcggagct cccctgtggt catcgacgcc tccactgcca ttgatgcacc 180
atccaacctg cgtttcctgg ccaccacacc caattccttg ctggtatcat ggcagccgcc 240
acgtgccagg attaccggtt acatcatcaa gtatgagaag cctgggtctc ctcccagaga 300
agtggctcct cggcccgccc ctggtgncac agaagctact attactggcc tggaaccggg 360
aaccgaatat acaatttatg tcattgcctt gaagaataat canaagagcg agcccctgat 420
tggaagg 427

```

&lt;210&gt; 256

&lt;211&gt; 535

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 347, 456, 475

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 256

```

agcgtgggtcg cggccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgcctt gtctttttcc 180
ttccaatcag gggctcgctc ttctgattat tcttcagggc aatgacataa attgtatatt 240
cggttcccgg ttccaggcca gtaatagtag cctctgtgac accagggcgg ggccgaggga 300
ccacttctct gggaggagac ccaggcttct catacttgat gatgtanccg gtaatcctgg 360
caccgtggcg gctgccatga taccagcaag gaattgggtg tgggtggcaa gaaacgcagg 420
ttggatgggtg catcaatggc agtggaggcg tcgatnacca caggggagct ccgancattg 480
tcattcaagg tggacaggta gaatcttgta atcagggtgcc tggttttaa acctg 535

```

<210> 257  
 <211> 544  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 495, 511  
 <223> n = A,T,C or G

<400> 257  
 tcgagcggcc gcccgggcag gtttcgtgac cgtgacctcg aggtggacac caccctcaag 60  
 agcctgagcc agcagatcga gaacatccgg agcccagagg gcagccgcaa gaaccccgcc 120  
 cgacactgcc gtgacctcaa gatgtgccac tctgactgga agagtggaga gtactggatt 180  
 gaccccaacc aaggctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggg 240  
 gagacctgcg tgtacccac tcagcccagt gtggcccaga agaactggta catcagcaag 300  
 aaccccaagg acaagaagca tgtctggttc ggcgaaagca tgaccgatgg attccagttc 360  
 gagtatggcg gccagggtc cgaccctgcc gatgtggacc tcggccgcga ccacgctaag 420  
 cccgaattcc agcacactgg cggccgttac tagtgggatc cgagcttcgg taccaagctt 480  
 ggcgtaatca tgggncatag ctgtttcctg ngtgaaaatg gtattccgct tcacaatttc 544  
 ccac

<210> 258  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<400> 258  
 agcgtggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60  
 ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120  
 gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180  
 agtctccatg ttgcagaaga ctttgatggc atccaggttg cagccttggt tggggtaaat 240  
 ccagtactct ccactcttcc agtcagagtg gcacatcttg aggtcacggc aggtgcgggc 300  
 ggggttcttg cggctgccct ctgggctccg gatgttctcg atctgctggc tcaagctctt 360  
 gaaggggtgt gtccacctcg aggtcacggt cgcgaaacct gcccgggcgg ccgctcga 418

<210> 259  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 320, 326, 342, 352  
 <223> n = A,T,C or G

<400> 259  
 agcgtggtcg cggccgaggt caagaacccc gcccgcacct gccgtgacct caagatgtgc 60  
 cactctgact ggaagagtgg agagtactgg attgacccca accaaggctg caacctggat 120  
 gccatcaaag tcttctgcaa catggagact ggtgagacct gcgtgtacct cactcagccc 180  
 agtgtggccc agaagaactg gtacatcagc aagaacccca aggacaagag gcatgtctgg 240  
 ttccggcgaga gcatgaccga tggattccag ttcgagtatg gcggccaggg ctccgacctt 300  
 gccgatgtgg acctgcccgn gccggncgcg tcgaaaagcc cnaatttcca gncacacttg 360  
 gccggccggt actactg 377

<210> 260  
 <211> 332

<212> DNA

<213> Homo sapiens

<400> 260

```
tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcgggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgt accagttctt ctgggccaca ctgggctgag tggggtacac gcaggtctca 180
ccagtctcca tgttgagaaa gactttgatg gcatccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcaggtgcgg 300
gcgggggttct tgacctcggc cgcgaccacg ct 332
```

<210> 261

<211> 94

<212> DNA

<213> Homo sapiens

<400> 261

```
cgagcggccg cccgggcagg tccccccct ttttttttt ttttttttt ttttttttt 60
ttttttttt ttttttttt ttttttttt tttt 94
```

<210> 262

<211> 650

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 412, 582, 612, 641, 646

<223> n = A,T,C or G

<400> 262

```
agcgtgggtcg cgcccgaggt ctggcattcc ttcgacttct ctccagccga gcttcccaga 60
acatcacata tcactgcaaa aatagcattg catacatgga tcaggccagt ggaaatgtaa 120
agaaggccct gaagctgatg gggcacaatg aagggtgaatt caaggctgaa ggaaatagca 180
aatcaccta cacagttctg gaggatgggt gcacgaaaca cactggggaa tggagcaaaa 240
cagtctttga atatcgaaca cgcaaggctg tgagactacc tattgtagat attgcaccct 300
atgacattgg tggctcctgat caagaatttg gtgtggacgt tggccctgtt tgctttttat 360
aaaccaaaact ctatctgaaa tccaacaaa aaaaatttaa ctccatagt gntcctcttg 420
ttctaattctt ggcaaccagt gcaagtgacc gacaaaattc cagttattta tttccaaaat 480
gtttggaac agtataattt gacaagaaa aaaggatact tctcttttt tggctgggtcc 540
accaaataca attcaaaagg ctttttggtt ttatttttt anccaattcc aatttcaaaa 600
tgtctcaatg gngcttataa taaaataaac tttcaccctt ntttntgat 650
```

<210> 263

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 453, 458, 544

<223> n = A,T,C or G

<400> 263

```
agcgtgggtcg cgcccgaggt ctgggatgct cctgctgtca cagtgagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcactgtgcc tgggagcaag 120
tctacagcta ccacagcggt ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa tttccattaa ttaccgaaca 240
```



```

gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagaa gtaaccacca ctcccaaaaa 360
tggaaccagga ccaacaaaaa ctaaaactgc aggtccagat caaacagaaa atggactatt 420
gaaggcttgc agcccacagt ggaagtatgt ggntaggngt ctatgctcag aatcccaagc 480
cggagaaagt cagccttctg gtttagactg cagtaaccaa cattgatcgc cctaaaggac 540
tggncattca cttggatggg ggatgtccaa ttc 573

```

```

<210> 264
<211> 550
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 39, 174, 352, 526
<223> n = A,T,C or G

```

```

<400> 264
tcgagcggcc gcccgggcag gtccttgcat ctctgcagng tcttcttcac catcaggtgc 60
agggaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagngaagtc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttgatttc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt ttttaagttt tgggtggcct gnccatttt 360
tggaagtggt ggggttactc tgtaaccagt aacaggggaa cttgaaggca gccacttgac 420
actaatgctg ttgtcctgaa catcggtcac ttgcatctgg ggatggtttt gacaatttct 480
ggttcggcaa attaatggaa attggcttgc tgcttgccgg ggctgnctcc acgggccagt 540
gacagcatac 550

```

```

<210> 265
<211> 596
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 347, 352, 353, 534, 555, 587
<223> n = A,T,C or G

```

```

<400> 265
tcgagcggcc gcccgggcag gtccttgcat ctctgcagtg tcttcttcac catcaggtgc 60
agggaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagtgaatgc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttgatttc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt ttttaagttt tgggtgncct gnnccatttt 360
tggaagtggt gtggttactc ttgtaaccag taacagggga acttgaagca gccacttgac 420
actaatgctg gtggcctgaa catcggtcac ttgcatctgg gatggtttgg tcaatttctg 480
ttcggttaatt aatgggaaat tggcttactg gcttgcgggg gctgtctcca cggncagtga 540
caagcatata caggngatgg gtataatcaa ctccaggttt aaggccnctg atggta 596

```

```

<210> 266
<211> 506
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature

```

&lt;222&gt; 393, 473

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 266

```

agcgtgggtcg cggccgaggt ctgggatgct cctgctgtca cagtgaagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agtaagccaa tttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagtg accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tcccaaaaat 360
gggaccagga ccaacaaaaa actaaaactg canggtccag atcaaacaga aatgactatt 420
gaaggcttgc agcccacagt ggagtatgtg ggtagtgtc tatgctcaga atnccaagcg 480
gagagagtca gcctctgggt cagact                                     506

```

&lt;210&gt; 267

&lt;211&gt; 548

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 346, 358, 432, 510, 512

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 267

```

tcgagcggcc gcccgggcag gtcagcgctc tcaggacgtc accaccatgg cctgggctct 60
gtcctcctc accctcctca ctcagggcac agggctcctg gccagctctg ccctgactca 120
gcctccctcc gcgtccgggt ctctgggaca gtcagtcacc atctcctgca ctggaaccag 180
cagtgcaggt ggtgcttatg aatttgtctc ctggtaccaa caacacccag gcaaggcccc 240
caaaactcatg atttctgagg tactaaagcg gccctcaggg gtccctgacg gcttctcttg 300
ctccaagtct ggcaacacgg cctccctgac cgtctctggg ctccangctg aggatganc 360
tgattattac tggaagctca tatgcaggca acaacaattg ggtgttcggc ggaagggacc 420
aagctgaccg tncctaaggte aagcccaagg cttgccccc tcggtcactc tgttcccacc 480
ctctctgaa gaagctttca agccaacaan gncacactgg gtgtgtctca taagtggact 540
ttctaccc                                     548

```

&lt;210&gt; 268

&lt;211&gt; 584

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 98, 380, 421, 454, 495, 506, 512, 561, 565, 579

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 268

```

agcgtgggtcg cggccgaggt ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc 60
tcaggtagct gctggccgag tacttggtgt tgccttgnnt ggaggggtgt gtggtctcca 120
ctcccgctt gacggggctg ctatctgcct tccaggccac tgtcacggct cccgggtaga 180
agtcaattat gagacacacc agtgtggcct tgttggttg aagctcctca gaggaggggtg 240
ggaacagagt gaccgagggg gcagccttg gctgacctag gacggtcagc ttggtccctc 300
cgccgaacac ccaattgttg ttgcctgcat atgagctgca gtaataatca gcctcctcct 360
cagcctggag ccagagacn gtcaaggag gcccgtgttt gccaaagactt ggaagccaga 420
naagcgatca gggacccctg agggccgctt tacngacctc aaaaaatcat gaatttgggg 480
ggcctttgcc tggngtttg ttggtnacca gnaaaacaaa atttcataaa gcaccaacgt 540
cactgctggt ttccagtga ngaanatggt gaactgaant gtcc                                     584

```

<210> 269  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 265, 329  
<223> n = A,T,C or G

<400> 269  
agcgtggtcg cggccgaggt ccagcatcag gagccccgcc ttgccggctc tggtcategc 60  
ctttcttttt gtggcctgaa acgatgtcat caattcgag tagcagaact gccgtctcca 120  
ctgctgtctt ataagtctgc agcttcacag ccaatggctc ccatatgcc agttccttca 180  
tgtccaccaa agtaccgctc tcaccattta caccacaggt ctacacagtc tcctgggtgt 240  
gcttgggccg aagggaggtg agtanacgga tgggtgctggt cccacagtc tggatcaggg 300  
tacgaggaat gacctctagg gcctgggcna caagccctgt atggacctgc ccgggcgggc 360  
ccgctcga 368

<210> 270  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 54, 163, 219, 229, 316  
<223> n = A,T,C or G

<400> 270  
tcgagcggcc gcccgggcag gtccatacag ggctgttgcc caggccctag aggnattcc 60  
ttgtaccctg atccagaact gtgggaccag caccatccgt ctacttacct cccttcgggc 120  
caagcacacc caggagaact gtgagacctg ggggtgtaa atgngagacgg gtactttggt 180  
ggacatgaag gaactgggca tatgggagcc attggctgng aagctgcana cttataagac 240  
agcagtgagg acggcagttc tgctactgag aattgatgac atcgtttcag gccacaaaaa 300  
gaaaggcgat gaccanagcc ggcaaggcgg ggcttcctga tgctggacct cggccgccga 360  
ccacgctt 368

<210> 271  
<211> 424  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 279, 329, 362, 384, 400  
<223> n = A,T,C or G

<400> 271  
agcgtggtcg cggccgaggt ccactagagg tctgtgtgcc attgcccagg cagagtctct 60  
gcgttacaaa ctcttaggag ggcttgctgt gcggagggcc tgctatggtg tgcgtcggtt 120  
catcatggag agtggggcca aaggctgcga ggttggtgtg tctgggaaac tccgaggaca 180  
gagggtctaaa tccatgaagt ttgtggatgg cctgatgac cacagcggag accctgttaa 240  
ctactacgtt gacactgctg tgcgccacgt gttgctcana cagggtgtgc tgggcatcaa 300  
ggtgaagatc atgctgccct gggacccanc tggcaaaaat ggcccttaaa aacccttgc 360  
cntgaccacg tgaaccattt gtgngaaccc caagatgaan atacttgccc accaccccc 420  
attc 424

<210> 272  
<211> 541  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 422, 442, 510, 513, 515, 525  
<223> n = A,T,C or G

<400> 272  
tcgagcggcc gcccgggcag gtctgccaa gagacctgt tatgctgtgg ggactggctg 60  
gggcatggca ggcggtctg gcttcccacc cttctgttct gagatggggg tggtagggcag 120  
tatctcatct ttgggttcca caatgctcac gtggtcaggc aggggttct tagggccaat 180  
cttaccagtt ggggtcccagg gcagcatgat cttcaccttg atgccagca cacctgtct 240  
gagcaacacg tggcgcacag cagtgtcaac gtagtagtta acagggtctc cgctgtggat 300  
catcaggcca tccacaaact tcatggattt agccctctgt cctcggagt tccaaaaaca 360  
ccacaacctc gccagccttt gggccccact tcttcatgaa tgaaaccgca gcacaccatt 420  
ancaaggccc ttccgcacag gnaagccctt cctaaggagt tttgtaaacy caaaaaactc 480  
ttgcctgggg caaatgggca cacagacctn tantnggacc ttggnccgag aaccaccgct 540  
t 541

<210> 273  
<211> 579  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 223, 265, 277, 308, 329, 346, 360, 366, 429, 448, 517, 524,  
531, 578  
<223> n = A,T,C or G

<400> 273  
agcgtggctg cggccgaggt ctggccctcc tggcaaggct ggtgaagatg gtcaccctgg 60  
aaaaccggga cgacctggtg agagaggagt tggtggacca cagggtgctc gtggtttccc 120  
tggaactcct ggacttcctg gcttcaaagg cattagggga cacaatggtc tggatggatt 180  
gaaggagcag cccggtgctc ctggtgtgaa gggtagacct ggngcccctg gtgaaaatgg 240  
aactccaggt caaacaggag cccgngggct tcctggngag agaggacgtg ttggtgcccc 300  
tggcccanac ctgcccgggc ggccgctcna aaagccgaaa tccagnacac tggcggccgn 360  
tactantgga atccgaactt cggtaccaa gcttggccgt aatcatggcc atagcttgtt 420  
ccctggggng gaaattggta ttccgctncc aattccacac aacataccga acccgaaag 480  
cattaaagtg taaaagccct gggggggcct aaatgangtg agcntaactc ncatttaatt 540  
ggcgttgccg ttcactgccc cgcttttcca gtccgggna 579

<210> 274  
<211> 330  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 171  
<223> n = A,T,C or G

<400> 274  
tcgagcggcc gcccgggcag gtctgggcca ggggcaccaa cacgtcctct ctcaccagga 60  
agccccaggg ctctgtttg acctggagtt ccattttcac caggggcacc aggttcaccc 120

```

ttcacaccag gagcaccggg ctgtcccttc aatccatcca gaccattgtg ncccctaattg 180
cctttgaagc caggaagtcc aggagttcca gggaaaccac gagcaccctg tggccaaca 240
actcctctct caccaggtcg tccgggtttt ccagggtgac catcttcacc agccttgcca 300
ggagggccag acctcgccg cgaccacgt 330

```

<210> 275

<211> 97

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 2, 35, 72

<223> n = A,T,C or G

<400> 275

```

ancgtgggtcg cggccgaggt cctcaccaga ggtgncacct acaacatcat agtggaggca 60
ctgaaagacc ancagaggca taagggtcgg gaagagg 97

```

<210> 276

<211> 610

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 358, 360, 363, 382, 424, 433, 464, 468, 477, 491, 499, 511, 558, 584, 588, 590

<223> n = A,T,C or G

<400> 276

```

tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaattctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagttaaaa gcctgattca gacattcggt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatccg taggttggtt 240
caagccttcg ttgacagagt tgtccacggt aacaacctct tccggaacct tatgcctctg 300
ctggtctttc agtgccctca ctatgatgtt gtaggtggca cctctggtga ggacctcngn 360
ccngaacaac gcttaagccc gnattctgca gaataatccc atcacacttg gcggccgctt 420
cgancatgca tcntaaaagg ggccccaatt tcccccttat aagngaancg gtatttncca 480
atttcaactg ncccgccgnt ttacaaaacg ncggtgaact ggggaaaaac cctggcggtt 540
acccaacttt aatcgccntt ggcagcacia tcccccttt tcgnccancn tgggcgtaaa 600
taaccgaaaa 610

```

<210> 277

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 2, 5, 18, 21, 31

<223> n = A,T,C or G

<400> 277

```

ancngngtcg cggccgangt nttttttctt nttttttt 38

```

<210> 278

<211> 443

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 156, 212, 233, 245, 327, 331, 336, 361, 364, 381, 391, 397, 419, 437

<223> n = A,T,C or G

<400> 278

```
agcgtggtcg cggccgaggt ctgaggttac atgcgtggtg gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gccgcgggag gagcagtaca acagcacgta cgggnggtc agcgtcctca ccgtcctgca 180
ccagaattgg ttgaatggca aggagtacaa gngcaagggt tccaacaaag cntcccagc 240
ccccntcgaa aaaaccattt ccaaagccaa agggcagccc cgagaaccac aggtgtacac 300
cctgccccca tcccgggagg aaaagancaa naaccnggtt cagccttaac ttgcttggtc 360
naangctttt tatccaacg nacttcccc ntggaantgg gaaaaacaa tgggccaanc 420
cgaaaaacaa ttacaanaac ccc                                     443
```

<210> 279

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 219, 256, 291, 297, 307, 314, 317

<223> n = A,T,C or G

<400> 279

```
tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagttgt 60
tctccggctg cccattgctc tcccactcca cggcgatgtc gctgggatag aagcctttga 120
ccaggcaggt caggetgacc tggttcttgg tcatctctc cgggatggg ggcagggtga 180
acacctgggg ttctcggggc ttgcccttgg gttttgaana tggttttctc gatgggggct 240
ggaagggtt tgttgnaaac cttgcacttg actccttgcc attcacccag ncctggngca 300
ggacgngag gacnctnacc acacggaacc gggctggtgg actgctcc                                     348
```

<210> 280

<211> 149

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 18, 34, 51, 118, 120, 140

<223> n = A,T,C or G

<400> 280

```
agcgtggtcg cggacgangt cctgtcagag tggactggt agaagttcca ngaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagnn 120
cctggaatgg ggcccatgan atggttgcc                                     149
```

<210> 281

<211> 404

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature  
 <222> 383, 386, 388, 393  
 <223> n = A,T,C or G

<400> 281  
 tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggtatc atggcagccg 60  
 ccacgtgccca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120  
 gaagtgggtcc ctcgcccccg ccctgggtgc acagaggcta ctattactgg cctggaaccg 180  
 ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240  
 attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300  
 catggaccag agatcttgga tgttccttcc acagttcaaa agaccctttt cggcaccccc 360  
 cctgggtatg aacctgggaa aanggnantt aanccttcct ggca 404

<210> 282  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 320, 341, 424, 450, 459, 487, 498  
 <223> n = A,T,C or G

<400> 282  
 agcgtgggtcg cgcccgaggt ctgggatgct cctgctgtca cagtgagata ttacaggatc 60  
 acttacggag aaacaggagg aaatagccct gtccaggagt tcactgtgcc tgggagcaag 120  
 tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180  
 gtcactggcc gtggagacag ccccgcaagc agcaagccaa tttccattaa ttaccgaaca 240  
 gaaattgaca aaccatccca gatgcaagtg accgatgttc aggacaacag cattagtgtc 300  
 aagtggctgc cttcaaggtn ccctgggtact gggttacaga ntaaccacca ctccccaaaa 360  
 tggaccagga accacaaaaa cttaaactgc aggttccaga tcaaaacaga aatgactatt 420  
 gaangcttgc agccacagtg gggagtatgn gggtagtgnc tatgcttcag aatccaagcg 480  
 gaaaaangtc aagccttntg ggttcaa 507

<210> 283  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 216, 292, 303, 304  
 <223> n = A,T,C or G

<400> 283  
 tcgagcggcc gcccgggcag gtccttgag ctctgcagtg tcttcttcac catcaggtgc 60  
 agggaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120  
 ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagtgaatgc 180  
 cagtccttta gggcgatcaa tgttggttac tgcagnctga accagaggct gactctctcc 240  
 gcttggtatc tgagcataga cactaaccac atactccaact gtgggctgca anccttcaat 300  
 aanncatttc tgtttgatct ggacc 325

<210> 284  
 <211> 331  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> misc\_feature  
 <222> 54, 59, 63, 121, 312, 327  
 <223> n = A,T,C or G

<400> 284  
 tcgagcggcc gcccgggcag gtctggtggg gtcctggcac acgcacatgg gggngttgnt 60  
 ctnatccagc tgcccagccc ccattggcga gtttgagaag gtgtgcagca atgacaacaa 120  
 naccttcgac tcttcctgcc acttccttgc cacaaagtgc accctggagg gcaccaagaa 180  
 gggccacaag ctccacctgg actacatogg gccttgcaaa tacatccccc cttgcctgga 240  
 ctctgagctg accgaattcc cccttgcgca tgcgggactg gctcaagaac cgtcctggca 300  
 cccttgatat anagggatga agacacnacc c 331

<210> 285  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 316, 319, 327, 329, 339, 344, 357, 384, 398, 427, 443, 450,  
 478  
 <223> n = A,T,C or G

<400> 285  
 agcgtggtcg cgcccgaggt ctgtcctaca gtcctcagga ctctactccc tcagcagcgt 60  
 ggtgaccgtg ccctccagca acttcggcac ccagacctac acctgcaacg tagatcacia 120  
 gccagcaac accaaggtgg acaagagagt tgagcccaa tcttgtaga aaactcacac 180  
 atgcccaccg tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccg 240  
 catccccctt ccaaacctgc ccgggcggcc gctcgaaagc cgaattccag cacactggcg 300  
 gccggtacta gtgganccna acttggnanc caacctggng gaantaatgg gcataantcg 360  
 tttctggggg gaaattggtg tccngtttac aattcccnca caacatacga gccggaagca 420  
 taaaagngta aaagcctggg gnggcctan tgaagtgaag ctaaactcac attaatngc 480  
 gttgccgctc actggcccgc ttttccage 509

<210> 286  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 188, 251, 267  
 <223> n = A,T,C or G

<400> 286  
 tcgagcggcc gcccgggcag gtttgaagg gggatgcggg ggaagaggaa gactgacggt 60  
 cccccagga gttcaggtgc tgggcacggt gggcatgtgt gattttgtc acaagatttg 120  
 ggctcaactc tcttgctcac cttggtgttg ctgggcttgt gatctacgtt gcagggtgtag 180  
 gtctggngc cgaagttgct ggaggcacg gtcaccacgc tgctgaggga gtagagtcct 240  
 gaggactgta ngacagacct cgcccgngac cacgctaagc cgaattctgc agatatccat 300  
 cacactggcg gccgctccga gcatgcattt tagagg 336

<210> 287  
 <211> 30  
 <212> DNA  
 <213> Homo sapiens

<220>



<221> misc\_feature  
 <222> 8, 18  
 <223> n = A,T,C or G

<400> 287  
 agcgtggncg cggacganga caacaacccc

30

<210> 288  
 <211> 316  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 22, 130  
 <223> n = A,T,C or G

<400> 288  
 tcgagcggcc gcccgggcag gnccacatcg gcagggtcgg agccctggcc gccatactcg 60  
 aactggaatc catcggtcat gctcttgccg aaccagacat gcctcttgtc cttgggggttc 120  
 ttgctgatgn accagttctt ctgggccaca ctgggctgag tgggggtacac gcaggtctca 180  
 ccagttctcca tgttgacagaa gactttgatg gcatccagggt tgcagccttg gttgggggtca 240  
 atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcaggtgcgg 300  
 gcgggggttct tgacct 316

<210> 289  
 <211> 308  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 36, 165, 191, 195, 218, 235  
 <223> n = A,T,C or G

<400> 289  
 agcgtgggtcg cgcccgagggt ccagcctgga gataanggtg aagggtggtgc ccccggaactt 60  
 ccaggtatag ctggacctcg tggtagccct ggtgagagag gtgaaactgg ccctccagga 120  
 cctgctgggtt tccctgggtgc tcctggacag aatggtgaac ctggnngtaa aggagaaaga 180  
 ggggctccgg ntganaaaagg tgaaggaggc cctcctgnat tggcagggggc cccangactt 240  
 agaggtggag ctggccccc tggcccccga ggaggaaagg gtgctgctgg tcctcctggg 300  
 ccacctgg 308

<210> 290  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 184  
 <223> n = A,T,C or G

<400> 290  
 tcgagcggcc gcccgggcag gtctgggcca ggaggaccaa taggaccagt aggaccctt 60  
 gggccatctt tccctgggac accatcagca cctggaccgc ctggttcacc cttgtcacc 120  
 tttggaccag gacttccaag acctcctctt tctccaggca ttccttgacg accaggagta 180  
 ccancagcac caggtggccc aggaggacca gcagcacctt ttctccttc gggaccaggg 240

ggaccagctc cacctctaag tcttggggcc cctgccaatc caggagggcc tccttcacct 300  
 ttctcaccgc gagccctctt ttct 324

<210> 291  
 <211> 278  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 249, 267  
 <223> n = A,T,C or G

<400> 291  
 tcgagcggcc gcccgggcag gtccaccggg atattcgggg gtctggcagg aatgggaggc 60  
 atccagaacg agaaggagac catgcaaagc ctgaacgacc gcctggcctc ttacctggac 120  
 agagtgagga gcctggagac cgacaaccgg aggcctggaga gcaaaatccg ggagcacttg 180  
 gagaagaagg gacccaggt cagagactgg agccattact tcaagatcat cgaggacctg 240  
 agggctcana tcttcgcaaa tactgcngac aatgcccg 278

<210> 292  
 <211> 299  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 6, 19, 25, 51, 53, 61, 63, 70, 109, 136, 157, 241, 276  
 <223> n = A,T,C or G

<400> 292  
 atgcgnggtc gcggccgang accanctctg gctcatactt gactctaaag nnttcaccag 60  
 nanttacggn cattgccaat ctgcagaacg atgcgggcat tgtccgcant atttgccaag 120  
 atctgagccc tcaggnccctc gatgatcttg aagtaanggc tccagtctct gacctggggt 180  
 cccttcttct ccaagtgtct ccggattttg ctctccagcc tccggttctc ggtctccaag 240  
 ncttctcact ctgtccagga aaagaggcca ggcggnccgat cagggttttt gcatggact 299

<210> 293  
 <211> 101  
 <212> DNA  
 <213> Homo sapiens

<400> 293  
 agcgtggtcg cggccgaggt tgtacaagct tttttttttt tttttttttt tttttttttt 60  
 tttttttttt tttttttttt tttttttttt tttttttttt t 101

<210> 294  
 <211> 285  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 64, 103, 110, 237, 282  
 <223> n = A,T,C or G

<400> 294  
 tcgagcggcc gcccgggcag gtctgccaac accaagattg gccccgccg catccacaca 60

```

gttngtgtgc ggggaggtaa caagaaatac cgtgccctga ggntggacgn ggggaatttc 120
tcctggggct cagagtgttg tactcgtaaa acaaggatca tcgatgttgt ctacaatgca 180
tctaataacg agctgggttcg taccaagacc ctggtgaaga attgcatcgt gctcatngac 240
agcacaccgt accgacagtg ggtaccgaag tcccactatg cncct 285

```

```

<210> 295
<211> 216
<212> DNA
<213> Homo sapiens

```

```

<400> 295
tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggtatc atggcagccg 60
ccacgtgccg ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtcc ctcgggcccg ccctggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaag 216

```

```

<210> 296
<211> 414
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 7, 10, 33, 61, 62, 63, 88, 109, 122, 255, 298, 307, 340,
355, 386, 393
<223> n = A,T,C or G

```

```

<400> 296
agcgtgntcn cggccgagga tggggaagct cgnctgtctt tttccttcca atcaggggct 60
nnntcttctg attattcttc agggcaanga cataaattgt atattcggnt cccggttcca 120
gnccagtaat agtagcctct gtgacaccag ggcggggccg agggaccact tctctgggag 180
gagacccagg cttctcatac ttgatgatga agccggtaat cctggcacgt gggcggtgtc 240
catgatacca ccaangaatt ggggtgtgtg gacctgcccc ggcggggccg tcgaaaancc 300
gaattcntgc aagaatatcc atcacacttg ggcggggccg tcgaaccatg catcntaaaa 360
gggcccgaat ttcccccta ttaggngaag ccncatttaa caaattccac ttgg 414

```

```

<210> 297
<211> 376
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 312, 326, 335, 361
<223> n = A,T,C or G

```

```

<400> 297
tcgagcggcc gcccgggcag gtctcgcggt cgcactggtg atgctggtcc tgttggtccc 60
cccggccctc ctggacctcc tggteccctt ggtcctcca gcgctggtt cgacttcagc 120
ttcttgcccc agccacctca agagaagget cactgatgtg gccgtacta ccgggctgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gaggcttgag 240
ccagcagaat cgaaaacatt cggaacccaa gaagggaag cccgaaaaga aaccccgccc 300
gcacctggcc gngaacctcc aagaangtgc ccacntcttg actgggaaaa aaagggaaaa 360
ntacttgga ttggac 376

```

```

<210> 298
<211> 357
<212> DNA

```

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 345, 346

<223> n = A,T,C or G

<400> 298

```
agcgtggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggttg cagccttggt tggggccaat 240
ccagtactct ccactcttcc agtcagaagt ggcacatctt gaggtcacgg caggggtcgg 300
gcgggggtct tgcgggctgc ccttctgggc tcccgggaatg ttctnngaac ttgctgg 357
```

<210> 299

<211> 307

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 281, 285, 306

<223> n = A,T,C or G

<400> 299

```
agcgtggtcg cggccgaggt ccactagagg tctgtgtgcc attgcccagg cagagtctct 60
gcgttacaaa ctccaggag ggcttgctgt gcggagggcc tgctatggtg tgctgcggtt 120
catcatggag agtggggcca aaggctgcga ggttggtgtg tctgggaaac tccaggaca 180
gagggtctaaa tccatgaagt ttgtggatgg cctgatgatc cacagcggag accctgttaa 240
ctactacgtt gacacttgct tgtgcgccac gtgttgctca nacanggggt ggctgggcat 300
caaggng 307
```

<210> 300

<211> 351

<212> DNA

<213> Homo sapiens

<400> 300

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tcgagcggcc gcccgggcag gtctgccaag gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggctctg gcttcccacc ctctgttctt gagatggggg tgggtggcag 120
tatctcatct ttgggttcca caatgctcac gtggtcaggc aggggcttct tagggccaat 180
cttaccagtt gggctccagg gcagcatgat cttcaccttg atgccagca caccctgtct 240
gagcaacacg tggcgcacag caagtgtcaa cgtaagtaag ttaacagggt ctccgctgtg 300
gatcatcagg ccatccacaa acttcatgga ttttaaccctc tgcctcgga g 351
```

<210> 301

<211> 330

<212> DNA

<213> Homo sapiens

<400> 301

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tcgagcggcc gcccgggcag gtgtttcaga ggttccaagg tccactgtgg aggtcccagg 60
agtgtgtgtg gtgggcacag aggtccgatg ggtgaaacca ttgacataga gactgttctt 120
gtccagggtg taggggcca gctctttgat gccattggcc agttggctca gctcccagta 180
cagccgctct ctgttgagtc cagggttttt ggggtcaaga tgatggatgc agatggcatc 240
cactccagtg gctgtcccat ctttctcgga cctgagagag gtcagtctgc agccagagta 300
cagagggcca aactggtgt tctttgaata 330
```

<210> 302  
<211> 317  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 129, 295  
<223> n = A,T,C or G

<400> 302  
agcgtggtcg cggccgaggt ctgtactggg agctaagcaa actgaccaat gacattgaag 60  
agctgggccc ctacaccctg gacaggaaca gtctctatgt caatggtttc acccatcaga 120  
gctctgtgnc caccaccagc actcctggga cctccacagt ggatttcaga acctcagggg 180  
ctccatcctc cctctccagc cccacaatta tggctgctgg ccctctcctg gtaccattca 240  
ccctcaactt caccatcacc aacctgcagt atggggagga catgggtcac cctgnctcca 300  
ggaagttcaa caccaca 317

<210> 303  
<211> 283  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 139, 146, 195  
<223> n = A,T,C or G

<400> 303  
tcgagcggcc gcccgagcag gtctgggcgg atagcaccgg gcatattttg gaatggatga 60  
ggtctggcac cctgagcagt ccagcgagga cttggtctta gttgagcaat ttggctagga 120  
ggatagtatg cagcacggnt ctgagnctgt gggatagctg ccatgaagta acctgaagga 180  
ggtgctggct ggtanggggt gattacaggg ttgggaacag ctctacact tgccattctc 240  
tgcatatact ggttagtgag gtgagcctgg ccctcttctt ttg 283

<210> 304  
<211> 72  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 59  
<223> n = A,T,C or G

<400> 304  
agcgtggtcg cggccgaggt gagccacagg tgaccggggc tgaagctggg gctgctggnc 60  
ctgctggtcc tg 72

<210> 305  
<211> 245  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 5, 11, 22, 98, 102

<223> n = A,T,C or G

<400> 305

```
cagcngctcc nacggggcct gngggaccaa caacaccgtt ttcaccctta ggccctttgg 60
ctctcttttc tccttttagca ccagggttgac cagcagcncc ancaggacca gcaaattccat 120
tggggccagc aggaccgacc tcaccacgtt caccagggtt tccccgagga ccagcaggac 180
cagcaggacc agcagcccca gcttcgcccc ggtcacctgt ggctcacctc ggccgcgacc 240
acgct 245
```

<210> 306

<211> 246

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 144, 159

<223> n = A,T,C or G

<400> 306

```
tcgagcggtc gcccgggcag gtccaccggg atagccgggg gtctggcagg aatgggaggc 60
atccagaacg agaaggagac catgcaaagc ctgaacgacc gcctggcctc ttacctggac 120
agaagtgagga gcctgggagac cganaaccgg aggctggana gcaaaatccg ggagcacttg 180
gagaagaagg gaccccagggt caagagactg gagccattac ttcaagatca tcgagggacc 240
tgaggg 246
```

<210> 307

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 5

<223> n = A,T,C or G

<400> 307

```
agcgnnggtcg cggccgaggt ccagctctgt ctcatacttg actctaaagt catcagcagc 60
aagacgggca ttgtcaatct gcagaacgat gcgggcattg tccgcagtat ttgcgaagat 120
ctgagccctc aggtcctcga tgatcttgaa gtaatggctc cagtctctga cctgggggtcc 180
cttcttctec aagtgtctcc ggattttgct ctccagcctc cggttctcgg tctccagget 240
cctcactctg tccaggtaag aaggcccagg cggtcgttca ggctttgcat ggtctccttc 300
tcgttctgga tgcttcccat tcctgccaga ccc 333
```

<210> 308

<211> 310

<212> DNA

<213> Homo sapiens

<400> 308

```
tcgagcggcc gcccgggcag gtcaggaagc acattggtct tagagccact gcctcctgga 60
ttccacctgt gctgcggaca tctccaggga gtgcagaagg gaagcaggtc aaactgctca 120
gatcagtcag actggctgtt ctcaattctc acctgagcaa ggtcagctctg cagccagagt 180
acagagggcc aacactgggtg ttcttgaaca agggcttgag cagaccctgc agaaccctct 240
tccgtggtgt tgaacttcct ggaaaccagg gtgttgcatg tttttcctca taatgcaagg 300
ttggtgatgg 310
```

<210> 309

<211> 429  
<212> DNA  
<213> Homo sapiens

<400> 309  
agcgtgggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60  
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tgggggttctt 120  
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagaccg caggtctcac 180  
cagttcccat gttgcagaag actttgatgg catccagggt gcagccttgg ttgggggtcaa 240  
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cgggccgggg gttcttgccg cttgccctct gggctccgga tgttctcgat ctgcttggct 360  
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cccgtcga 429

<210> 310  
<211> 430  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 342  
<223> n = A,T,C or G

<400> 310  
tcgagcggtc gcccgggcag gtttcgtgac cgtgacctcg aggtggacac caccctcaag 60  
agcctgagcc agcagatcga gaacatccgg agcccagagg gcagccgcaa gaaccccgcc 120  
cgacactgcc gtgacctcaa gatgtgccac tctgactgga agagtggaga gtactggatt 180  
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gaccaccgct 430

<210> 311  
<211> 2996  
<212> DNA  
<213> Homo sapiens

<400> 311  
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```

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gatctgcaat gactggaaact tgccggtgcc tggggtgect ttcccccagc cagggtccaa 2940
agaagcttgg ctggggcaga aataaaccat attggtcgga cacaaaaaaa aaaaaa 2996

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&lt;210&gt; 312

&lt;211&gt; 914

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 312

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Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
 1          5          10          15
Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
 20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
 35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
 50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
 65          70          75          80
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
 85          90          95
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
100          105          110
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
115          120          125
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
130          135          140
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr

```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| His | Arg | Ser | Ser | Val | Ser | Thr | Thr | Ser | Thr | Pro | Gly | Thr | Pro | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Tyr | Leu | Gly | Ala | Ser | Lys | Thr | Pro | Ala | Ser | Ile | Phe | Gly | Pro | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Ala | Ser | His | Leu | Leu | Ile | Leu | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Leu | Arg | Tyr | Glu | Glu | Asn | Met | Trp | Pro | Gly | Ser | Arg | Lys | Phe | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Thr | Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Arg | Pro | Leu | Phe | Lys | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Ser | Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr | Leu | Leu | Arg |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |
| Glu | Lys | Asp | Gly | Glu | Ala | Thr | Gly | Val | Asp | Ala | Ile | Cys | Thr | His |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Pro | Asp | Pro | Thr | Gly | Pro | Gly | Leu | Asp | Arg | Glu | Gln | Leu | Tyr | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Leu | Ser | Gln | Leu | Thr | His | Ser | Ile | Thr | Glu | Leu | Gly | Pro | Tyr | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Asp | Arg | Asp | Ser | Leu | Tyr | Val | Asn | Gly | Phe | Thr | His | Arg | Ser | Ser |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Thr | Thr | Ser | Thr | Gly | Val | Val | Ser | Glu | Glu | Pro | Phe | Thr | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |
| Phe | Thr | Ile | Asn | Asn | Leu | Arg | Tyr | Met | Ala | Asp | Met | Gly | Gln | Pro |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |
| Ser | Leu | Lys | Phe | Asn | Ile | Thr | Asp | Asn | Val | Met | Lys | His | Leu | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |
| Pro | Leu | Phe | Gln | Arg | Ser | Ser | Leu | Gly | Ala | Arg | Tyr | Thr | Gly | Cys |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |
| Val | Ile | Ala | Leu | Arg | Ser | Val | Lys | Asn | Gly | Ala | Glu | Thr | Arg | Val |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |
| Leu | Leu | Cys | Thr | Tyr | Leu | Gln | Pro | Leu | Ser | Gly | Pro | Gly | Leu | Pro |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |
| Lys | Gln | Val | Phe | His | Glu | Leu | Ser | Gln | Gln | Thr | His | Gly | Ile | Thr |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |
| Leu | Gly | Pro | Tyr | Ser | Leu | Asp | Lys | Asp | Ser | Leu | Tyr | Leu | Asn | Gly |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |
| Asn | Glu | Pro | Gly | Pro | Asp | Glu | Pro | Pro | Thr | Thr | Pro | Lys | Pro | Ala |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |
| Thr | Phe | Leu | Pro | Pro | Leu | Ser | Glu | Ala | Thr | Thr | Ala | Met | Gly | Tyr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |
| Leu | Lys | Thr | Leu | Thr | Leu | Asn | Phe | Thr | Ile | Ser | Asn | Leu | Gln | Tyr |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |
| Pro | Asp | Met | Gly | Lys | Gly | Ser | Ala | Thr | Phe | Asn | Ser | Thr | Glu | Gly |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |
| Leu | Gln | His | Leu | Leu | Arg | Pro | Leu | Phe | Gln | Lys | Ser | Ser | Met | Gly |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     |     | 525 |     |
| Phe | Tyr | Leu | Gly | Cys | Gln | Leu | Ile | Ser | Leu | Arg | Pro | Glu | Lys | Asp |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |
| Ala | Ala | Thr | Gly | Val | Asp | Thr | Thr | Cys | Thr | Tyr | His | Pro | Asp | Pro |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     | 560 |
| Gly | Pro | Gly | Leu | Asp | Ile | Gln | Gln | Leu | Tyr | Trp | Glu | Leu | Ser | Gln |
|     |     |     | 565 |     |     |     |     |     | 570 |     |     |     |     | 575 |
| Thr | His | Gly | Val | Thr | Gln | Leu | Gly | Phe | Tyr | Val | Leu | Asp | Arg | Asp |
|     |     | 580 |     |     |     |     |     | 585 |     |     |     |     | 590 |     |
| Leu | Phe | Ile | Asn | Gly | Tyr | Ala | Pro | Gln | Asn | Leu | Ser | Ile | Arg | Gly |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |
| Tyr | Gln | Ile | Asn | Phe | His | Ile | Val | Asn | Trp | Asn | Leu | Ser | Asn | Pro |

|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 610   |     | 615 |     | 620 |
| Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys |     |     |     |     |
| 625   |     | 630 |     | 635 |
| Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe |     |     |     |     |
|   | 645 |     | 650 | 655 |
| Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys |     |     |     |     |
|   | 660 |     | 665 | 670 |
| Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe |     |     |     |     |
|   | 675 |     | 680 | 685 |
| Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr |     |     |     |     |
|   | 690 |     | 695 | 700 |
| Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln |     |     |     |     |
| 705   |     | 710 |     | 715 |
| Pro Thr Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile     |     |     |     |     |
|   | 725 |     | 730 | 735 |
| Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn |     |     |     |     |
|   | 740 |     | 745 | 750 |
| Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe |     |     |     |     |
|   | 755 |     | 760 | 765 |
| Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr |     |     |     |     |
|   | 770 |     | 775 | 780 |
| Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys |     |     |     |     |
| 785   |     | 790 |     | 795 |
| Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu |     |     |     |     |
|   | 805 |     | 810 | 815 |
| Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr |     |     |     |     |
|   | 820 |     | 825 | 830 |
| Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn |     |     |     |     |
|   | 835 |     | 840 | 845 |
| Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu |     |     |     |     |
|   | 850 |     | 855 | 860 |
| Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly |     |     |     |     |
| 865   |     | 870 |     | 875 |
| Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val |     |     |     |     |
|   | 885 |     | 890 | 895 |
| Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp |     |     |     |     |
|   | 900 |     | 905 | 910 |
| Leu Gln   |     |     |     |     |

&lt;210&gt; 313

&lt;211&gt; 656

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 313

```

acagccagtc ggagctgcaa gtgttctggg tggatcgcyg atatgcactc aaaatgctct 60
ttgtaaagga aagccacaac atgtccaagg gacctgaggg gacttggagg ctgagcaaag 120
tgcagtttgt ctacgactcc tcggagaaaa cccacttcaa agacgcagtc agtgctggga 180
agcacacagc caactcgcac cacctctctg ccttggtcac ccccgctggg aagtcctatg 240
agtgtcaagc tcaacaaacc atttactggg cctctagtga tccgcagaag acggtcacca 300
tgatcctgtc tgcggtccac atccaacctt ttgacattat ctcagatttt gtcttcagt 360
aagagcataa atgcccagtg gatgagcggg agcaactgga agaaaccttg cccctgattt 420
tggggctcat cttgggcctc gtcacatcatg taacactcgc gatttaccac gtccaccaca 480
aaatgactgc caaccagggtg cagatccctc gggacagatc ccagtataag cacatgggct 540
agaggccggt aggcaggcac cccctattcc tgctcccca actggatcag gtagaacaac 600
aaaagcactt ttccatcttg tacacgagat acaccaacat agctacaatc aaacag 656

```

100

<210> 314  
<211> 519  
<212> DNA  
<213> Homo sapiens

<400> 314  
tgtgctgga ccagtcagct tccgggtgtg actggagcag ggcttgtcgt cttcttcaga 60  
gtcactttgc aggggttggt gaagctgctc ccatccatgt acagctcca gtctactgat 120  
gtttaaggat ggtctcgggt gttaggccca ctagaataaa ctgagtcaca tacctctaca 180  
cagttatgtt taactgggct ctctgacacc gggaggaagg tggcgggggt taggtgttgc 240  
aaacttcaat ggttatgcgg ggatgttcac agagcaagct ttggtatcta gctagtctag 300  
cattcattag ctaatggtgt cctttggtat ttattaaaat caccacagca tagggggact 360  
ttatgttttag gttttgtcta agagttagct tatctgcttc ttgtgctaac agggctattg 420  
ctaccaggga ctttggacat gggggccagc gtttggaac ctcatctagt ttttttgaga 480  
gataggccac tggccttgga cctcggccgc gaccacgct 519

<210> 315  
<211> 441  
<212> DNA  
<213> Homo sapiens

<400> 315  
cacagagcgt ttattgacac caccactcct gaaaattggg atttcttatt aggttccct 60  
aaaagttccc atgttgatta catgtaaata gtcacatata tacaatgaag gcagtttctt 120  
cagaggcaac cagggtttat agtgctaggt aaatgtcatc tcttttgtgc tactgactca 180  
ttgtcaaacg tctctgcaact gttttcagcc tctccacgtt gcctctgtcc tgcttcttag 240  
ttccttcttt gtgacaaacc aaaagaataa gaggatttag aacaggactg cttttccct 300  
atgatttaaa aattccaatg actttcgccc ttgggagaaa tttccaagga aatctctctc 360  
gctcgctctc tccgttttcc tttgtgagct tctgggggag ggtagtggt gactttttga 420  
tacgaaaaaa tgcattttgt g 441

<210> 316  
<211> 247  
<212> DNA  
<213> Homo sapiens

<400> 316  
tggcgggct gctggatttc accttcttgc acctgccggt gagcgccctg ggtctaaagg 60  
ggcgggatac tccattatgg cccctcgccc tgtagggtg gaatagttag aaaaggcaac 120  
ccagtctagc ttgtaagaa gagagacatg cccccaacct cggcgccctt tttcctcacg 180  
atctgctgtc cttacttcag cgactgcagg agcttcacct gcaagaaaac agcattgagc 240  
tgctgac 247

<210> 317  
<211> 409  
<212> DNA  
<213> Homo sapiens

<400> 317  
tgacagggct cctggagttg ttaagtcacc aagtagctgc aggggatgga cactgcccc 60  
cacgatgtgg gatgaacagc agccttggtt ttagctccag ggtgtccatg gatttgacct 120  
gaatgctccc tggaggccct gtggcgagga caggcactgg atggtccaga ccctctggct 180  
ggaggagtgg tggagccagg actgggctt cagccatgag ggctagaata acctgacctc 240  
ttgcatctta aactgggtc attaatgaca cttttccagt ggatgttgca aaaaccaaca 300  
ctgtcaggaa cctggccctg ggagggctca ggtgagctca caaggagagg tcaagccaag 360  
ccaaagggta ggkaacacac aacaccaggg gaaaccagcc cccaaacca 409

<210> 318  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc feature  
 <222> 6, 17, 24, 271  
 <223> n = A,T,C or G

<400> 318  
 caaggnagat cttaagnggg gtentatgta agtgtgctcc tggctccagg gttcctggag 60  
 cctcacgagg tcaggggaac cctttagtaa ctccaccagg agcatcatct cgtgaaggat 120  
 gtcattgggtc aggaagctgt cctggacgta ggccatctcc acatccatgg ggatgccata 180  
 gtcaactgggc ctttgcctcg gaggaggcat caccagaaaa ggagagatct tggactcggg 240  
 gcctggggtt ccagaatagt aaggggagca naggaggcg aggcagggtt ggaagccatt 300  
 gctggagccc tgcagccgca 320

<210> 319  
 <211> 212  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc feature  
 <222> 172  
 <223> n = A,T,C or G

<400> 319  
 tgaagcaata gcgcccccat ttacaggcg gagcatggaa gccagagagg tgggtggggg 60  
 aggggggtcct tccctggctc aggcagatgg gaagatgagg aagccgctga agacgctgtc 120  
 ggccctcagag ccctggtaaa tgtgaccctt tttggggtct tttcaacc anacctgggc 180  
 accctgctgc agacctggc cgcgaccacg ct 212

<210> 320  
 <211> 769  
 <212> DNA  
 <213> Homo sapiens

<400> 320  
 tggaggtgta gcagtgagag gagatytgag gcaagagtgt cacagcagag ccctaaascc 60  
 tccaactcac cagttagaga tgagactgcc cagtactcag ccttcatctc ctggggccacc 120  
 tggagggcgt ctttctccat cagcgcatat tgagcagggg tactcagatc cttcttggaa 180  
 cctacaagga agagaagcac actggaaggg tcattctcct tcagggcacg ggccagccac 240  
 tgctgcatc gggaggtgga aagtaaggga tgagttagtc tgcagggccg ctccactga 300  
 cattcatagg cccaattacc ccctctctgg tcctacatgc attcttcttc ttccctgacca 360  
 cccctctgtt ctgaacctc tcttcccgga gcctccatt atattgcagg atgtcactt 420  
 acttgggtatg ttccagagat gccacatcat tcagggtgaa gacaatgatg atggcttga 480  
 agagtggcag aaacagcccc aggttgacag ggaagacact actgctcatt tcccaatcc 540  
 ttccagctcc atatgagaaa gccatgtgca ctctgagacc cactacccc acttcaccca 600  
 gccccttacc ttgagctcct ctatagtagg ttgatgcaat gcatttgaac ctctcctgcc 660  
 cagcggatc ccaactggaa ggaaggaaga gtgaagcaca ggtatgtatc ttgggggggtg 720  
 tgggtgctgg ggagaaggga tagctggaa ggggtgtgaa gcactcaca 769

<210> 321  
 <211> 690  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 633, 666

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 321

```
tgggctgtgg gcggcacctg tgctctgcag gccagacagc gatagaagcc tttgtctgtg 60
cctactcccc cggaggcaac tgggaggtca acgggaagac aatcatcccc tataagaagg 120
gtgcctgggtg ttgcctctgc acagccagtg tctcaggtcg cttcaaagcc tgggaccatg 180
caggggggct ctgtgaggtc cccaggaatc cttgtcgcat gagctgccag aaccatggac 240
gtctcaacat cagcacctgc cactgccact gtccccctgg ctacacgggc agatactgcc 300
aagtgaggtg cagcctgcag tgtgtgcacg gccggttccg ggaggaggag tgctcgtgcg 360
tctgtgacat cggctacggg ggagcccagt gtgccaccaa ggtgcatttt cccttcaca 420
cctgtgacct gaggatcgac ggagactgct tcatggtgtc ttcagaggca gacacctatt 480
acagaagcca ggatgaaatg tcagaggaat ggcggggtgc tggccagat caagagccag 540
aaagtgcagg acatcctcgc cttctatctg ggccgcctgg agaccaccaa cgaggtgact 600
gacagtgact ttgagaccag gaacttctgg atngggctca cctacaagac cgccaaggac 660
tccttncgct gggccacagg ggagcaccag                                     690
```

&lt;210&gt; 322

&lt;211&gt; 104

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 322

```
gtcgcaagcc ggagcaccac catgtagcct ttcccgaagt accggacctt ctctcctcc 60
acgtcacat cacggacatc atggagcagg accaccacct ggtc                                     104
```

&lt;210&gt; 323

&lt;211&gt; 118

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 323

```
gggccctggg cgcttccaaa tgacccagga ggtggtctgc gacgaatgcc ctaatgtcaa 60
actagtgaat gaagaacgaa cactggaagt agaaatagag cctgggggtga gagacgga 118
```

&lt;210&gt; 324

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 324

```
tgctctccgg gagcttgaag aagaaactgg ctacaaaggg gacattgccg aatgttctcc 60
agcgggtctgt atggaccag gcttgtcaaa ctgtactata cacatcgtga cagtcaccat 120
taacggagat gatgccgaaa acgcaaggcc gaagccaaag ccaggggatg gagagtttgt 180
ggaagtcatt tctttacca agaatgacct gctgcagaga cttgatgctc tggtagctga 240
agaacatctc acagtggacg ccagggtcta ttcctacgct ctacgctga aacatgcaaa 300
tgcaagcca tttgaagtgc cttcttgaa attttaagcc caaatatgac actg                                     354
```

&lt;210&gt; 325

&lt;211&gt; 642

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 1

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 325

```

ncatgcttga atgggctcct ggtgagagat tgccccctgg tggtgaaaca atcgtgtgtg 60
cccactgata ccaagaccaa tgaaagagac acagttaagc agcaatccat ctcatttcca 120
ggcacttcaa taggtcgctg attggtcctt gcaccagcag tggtagtcgt acctatttca 180
gagaggtctg aaattcaggt tcttagtttg ccaggacag gccctacctt atattttttt 240
ccatcttcat catccacttc tgcttacagt ttgtgctta caataactta atgatggatt 300
gagtattctg ggtggtctct agccatctgg gcagtgtggg tctgtctaac caaagggcat 360
tggcctcaaa cctgcattt ggtttagggg ctaacagagc tcctcagata atcttcacac 420
acatgtaact gctggagatc ttattctatt atgaataaga aacgagaagt ttttccaaag 480
tgtagtcag gatctgaagg ctgtcattca gataaccag cttttccttt tggcttttag 540
cccattcaga ctttgccaga gtcaagccaa ggattgcttt tttgctacag ttttctgcca 600
aatggcctag ttcttgagta cctggaaacc agagagaaag ag 642

```

&lt;210&gt; 326

&lt;211&gt; 455

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 326

```

tccgtgagga tgagcttoga gtccttcacc aggcactgca ggggcacagt cacgtcaatc 60
accttcacct tctcgctctt cctgctcttg tcattgacaa acttcccgtg ccaggcattg 120
acgatgatga ggccattctt ggactcttct gcctcaatta tccttcggac agattcctgc 180
atcagccgga cagcggactc cgctcttgc ttcttctgca gcacatcggg ggcggcgctt 240
tccctctgct tctccaattc cttctctttc tgagccctga ggtatggttt gatgatcaga 300
cgggtgatgg caaagtagac cactagaggc cccacgggtg catagaacat ggcgctgggc 360
agaagctggg ccgtcaagtg aataggggaag aagtatgtct gactggccct gttgagcttg 420
actttgagag aaacgccctg tggaactcca acgct 455

```

&lt;210&gt; 327

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 327

```

ttcactgtga actcgcagtc ctcgatgaac tcgcacagat gtgacagccc tgtctccttg 60
ctctctgagt tctcttcaat gatgctgatg atgcagtcca cgatagcgcg cttatactca 120
aagccaccct cttcccgag catggtgaac aggaagttca taaggacggc gtgtttgcga 180
ggatatttct gacacagggc actgatggcc tggacaacca ccaccttgaa ttcacccgag 240
atttctgaca tgaaggagga gatctgcttc atgaggcggg cgatgctgct ctcgctgccc 300
gtcttaagga ggggtggtgat g 321

```

&lt;210&gt; 328

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 302, 311

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 328

```

tgcaggaggg gccatggggg ctgtgaatgg gatgcagccc catggtgtcc ctgataaatc 60
cagtgtgcag tctgatgaag tctgggtggg tgtggtctac gggctggcag ctacccatgat 120
ccaagaggta atgcactcct tttcccatct ctccaccatc tgtatcctgg ccmagaaaaa 180

```

```

cttcccttca aaccaacca aatttccttt caaaggcata acccaaatgc catccttggt 240
ccggtctaataaagcctccc ccatttttcc cctggatatgc attcccaggc tccctggcct 300
tncagggtt nctgtctgtg ggtcatagtt tatctcctcc cacttgctgg gagtccttg 360
aaggcaaaga ctctactgcc tccatctatc cagtggaaagt ggctcttcag agggtgccaa 420
gttagtatgt atgactgtca tctctcccaa cagggcctga cttggsaggg cttcca 476

```

&lt;210&gt; 329

&lt;211&gt; 340

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 329

```

cgaggagat tgccagcacc ctgatggaga gtgagatgat ggagatcttg tcagtgctag 60
ctaagggtga ccacagccct gtcacaaggg ctgctgcagc ctgcctggac aaagcagtgg 120
aatatgggct tatccaaccc aaccaagatg gagagtgagg gggttgtccc tgggcccag 180
gtcatgcac acgtaccta ttgtggcacg gagagtaagg acggaagcag ctttggtgg 240
tggtggctgg catgcccaat actcttgccc atcctcgctt gctgccctag gatgtcctct 300
gttctgagtc agcgccacg ttcagtcaca cagccctgct 340

```

&lt;210&gt; 330

&lt;211&gt; 277

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 330

```

tgtcaccatc acattggtgc caaataccca gaagacatcg tagatgaaga gtccgcccag 60
caggatgcag ccagtgtgta cattgttgag gtgcaggagc tctactccat taaggagaa 120
ggccaggcca aaaagggtgt tggcaatcca gtgcttcctc agcaggtaac agacgccaac 180
gatgctgctc aggccaggc acaccaggtc cttggtgtca aattcataat tgatgatctc 240
ctccttgttt tcccagaacc ctgtgtgaag agcagac 277

```

&lt;210&gt; 331

&lt;211&gt; 136

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 331

```

ttgcttccca cctcctttct ctgtcctctc ctgaggttct gccttacaat ggggacactg 60
atacaaacca cacacacaat gaggatgaaa acagataaca ggtaaaatga cctcacctgc 120
ccgggcggcc gctcga 136

```

&lt;210&gt; 332

&lt;211&gt; 184

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 332

```

ttgtgagata aacgcagata ctgcaatgca ttaaaacgct tgaaatactc atcagggatg 60
ttgtgatctc tattgttgtc taagtagaga gttagaagag agacagggag accagaaggc 120
agtctggcta tctgattgaa gctcaagtca aggtattcga gtgatttaag acctttaaaa 180
gcag 184

```

&lt;210&gt; 333

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 333

```

cggaaaactt cgaggaattg ctcaaagtgc tgggggtgaa tgtgatgctg aggaagattg 60
ctgtggctgc agcgtccaag ccagcagtgg agatcaaaca ggagggagac actttctaca 120
tcaaaacctc caccaccgtg cgaccacag agattaactt caaggttggg gaggagtgtg 180
aggagcagac tgtggatggg aggccctgta agagcctggt gaaatgggag agtgagaata 240
aatgggtctg tgagcagaag ctctgaagg gagagggccc caagacctcg tggaccagag 300
aactgaccaa cgatggggaa ctgatcctga ccatgacggc ggatgacgtt gtgtgcacca 360
gggtctacgt ccgagagtga gcgg                                     384

```

<210> 334  
 <211> 169  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 2, 165  
 <223> n = A,T,C or G

```

<400> 334
cnacaaacag agcagacacc ctggatccgg tcctgtact ggccaggacg gctggaccgt 60
aaaattgaat ttccacttcc tgaccgcgcg cagaagagat tgattttctc cactatcact 120
agcaagatga acctctctga ggaggttgac ttggaagact atgtngccc          169

```

<210> 335  
 <211> 185  
 <212> DNA  
 <213> Homo sapiens

```

<400> 335
ccaggtttgc agccaggct gcacatcagg ggactgcctc gcaatacttc atgctgttgc 60
tgctgactga tgggtgctgt acggatgtgg aagccacacg tgaggctgtg gtgcgtgcct 120
cgaacctgcc catgtcagt atcattgtgg gtgtgggtgg tgctgacttt gaggccatgg 180
agcag                                     185

```

<210> 336  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 26  
 <223> n = A,T,C or G

```

<400> 336
ctgccctgc cttacggcgg ccaganacac acccaggatg gcattggccc caaacttggg 60
tttgttctca gtcccatcca actccagcat caggttgtcc agtttctctt gctccaccac 120
agagagacct gagctgatga gggctggcgo gatggtggag ttgatgtggt cactgcctt 180
caggacacct ttgcctaagt aacgctgttt gtctccatcc ctgagctcca ggccctcata 240
gatgcccgta gaggtccac tgggcactgc agcccggaaa agacctttgg cagtatagag 300
atccacctcc actgtggggt tcccgcggga gtccaggatc tcccggggcc agatcttc 358

```

<210> 337  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens

<220>



<221> misc\_feature

<222> 17

<223> n = A,T,C or G

<400> 337

```
cacaaagcca ccagccnggg aaatcagaat ttacttgatg caactgactt gtaatagcca 60
gaaatcctgc ccagcatggg attcagaacc tggctctgcaa ccaaatccac cgtcaaagtt 120
catacaggat aaaacaaatt caattgcctt ttccacatta atagcatcaa gtttcccca 180
caaagccaaa gttgccaccg cacaaaaaga gaatcttggt tcaatttctc cctactttat 240
aaaagtagat ttttcacatc ccatgaagca g                                     271
```

<210> 338

<211> 326

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 15, 17, 18

<223> n = A,T,C or G

<400> 338

```
ctgtgctccc gactngnnca tctcaggtac caccgactgc actgggcggg gccctctggg 60
gggaaaggct ccacggggca gggatacatc tcgaggccag tcctcctctg gaggcagccc 120
aatcagggtca aagattttgc ccaactgggc ggcttcagag tttccacaga agagaggctt 180
tcgacgaaac atctctgcaa agatacagcc aacactccac atgtccacag gtgttgcata 240
tgtggactgc agaagaactt cgggagctcg gtaccagagt gtaacaacca cgggtgtaag 300
tgccatctgg tagctgtaga ttctgg                                     326
```

<210> 339

<211> 260

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 47, 54, 60, 69, 90, 91, 96, 113, 117, 119, 195

<223> n = A,T,C or G

<400> 339

```
ttcacctgag gactcatttc gtgccctttg ttgacttcaa gcaaagncct tcanggtctn 60
caaggacgnc acattttccac ttgcgaatgn nctcanggct catcttgag aanaagnanc 120
ccaagtgtcg gatcccagac tcgggggtaa ccttggtggg aagagctcat ccagtttatg 180
ctttaggacg tccanctact cgggggagct ggaagcctgc gtggatgcgg ccctgctgga 240
cctcggccgc gaccacgcta                                     260
```

<210> 340

<211> 220

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 15, 18

<223> n = A,T,C or G

<400> 340

```
ctggaagccc ggctnggnct ggcagcggaa ggagccaggc aggttcacgc agcgggtgctg 60
```

```
gcagtagcgg tagcggcact cgtctatgtc cacacactcg ggcccgatct tgcggtaacc 120
atcagggcag gtgcactgat aggagccagg caagttatgg cagtcctggc tggggcgaca 180
gtcgtgcagg gcctgggcac actcgtccac atccacacag                220
```

```
<210> 341
<211> 384
<212> DNA
<213> Homo sapiens
```

```
<400> 341
ctgctaccag gggagcgaga gctgactatc ccagcctcgg ctaatgtatt ctacgccatg 60
gatggagctt cacacgattt cctcctgcgg cagcggcgaa ggtcctctac tgctacaccg 120
ggcgtcacca gtggcccgtc tgcctcagga actcctccga gtgagggagg agggggctcc 180
tttcccagga tcaaggccac agggaggaag attgcacggg cactgttctg aggaggaagc 240
cccgttggct tacagaagtc atggtgttca taccagatgt gggtagccat cctgaatggg 300
ggcaattata tcacattgag acagaaatc agaaagggag ccagccaccc tggggcagtg 360
aagtgccact ggtttaccag acag                384
```

```
<210> 342
<211> 245
<212> DNA
<213> Homo sapiens
```

```
<400> 342
ctggctaagc tcatcattgt tactgggtggg caccatgtcc ttgaagcttc aggcaagcaa 60
tgtaaccaac aagaatgacc ccaagtccat caactctcga gtcttcattg gaaacctcaa 120
cacagctctg gtgaagaaat cagatgtgga gaccatcttc tctaagtatg gccgtgtggc 180
cggctgttct gtgcacaagg gctatgcctt tgttcagtag tccaatgagc gccatgcccg 240
ggcag                245
```

```
<210> 343
<211> 611
<212> DNA
<213> Homo sapiens
```

```
<400> 343
ccaaaaaaat caagatttaa ttttttttatt tgcactgaaa aactaatcat aactgttaat 60
tctcagccat ctttgaagct tgaaagaaga gtctttggta ttttgtaaac gttagcagac 120
tttcctgccg gtgtcagaaa atcctattta tgaatcctgt cggatttcct tggatatctga 180
aaaaaatacc aaatagtacc atacatgagt tatttctaag tttgaaaaat aaaaagaaat 240
tgcatcacac taattacaaa atacaagttc tggaaaaaat atttttcttc attttaaaac 300
tttttttaac taataatggc tttgaaagaa gaggcttaat ttgggggtgg taactaaaat 360
caaaagaaat gattgacttg agggctctctg tttggtaaga atacatcatt agcttaaata 420
agcagcagaa ggtagtttt aattatgtag cttctgttaa tattaagtgt tttttgtctg 480
ttttacctca atttgaacag ataagtttgc ctgcatgctg gacatgcctc agaaccatga 540
atagcccgta ctagatcttg ggaacatgga tcttagagtc ctttggaata agttcttata 600
taaatacccc c                611
```

```
<210> 344
<211> 311
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> 1, 275, 284, 296, 297, 300
<223> n = A,T,C or G
```

<400> 344  
nctcgaaaaa gcccaagaca gcagaagcag acacctccag tgaactagca aagaaaagca 60  
aagaagtatt cagaaaagag atgtcccagt tcctcgtcca gtgcctgaac ccttaccgga 120  
aacctgactg caaagtggga agaattacca caactgaaga ctttaaacat ctggctcgca 180  
agctgactca cgggtgtatg aataaggagc tgaagtactg taagaatcct gaggacctgg 240  
agtgcattga gaatgtgaaa cacaaaacca aggantacat taanaagtag atgcannan 300  
tttggggctt g 311

<210> 345  
<211> 201  
<212> DNA  
<213> Homo sapiens

<400> 345  
cacacggtca tcccgaactgc caacctggag gcccaggccc tgtggaagga gccgggcagc 60  
aatgtcacca tgagtgtgga tgctgagtgt gtgcccatgg tcagggacct tctcaggtac 120  
ttctactccc gaaggattga catcacctcg tcgtcagtca agtgcttcca caagctggcc 180  
tctgcctatg gggccaggca g 201

<210> 346  
<211> 370  
<212> DNA  
<213> Homo sapiens

<400> 346  
ctgctccagg gcgtggtgtg ccttcgtggc ctctgcctcc tccgaggagc caggctgtgt 60  
tctcttcaga atgttctgga gcagcagttt gaggcgggtg atgcgttgga agggcagaat 120  
cagaaaggac ttgagggaaa ggcgctggca gacggggtcg ctctccagct tctccaagac 180  
ctcccggaaa ttgctgttgc tattcatcag gctctggaag gtgcgttcct gataggtctg 240  
gttggtgaca taaggcaggt agaccggcg gaagtctggg gcgtggttca ggactacgtc 300  
acatacttgg aaggagaaga tattgttctc aaagttctct tccagggtctg aaaggaacgt 360  
ggcgctgacg 370

<210> 347  
<211> 416  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 416  
<223> n = A,T,C or G

<400> 347  
ctgttgtgct gtgtatggac gtgggcttta ccatgagtaa ctccattcct ggtatagaat 60  
ccccatttga acaagcaaag aaggtgataa ccatgtttgt acagcgacag gtgtttgctg 120  
agaacaagga tgagattgct ttagtcctgt ttggtacaga tggcactgac aatccccttt 180  
ctggtgggga tcagtatcag aacatcacag tgcacagaca tctgatgcta ccagattttg 240  
atttgctgga ggacattgaa agcaaaatcc aaccagggtc tcaacaggct gacttcctgg 300  
atgcactaat cgtgagcatg gatgtgattc aacatgaaac aataggaaag aagtttggag 360  
aagaggcata ttgaaatatt cactgacctc aagcagcccg attcagcaaa agtcan 416

<210> 348  
<211> 351  
<212> DNA  
<213> Homo sapiens

<400> 348

```

gtacaggaga ggatggcagg tgcagagcgg gactgagct ctgcagggtga aagggtcgg 60
cagttggatg ctctcctgga ggctctgaaa ttgaaacggg caggaaatag tctggcagcc 120
tctacagcag aagaaacggc aggcagtgcc cagggacgag caggagacag atgccttcct 180
cttgtctcaa ctgcaaagag gcgttccttc ctctttcact aatcctcctc agcacagacc 240
ctttacgggt gtcaggctgg gggacagtaa ggtctttccc ttcccacaag gccatatctc 300
aggctgtctc agtgggggga aaccttggac aatacccggg ctttcttggg c 351

```

```

<210> 349
<211> 207
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 1
<223> n = A,T,C or G

```

```

<400> 349
nccgggacat ctccaccctc aacagtggca agaagagcct ggagactgaa cacaaggcct 60
tgaccagtga gattgcactg ctgcagtcca ggctgaagac agagggctct gatctgtgcg 120
acagagtgag cgaaatgcag aagctggatg cacaggtcaa ggagctggtg ctgaagtcgg 180
cgggtggaggc tgagcgcctg gtggctg

```

```

<210> 350
<211> 323
<212> DNA
<213> Homo sapiens

```

```

<400> 350
ccatacaggg ctgttgccca ggccttagag gtcattcctc gtaccctgat ccagaactgt 60
ggggccagca ccatcgtct acttacctcc cttcgggcca agcacacca ggagaactgt 120
gagacctggg gtgtaaatgg tgagacgggt actttggtgg acatgaaggga actgggcata 180
tgggagccat tggctgtgaa gctgcagact tataagacag cagtggagac ggcagttctg 240
ctactgcgaa ttgatgacat cgtttcaggc cagcaaaaga aaggcgatga ccagagccgg 300
caaggcgggg ctcctgatgc tgg

```

```

<210> 351
<211> 353
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 12, 25, 39, 42
<223> n = A,T,C or G

```

```

<400> 351
cgccgcaccc cntgggtccct tccantccct tttcctttnt cngggaacgt gtatgcgggt 60
tgtttttgtt ttgtagggtt tttttccttc tccacctctc cctgtctctt ttgtccatg 120
ttgtccgttt ctgtggggtt aggtttatgt ttttaacat ctgaggtcac gtctatttc 180
tccggactcg cctgcttggt ggcgattctc caccggttaa tatggtgcgt cccctttttc 240
ttttgttgcg aatctgagcc ttcttcctcc agcttctgcc ttttgaactt tgttcttcgg 300
ttctgaaacc atacttttac ctgagtttcc gtgaggctga ggctgtgtgc caa 353

```

```

<210> 352
<211> 467
<212> DNA
<213> Homo sapiens

```

&lt;400&gt; 352

```

ctgcccacac tgatcacttg cgagatgtcc ttagggtaca agaacaggaa ttgaagtctg 60
aatttgagca gaacctgtct gagaaactct ctgaacaaga attacaattt cgctgtctca 120
gtcaagagca agttgacaac tttactctgg atataaatac tgcctatgcc agactcagag 180
gaatcgaaca ggctgttcag agccatgcag ttgctgaaga ggaagccaga aaagcccacc 240
aactctggct ttcagtggag gcattaaagt acagcatgaa gacctcatct gcagaaacac 300
ctactatccc gctgggtagt gcagttgagg ccatcaaagc caactgttct gataatgaat 360
tcaccaagc ttttaaccga gctatccctc cagagtcctt gacctgtggg gtgtacagtg 420
aagagaccct tagagcccgt ttctatgctg ttcaaaaact ggcccga 467

```

&lt;210&gt; 353

&lt;211&gt; 350

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 353

```

ctgctgcagc cacagtagtt cctcccatgg tgggtggccc tcctggctct gctggcccag 60
gaaatctgtc cccaccagga acagcccctg gaaaacggcc ccgtcctcta ccaccttggt 120
gaaatgctgc acgggaactg cctcctggag gaccagcttt accttcccca gacatttgtc 180
ctgattgtgt agttttcctg gactgcattt caaattgact caggaactgt ttattgcatg 240
gagttacaac aggattctga ccatgaagtt ctcttttagg taacagatcc attactttt 300
ttgaagatgc ttcagatcca acaccaacaa gggcaaacc ctttgactgg 350

```

&lt;210&gt; 354

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 354

```

atttagatga gatctgaggc atggagacat ggagacagta tacagactcc tagatttaag 60
ttttagggtt tttgcttttc taatcaccaa ttcttatata caatgtatat tttagactcg 120
agcagatgat catcttcac ctttaagtcatt ctttttgact gagtatggca ggattagagg 180
gaatggcagt atagatcaat gtctttttct gtaaagtata ggaaaaacca gagaggaaaa 240
aaagagctga caattggaag gtagtagaaa attgacgata atttcttctt aacaaataat 300
agttgtatat acaaggaggc tagtcaacca gattttattt gttgagggcg a 351

```

&lt;210&gt; 355

&lt;211&gt; 308

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 355

```

ttttggcgca agttttacag attttattaa agtcgaagct attggtcttg gaagatgaaa 60
atgcaaatgt tgatgaggtg gaattgaagc cagatacctt aataaaaatta tatcttggtt 120
ataaaaaataa gaaattaagg gttaacatca atgtgccaat gaaaaccgaa cagaagcagg 180
aacaagaaac cacacacaaa aacatcgagg aagaccgcaa actactgatt caggcggcca 240
tcgtgagaat catgaagatg aggaaggttc tgaaacacca gcagttactt ggcgaggtcc 300
tcactcag 308

```

&lt;210&gt; 356

&lt;211&gt; 207

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 356

```

ctgtcccaag tgctccaga aggcaggatt ctgaagacca ctccagcgat atgttcaact 60
atgaagaata ctgcaccgcc aacgcagtca ctgggccttg ccgtgcatcc ttcccagct 120

```

ggtacttttga cgtggagagg aactcctgca ataacttcat ctatggaggc tgccggggca 180  
 ataagaacag ctaccgctct gaggagg 207

<210> 357  
 <211> 188  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 25, 29  
 <223> n = A,T,C or G

<400> 357  
 tcgaccacgc cctcgtagcg catgngctnc aggacgatgc tcagagtgat gaacacccccg 60  
 gtgcggccca cgccagcact gcagtgcacc gtgataggcc catcctgtcc aaactgtctc 120  
 ttggtcttat gcacctgcc gatgaagtca atgaatccct cgctgtctt gggcacgccc 180  
 tgctctgg 188

<210> 358  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 358  
 ctgggagcat cggcaagcta ctgccttaaa atccgatctc cccgagtgca caatttctgt 60  
 cccttttaag ggttcacaac actaaagatt tcacatgaaa gggttgtgat tgatttgagc 120  
 aggcaggcgg tacgtgacag gggctgcatg caccggtggt cagagagaaa cagaacaggg 180  
 cagggaattt cacaatgttc ttctatacaa tggctggaat ctatgaataa catcagtttc 240  
 taagttatgg gttgattttt aactactggg tttaggccag gcaggcccag g 291

<210> 359  
 <211> 117  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 79, 98, 100  
 <223> n = A,T,C or G

<400> 359  
 gccaccacac tccagcctgg gcaatacagc aagactgtct caaaaaaaaa aaaaaaaaaa 60  
 ccaaaaaaaaa ctcaaaaang taatgaatga tacccaangn gccttttcta gaaaaag 117

<210> 360  
 <211> 394  
 <212> DNA  
 <213> Homo sapiens

<400> 360  
 ctgttcctct ggggtggtcc agttctagag tgggagaaa ggagtcaggc gcattgggaa 60  
 tcgtgggtcc agtctggttg cagaatctgc acatttgcca agaaattttc cctgtttgga 120  
 aagtttggcc cagctttccc gggcacacca cttttgtcc caagtgtctg ccggtcgacc 180  
 aatctgcctg ccacacattg accaagccag acccggttca cccagctcga ggatcccagg 240  
 ttgaagagtg gcccttgag gccctggaaa gaccaatcac tggacttctt cccttgagag 300  
 tcagaggtea cccgtgatcc tgccctgacc ttatcattga tctgcagtga tttctgcaaa 360  
 tcaagagaaa ctctgcaggg cactcccctg tttc 394

<210> 361  
<211> 394  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 28, 31  
<223> n = A,T,C or G

<400> 361  
ctgggcggat agcaccgggc atattttntt natggatgag gtctggcacc ctgagcagtc 60  
cagcaggagac ttggtcttag ttgagcaatt tggctaggag gatagtatgc agcacggttc 120  
tgagtctgtg ggatagctgc catgaagtaa cctgaaggag gtgctggctg gtaggggttg 180  
attacagggg tgggaacagc tcgtacactt gccattctct gcatatactg gttagtgagg 240  
tgagcctggc gctcttcttt gcgctgagct aaagctacat acaatggctt tgtggacctc 300  
ggccgcgacc acgctaagcc gaattccagc aactggcgg ccgttactag tggatccgag 360  
ctcggtacca agcttggcgt aatcatggtc atag 394

<210> 362  
<211> 268  
<212> DNA  
<213> Homo sapiens

<400> 362  
ctgcgcgtgg accagtcagc ttccgggtgt gactggagca gggcttgtcg tcttcttcag 60  
agtcactttg caggggttgg tgaagctgct cccatccatg tacagctccc agtctactga 120  
tgtttaagga tggctcgggt ggtaggccc actagaataa actgagtcca atacctctac 180  
acagttatgt ttaactgggc tctctgacac cgggaggaag gtggcggggg ttaggtgttg 240  
caaacttcaa tggttatgcg gggatgtt 268

<210> 363  
<211> 323  
<212> DNA  
<213> Homo sapiens

<400> 363  
ccttgacctt ttcagcaagt gggaagggtgt aatccgtctc cacagacaag gccaggactc 60  
gtttgtaccc gttgatgata gaatggggta ctgatgcaac agttgggtag ccaatctgca 120  
gacagacact ggcaacattg cggacaccct ccaggaagcg agaatgcaga gtttcctctg 180  
tgatatcaag cacttcaggg ttgtagatgc tgccattgtc gaacacctgc tggatgacca 240  
gccc aaagga gaagggggag atgttgagca tgttcagcag cgtggcttcg ctggctccca 300  
ctttgtctcc agtcttgatc aga 323

<210> 364  
<211> 393  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 29  
<223> n = A,T,C or G

<400> 364  
ccaagctctc catcgtcccc gtgcgcagng gctactgggg gaacaagatc ggcaagcccc 60  
aactgtccc ttgcaagggtg acaggccgct gcggctctgt gctggtacgc ctcatcactg 120

```

caccagggg cactggcatc gtctccgcac ctgtgcctaa gaagctgctc atgatggctg 180
gcatcgatga ctgctacacc tcagcccggg gctgcaactgc caccctgggc aacttcgcca 240
aggccacctt tgatgccatt tctaagacct acagctacct gacccccgac ctctggaagg 300
agactgtatt caccaagtct ccctatcagg agttcactga ccacctcgtc aagaccaca 360
ccagagtctc cgtgcagcgg actcaggctc cag
393

```

```

<210> 365
<211> 371
<212> DNA
<213> Homo sapiens

```

```

<400> 365
cctcctcaga gcggtagctg ttcttattgc cccggcagcc tccatagatg aagttattgc 60
aggagttcct ctccacgtca aagtaccagc gtgggaagga tgeacggcaa ggcccagtga 120
ctgcgttggc ggtgcagtat tcttcatagt tgaacatata gctggagtgg tcttcagaat 180
cctgccttct gggagcactt gggacagagg aatccgctgc attcctgctg gtggacctcg 240
gccgcgacca cgctaagccg aattccagca cactggcggc cgttactagt ggatccgagc 300
tcggtaccaaa gcttggcgta atcatgggtca tagctgtttc ctgtgtgaaa ttgttatccg 360
ctcacaaattc c
371

```

```

<210> 366
<211> 393
<212> DNA
<213> Homo sapiens

```

```

<400> 366
atttcttgcc agatgggagc tctttggtga agactccttt cgggaaaagt tttttggctt 60
ctttcttcagg gatggttggg aggaccatca cactatcccc atccttccaa tcaactgggg 120
tggaaccctt tttttctgct gtcagctgga gagagatgac taccctgaga atctcatcaa 180
agttcctgcc agtggtagct gggtagagga tagacagctt cagcttctta tcaggaccaa 240
aaacaaacac cacacgagct gccacaggca tgcccttttc atccttctct gctggatcca 300
gcatgcccaa caggatggca agctcccgat tcctatcatc gatgatggga aaaggtaact 360
tttctgtggg ctcttcacaa ttgtaagcat tga
393

```

```

<210> 367
<211> 327
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 34, 54, 55
<223> n = A,T,C or G

```

```

<400> 367
ccagctctgt ctcatacttg actctaaagt cttnagcagc aagacgggca ttgnnaatct 60
gcagaacgat gcgggcattg tccacagtat ttgcgaagat ctgagccctc aggtcctcga 120
tgatcttgaa gtaatggctc cagtctctga cctggggctc cttcttctcc aagtgtctcc 180
ggattttgct ctccagcctc cggttctcgg tctccaggct cctcactctg tccaggtaag 240
aggccaggcg gtcgttcagg ctttgcatgg tctccttctc gttctggatg cctcccatte 300
ctgccagacc cccggctatc ccggtgg
327

```

```

<210> 368
<211> 306
<212> DNA
<213> Homo sapiens

```

```

<220>

```



&lt;221&gt; misc\_feature

&lt;222&gt; 24

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 368

```

ctggagaagg acttcagcag tttnaagaag tactgccaaag tcatccgtgt cattgcccac 60
accagatgc gcttgcttcc tctgcgccag aagaaggccc acctgatgga gatccaggtg 120
aacggaggca ctgtggccga gaagctggac tgggcccgcg agaggcttga gcagcaggta 180
cctgtgaacc aagtgtttgg gcaggatgag atgatcgacg tcatcggggt gaccaagggc 240
aaaggctaca aaggggtcac cagtcgttgg cacaccaaga agctgccccg caagaccac 300
cgagga                                           306

```

&lt;210&gt; 369

&lt;211&gt; 394

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 369

```

tcgaccaca ccggaacacg gagagctggg ccagcattgg cacttgatag gatttcccgt 60
cggctgcac gaaagtgcgt ttctttgtgt tctcgggttg gaaccgtgat ttccacagac 120
ccttgaata cactgcgttg acgaggacca gtctggtag cacaccatca ataagatctg 180
gggacagcag attgtcaatc atatccctgg ttccattttt aacctatgca ttgatggaat 240
cacaggcaga ggctggatcc tcaaagttca cattccggac ctcaactgg aacacatctt 300
tgttccttgt aacaaaaggc acttcaattt cagaggcatt cttaacaaac acggcggttag 360
ccactgtcac aatgtcttta ttcttcttgg agac                                           394

```

&lt;210&gt; 370

&lt;211&gt; 653

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 370

```

ccaccacacc caattccttg ctggtatcat ggcagccgcc acgtgccagg attacggct 60
acatcatcaa gtatgagaag cctgggtctc ctcccagaga agtgggtccct cggccccgcc 120
ctggtgtcac agaggctact attactggcc tggaaccggg aaccgaatat acaatttatg 180
tcattgccct gaagaataat cagaagagcg agccccgat tggaaggaaa aagacagacg 240
agcttccccca actgtaacc ctccacacc ccaatcttca tggaccagag atcttggatg 300
ttccttccac agttcaaaag acccctttcg tcaccacccc tgggtatgac actggaaatg 360
gtattcagct tcctggcact tctggtcagc aaccagtggt tgggcaacaa atgatctttg 420
aggaacatgg ttttaggcgg accacaccgc ccacaacggc caccacctata aggcataaggc 480
caagaccata cccgccgaat gtaggacaag aagctctctc tcagacaacc atctcatggg 540
ceccattcca ggacacttct gagtacatca tttcatgtca tcctgttggc actgatgaag 600
aacccttaca gttcagggtt cctggaactt ctaccagtgc cactctgaca gga                                           653

```

&lt;210&gt; 371

&lt;211&gt; 268

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 371

```

ctgcccagcc ccatttggcg agtttgagaa ggtgtgcagc aatgacaaca agaccttcga 60
ctcttcttgc cacttctttg ccacaaagtg caccctggag ggcaccaaga agggccacaa 120
gctccacctg gactacatcg ggccttgcaa atacatcccc ccttgccctgg actctgagct 180
gaccgaattc ccctgcgca tgcgggactg gctcaagaac gtccctgttca ccctgtatga 240
gagggatgag gacaacaacc ttctgact                                           268

```

&lt;210&gt; 372

&lt;211&gt; 392

<212> DNA  
<213> Homo sapiens

<400> 372  
gctggtgccc ctggtgaacg tggacctcct ggattggcag gggccccagg acttagaggt 60  
ggaaactggtc cccctgggtc cgaaggagga aagggtgctg ctggctcctc tgggccacct 120  
ggtgctgctg gtactcctgg tctgcaagga atgcctggag aaagaggagg tcttggaagt 180  
cctggtccaa agggtgacaa ggggaacca ggcgtccag gtgctgatgg tgtcccaggg 240  
aaagatggcc caaggggtcc tactggtcct attggtcctc ctggcccagc tggccagcct 300  
ggagataagg gtgaagggtg tgcccccgga cttccaggta tagctggacc tcgtggtagc 360  
cctggtgaga gaggtgaaac ctggccgcg ac 392

<210> 373  
<211> 388  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 30  
<223> n = A,T,C or G

<400> 373  
ccaagcgctc agatcgga ggggcaccan ttttgatctg ccagtgac agccccacaa 60  
ccaggtcagc gatgaaggta tcttcagtct cccccaagc atgagacacc atgacgccc 120  
aaccattggc ctgggccagc ttgcagcct gaagagactc ggtcacggag ccaatctggt 180  
tgactttgag caggaggcag ttgcaggact tctcgttcac ggccttggcg atcctctttg 240  
ggttggtcac tgtgagatca tccccacta cctggattcc tgactggct gtgaacttct 300  
gccaagctcc ccagtcaccc tggtaaagg gatcttcgat agacaccact gggtagtcc 360  
tgatgaagga cttgtacagg tcagccag 388

<210> 374  
<211> 393  
<212> DNA  
<213> Homo sapiens

<400> 374  
ctgacgaccg cgtgaacccc tgcattgggg gtgtcatcct cttccatgag acactctacc 60  
agaaggcgga tgatgggctg ccctccccc aagtatcaa atccaagggc ggtgttgtgg 120  
gcatcaaggt agacaagggc gtggtccccc tggcaggagc aaatggcgag actaccacc 180  
aagggttga tgggctgtct gagcgtgtg cccagtaca gaaggacgga gctgacttcg 240  
ccaagtggcg ttgtgtgctg aagattgggg aacacacccc ctgagccctc gccatcatgg 300  
aaaatgccaa tgttctggcc cgttatgcca gtatctgcca gcagaatggc attgtgcca 360  
tcgtggagcc tgagatcctc cctgatggg acc 393

<210> 375  
<211> 394  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 30, 33  
<223> n = A,T,C or G

<400> 375  
ccacaaatgg cgtgggtccat gtcatcaccn ttnttctgca gcctccagcc aacagacctc 60  
aggaaagagg ggatgaactt gcagactctg cgcttgagat cttcaaaca gcatcagcgt 120

116

```

tttccagggc ttccagaggg tctgtgcgac tagccctgt ctatcaaaag ttattagaga 180
ggatgaagca ttagcttgaa gcactacagg aggaatgcac caccgcagct ctccgccaat 240
ttctctcaga ttccacaga gactgtttga atgttttcaa aaccaagtat cacactttaa 300
tgtacatggg ccgcaccata atgagatgtg agccttgtgc atgtggggga ggagggagag 360
agatgtactt tttaaatcat gttcccccta aaca 394

```

&lt;210&gt; 376

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 30

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 376

```

ctgcccagcc cccattggcg agtttgattn ggtgtgcagc aatgacaaca agaccttcga 60
ctcttcctgc cacttctttg ccacaaagtg caccctggag ggcaccaaga agggccacaa 120
gtccacctg gactacatcg ggccttgcaa atacatcccc ccttgectgg actctgagct 180
gaccgaattc cccctgcgca tgcgggactg gctcaagaac gtcctggtca ccctgtatga 240
gagggatgag gacaacaacc ttctgactga gaagcagaag ctgcgggtga agaagatcca 300
tgagaatgag aagcgcttg aggcaggaga ccaccccggt gagctgctgg cccgggactt 360
cgagaagaac tataacatgt acatcttccc tg 392

```

&lt;210&gt; 377

&lt;211&gt; 292

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 377

```

caatgtttga tgcttaaccc ccccaatttc tgtgagatgg atggccagtg caagcgtgac 60
ttgaagtgtt gcatgggcat gtgtgggaaa tctgcgttt cccctgtgaa agcttgatc 120
ctgccatatg gaggaggctc tggagtcctg ctctgtgtgg tccaggtcct ttccaccctg 180
agacttggct ccaccactga tatctcctt tggggaaagg cttggcacac agcaggcttt 240
caagaagtgc cagttgatca atgaataaat aaacgagcct atttctcttt gc 292

```

&lt;210&gt; 378

&lt;211&gt; 395

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 378

```

ctgctgcttc agcgaagggt ttctggcata tccaatgata aggctgcaa agactgttcc 60
aataccagca ccagaaccag ccactcctac tggtgcagca cctgcaccaa taaatttggc 120
agcagtatca atgtctctgc tgattgcaact ggtctgaaac tccctttgga ttagctgaga 180
cacaccattc tgggcctga ttttcctaag atagaactcc aactctttgc cctctagcac 240
atagccatct gctcgccac actgtcccgg ccttgaagcg atgcacgcaa gaagcttgcc 300
ctgctggaac tgctcctcca ggagactgct gattttggca ttctttttcc ttcatcata 360
tttcttctga attttttaga tcgtttttt tttaa 395

```

&lt;210&gt; 379

&lt;211&gt; 223

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 379

```

ccagatgaaa tgctgccgca atggctgtgg gaaggtgtcc tgtgtcactc ccaatttctg 60

```

```

agctccagcc accaccaggc tgagcagtga ggagagaaag tttctgcctg gccctgcac 120
tggttccagc ccacctgccc tcccctttt cgggactctg tattccctct tgggctgacc 180
acagcttctc ctttcccaa ccaataaagt aaccactttc agc 223

```

```

<210> 380
<211> 317
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 30, 32
<223> n = A,T,C or G

```

```

<400> 380
tcgaccacag tattccaacc ctctgtgcn tngagaagt atggagggtg ctgacaacca 60
gggtgcagga gaacaaggta gaccagttag gcagaatatg tatcggggat atagaccacg 120
attccgcagg ggccctcctc gccaaagaca gcctagagag gacggcaatg aagaagataa 180
agaaaaatca ggagatgaga cccaaggta gcagccacct caacgtcggg accgccgcaa 240
cttcaattac cgacgcagac gccagaaaa ccctaaacca caagatggca aagagacaaa 300
agcagccgat ccaccag 317

```

```

<210> 381
<211> 392
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 29, 30, 31
<223> n = A,T,C or G

```

```

<400> 381
cctgaaggaa gagctggcct acctgaatnn naaccatgag gaggaaatca gtacgctgag 60
gggccaagtg ggaggccagg tcagtgtgga ggtggattcc gctccgggca ccgatctcgc 120
caagatcctg agtgacatgc gaagccaata tgaggatcat gccgagcaga accggaagga 180
tgctgaagcc tggttcacca gccggactga agaattgaac cgggaggtcg ctggccacac 240
ggagcagctc cagatgagca ggtccgaggt tactgacctg cggcgcaccc ttcagggtct 300
tgagattgag ctgcagtcac agacctcggc cgcgaccacg ctaagccgaa ttccagcaca 360
ctggcgcccg ttactagtgg atccgagctc gg 392

```

```

<210> 382
<211> 234
<212> DNA
<213> Homo sapiens

```

```

<400> 382
cctcgatgtc taaatgagcg tggtaaagga tgggtgcctgc tgggggtctcg tagatacctc 60
gggacttcat tccaatgaag cggttctcca cgatgtcaat acggcccacg ccatgcttgc 120
ccgcgacttc gttcaggtag atgaagagct ccaaggaggt ctggtgggtg gtgccatcct 180
tgacgttggg caccttcaca gggaccctt ttttgaactc catctccaga atgt 234

```

```

<210> 383
<211> 396
<212> DNA
<213> Homo sapiens

```

```

<220>

```

&lt;221&gt; misc\_feature

&lt;222&gt; 66

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 383

```

ccttgacctt ttcagcaagt ggggaaggtgt tttccgtctc cacagacaag gccaggactc 60
gtttgnaccc gttgatgata gaatggggtg ctgatgcaac agttgggtag ccaatctgca 120
gacagacact ggcaacattg cggacaccca ggatttcaat ggtgccctg gagattttag 180
tggtgatacc taaagcctgg aaaaaggagg tcttctcggg cccgagacca gtgttctggg 240
ctggcacagt gacttcacat ggggcaatgg caccagcacg ggcagcagac ctgcccgggc 300
ggccgctcga aagccgaatt ccagcacact ggcgccgctt actagtggat ccgagctcgg 360
taccaagctt ggcgtaatca tggtcatagc tgtttc 396

```

&lt;210&gt; 384

&lt;211&gt; 396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 384

```

gctgaatagg cacagagggc acctgtacac cttcagacca gtctgcaacc tcaggctgag 60
tagcagtga ctcaggagcg ggagcagtc attcaccctg aaattcctcc ttgggtcactg 120
ccttctcagc agcagcctgc tcttctttt caatctcttc aggatctctg tagaagtaca 180
gatcaggcat gacctcccat ggggtgtcac gggaaatggg gccacgcatg cgcagaactt 240
cccgagccag catccaccac atcaaaccac ctgagtgagc tcccttggtg ttgcatggga 300
tggaatgtc cacatagcgc agaggagaat ctgtgttaca cagcgcaatg gtaggtaggt 360
taacataaga tgccctccgtg agaggctggg ggtcag 396

```

&lt;210&gt; 385

&lt;211&gt; 2943

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 385

```

cagccaccgg agtggatgcc atctgcaccc accgccctga cccacaggc cctgggctgg 60
acagagagca gctgtatttg gagctgagcc agctgaccca cagcatcact gagctgggcc 120
cctacadcct ggacagggac agtctctatg tcaatggttt cacacagcgg agctctgtgc 180
ccaccactag ccttctggg acccccacag tggacctggg aacatctggg actccagttt 240
ctaaacctgg tccctcggt gccagccctc tcctggtgct attcactctc aacttcacca 300
tcaccaacct gcggtatgag gagaacatgc agcaccctgg ctccaggaag ttcaacacca 360
cggagagggg ccttcagggc ctgggtccctg ttcaagagca ccagtgttg ccctctgtac 420
tctggctgca gactgacttt gctcaggcct gaaaaggatg ggacagccac tggagtggat 480
gccatctgca cccaccaccc tgaccccaaa agccctaggc tggacagaga gcagctgtat 540
tggaagctga gccagctgac ccacaatatc actgagctgg gccctatgc cctggacaac 600
gacagcctct ttgtcaatgg tttcactcat cggagctctg tgtccaccac cagcactcct 660
gggaccccca cagtgtatct gggagcatct aagactccag cctcgatatt tggcccttca 720
gctgccagcc atctctgat actattcacc ctcaacttca ccatcactaa cctgcggtat 780
gaggagaaca tgtggcctgg ctccaggaag ttcaacacta cagagagggg ccttcagggc 840
ctgctaaggc ccttggtcaa gaacaccagt gttggccctc tgtactctgg ctgcaggctg 900
accttgctca ggccagagaa agatggggaa gccaccggag tggatgccat ctgcaccac 960
cgccctgacc ccacaggccc tgggctggac agagagcagc tgtatttga gctgagccag 1020
ctgaccaca gcatcactga gctgggcccc tacacactgg acagggacag tctctatgtc 1080
aatggtttca cccctcggag ctctgtacc accaccagca ccggggtggg cagcaggagg 1140
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ggctccctca agttcaacat cacagacaac gtcatgaagc acctgctcag tcccttgttc 1260
cagaggagca gcctgggtgc acggtacaca ggctgcaggg tcatcgact aaggtctgtg 1320
aagaacggtg ctgagacacg ggtggacctc ctctgcacct acctgcagcc cctcagcggc 1380
ccaggtctgc ctatcaagca ggtgttccat gagctgagcc agcagacca tggcatcacc 1440
cggctggggc cctactctct ggacaaagac agcctctacc ttaacggtta caatgaacct 1500

```

```

ggtccagatg agcctcctac aactcccaag ccagccacca cattcctgcc tctctgtca 1560
gaagccacaa cagccatggg gtaccacctg aagaccctca cactcaactt caccatctcc 1620
aatctccagt attcaccaga tatgggcaag ggctcagcta cattcaactc caccgagggg 1680
gtccttcagc acctgtcag acccttggtc cagaagagca gcatggggcc cttctacttg 1740
ggttgccaac tgatctccct caggcctgag aaggatgggg cagccactgg tgtggacacc 1800
acctgacct accaccctga ccctgtgggc cccgggctgg acatacagca gctttactgg 1860
gagctgagtc agctgaccca tgggtgcacc caactgggct tctatgtcct ggacagggat 1920
agcctcttca tcaatggcta tgcacccag aatttatcaa tccggggcga gtaccagata 1980
aatttcaca ttgtcaactg gaacctcagt aatccagacc ccacatcctc agagtacatc 2040
acctgaactga gggacatcca ggacaaggtc accacactct acaaaggcag tcaactacat 2100
gacacattcc gcttctgcct ggtcaccaac ttgacgatgg actccgtgtt ggctactgtc 2160
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acagaaatgg agtcatcagt ttatcaacca acaagcagct ccagcacca gcactttac 2340
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aattaccaga ggaacaaaag gaatatgag gatcgggcac cacaccgggg tggactccct 2460
gtgtaacttc tgcgactgg ctcgagagt accacagatt gccatctatg aggaatttct 2520
gcggatgacc cggaatggta cccagctgca gaacttcacc ctggacagga gcagtgtcct 2580
tgtggatggg tattttccca acagaaatga gcccttaact gggaattctg accttccctt 2640
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cgggtgcctg gtgaccaccc gccggcggaa gaagggaagga gaatacaacg tccagcaaca 2760
gtgccaggc tactaccagt cacacctaga cctggaggat ctgcaatgac tggaaactgc 2820
cggtgcttg gggtgccttc cccagccag ggtccaaaga agcttggtg gggcagaaat 2880
aaaccatatt ggtcggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2940
aaa

```

<210> 386  
 <211> 2608  
 <212> DNA  
 <213> Homo sapiens

```

<400> 386
gttcaagagc accagtgttg gccctctgta ctctggctgc agactgactt tgetcaggcc 60
tgaaaaggat gggacagcca ctggagtggg tgccatctgc acccaccacc ctgaccccaa 120
aagccctagg ctggacagag agcagctgta ttgggagctg agccagctga cccacaatat 180
cactgagctg ggccctatg ccctggacaa cgacagcctc tttgtcaatg gtttactca 240
tcggagctct gtgtccacca ccagactcc tgggaccccc acagtgtatc tgggagcatc 300
taagactcca gctcgatat ttggcccttc agctgccagc catctcctga tactattcac 360
cctcaacttc accatcacta acctgcggtg tgaggagaac atgtggcctg gctccaggaa 420
gttcaacact acagagaggg tcttcaggg cctgctaagg cccttgttca agaaccaccg 480
tgttggccct ctgtactctg gctgcaggct gaccttgctc aggccagaga aagatgggga 540
agccaccgga gtggatgcca tctgcaccca ccgccctgac cccacaggcc ctgggctgga 600
cagagagcag ctgtatttgg agctgagcca gctgaccac agcatcactg agctggggcc 660
ctacacactg gacagggaca gtctctatgt caatggtttc acccatcgga gctctgtacc 720
caccaccagc accggggtgg tcagcgagga gccattcaca ctgaacttca ccatcaacaa 780
cctgcgctac atggcggaaca tgggccaacc cggctccctc aagttcaaca tcacagacaa 840
cgtcatgaag cacctgctca gtctttgtt ccagaggagc agcctgggtg cacggtacac 900
aggctgcagg gtcatgcac taaggctctg gaagaacggg gctgagacac ggggtggacct 960
cctctgcacc tacttgcagc ccctcagcgg cccaggtctg cctatcaagc aggtgttcca 1020
tgagctgagc cagcagaccc atggcatcac ccggctgggc ccctactctc tggacaaaga 1080
cagcctctac cttaacggtt acaatgaacc tgggtccagat gagcctccta caactcccaa 1140
gccagccacc acattcctgc ctctctgtc agaagccaca acagccatgg ggtaccacct 1200
gaagaccctc aactcaact tcaccatctc caatctccag tattcaccag atatgggcaa 1260
gggctcagct acattcaact ccaccgaggg ggtccttcag cacctgctca gaccttgtt 1320
ccagaagagc agcatgggac cttctactt ggggttgcaa ctgatctccc tcaggcctga 1380
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ccccgggctg gacatacagc agctttactg ggagctgagt cagctgaccc atggtgtcac 1500
ccaactgggc ttctatgtcc tggacaggga tagcctcttc atcaatggct atgcacccca 1560

```

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gaatttatca atccggggcg agtaccagat aaatttccac attgtcaact ggaacctcag 1620
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cagcctggtg gagcaagtct ttctagataa gaccctgaat gcctcattcc attggctggg 1860
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ctggggtgcc ttccccag ccagggtcca aagaagcttg gctggggcag aaataacca 2580
tattggtcgg acacaaaaaa aaaaaaaa 2608

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&lt;210&gt; 387

&lt;211&gt; 1761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 387

```

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gctgagacac ggggtggacct cctctgcagg taggtgcaga ggaggtccac ggcatcacc 240
ggctgggccc ctactctctg gacaaagaca gcctctacct taacgtccc aagccagcca 300
ccacattcct gcctcctctg tcagaagcca caacagccat ggggtaccac ctgaagacc 360
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cctttcccc agccagggtc caaagaagct tggctggggc agaaataaac catattgggtc 1740
ggacacaaaa aaaaaaaaaa a 1761

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&lt;210&gt; 388

&lt;211&gt; 772

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 388

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Met | Val | Ser | His | Ser | Gly | Ala | Leu | Cys | Pro | Pro | Leu | Ala | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gly | Pro | Pro | Gln | Trp | Thr | Trp | Glu | His | Leu | Gly | Leu | Gln | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Leu | Val | Pro | Arg | Leu | Pro | Ala | Leu | Ser | Trp | Cys | Tyr | Ser | Leu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ser | Pro | Ser | Pro | Thr | Cys | Gly | Met | Arg | Arg | Thr | Cys | Ser | Thr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Pro | Gly | Ser | Ser | Thr | Pro | Arg | Arg | Gly | Ser | Phe | Arg | Ala | Trp | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Phe | Lys | Ser | Thr | Ser | Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Leu | Leu | Arg | Pro | Glu | Lys | Asp | Gly | Thr | Ala | Thr | Gly | Val | Asp | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Cys | Thr | His | His | Pro | Asp | Pro | Lys | Ser | Pro | Arg | Leu | Asp | Arg | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gln | Leu | Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr | His | Asn | Ile | Thr | Glu | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Pro | Tyr | Ala | Leu | Asp | Asn | Asp | Ser | Leu | Phe | Val | Asn | Gly | Phe | Thr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Arg | Ser | Ser | Val | Ser | Thr | Thr | Ser | Thr | Pro | Gly | Thr | Pro | Thr | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Leu | Gly | Ala | Ser | Lys | Thr | Pro | Ala | Ser | Ile | Phe | Gly | Pro | Ser | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ser | His | Leu | Leu | Ile | Leu | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Thr | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Arg | Tyr | Glu | Glu | Asn | Met | Trp | Pro | Gly | Ser | Arg | Lys | Phe | Asn | Thr |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Thr | Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Arg | Pro | Leu | Phe | Lys | Asn | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr | Leu | Leu | Arg | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Lys | Asp | Gly | Glu | Ala | Thr | Gly | Val | Asp | Ala | Ile | Cys | Thr | His | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Asp | Pro | Thr | Gly | Pro | Gly | Leu | Asp | Arg | Glu | Gln | Leu | Tyr | Leu | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Ser | Gln | Leu | Thr | His | Ser | Ile | Thr | Glu | Leu | Gly | Pro | Tyr | Thr | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Arg | Asp | Ser | Leu | Tyr | Val | Asn | Gly | Phe | Thr | His | Arg | Ser | Ser | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Thr | Thr | Ser | Thr | Gly | Val | Val | Ser | Glu | Glu | Pro | Phe | Thr | Leu | Asn |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Phe | Thr | Ile | Asn | Asn | Leu | Arg | Tyr | Met | Ala | Asp | Met | Gly | Gln | Pro | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Leu | Lys | Phe | Asn | Ile | Thr | Asp | Asn | Val | Met | Lys | His | Leu | Leu | Ser |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Pro | Leu | Phe | Gln | Arg | Ser | Ser | Leu | Gly | Ala | Arg | Tyr | Thr | Gly | Cys | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Ile | Ala | Leu | Arg | Ser | Val | Lys | Asn | Gly | Ala | Glu | Thr | Arg | Val | Asp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Leu | Cys | Thr | Tyr | Leu | Gln | Pro | Leu | Ser | Gly | Pro | Gly | Leu | Pro | Ile |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Gln | Val | Phe | His | Glu | Leu | Ser | Gln | Gln | Thr | His | Gly | Ile | Thr | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |



Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr  
 435 440 445  
 Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr  
 450 455 460  
 Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His  
 465 470 475 480  
 Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser  
 485 490 495  
 Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val  
 500 505 510  
 Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro  
 515 520 525  
 Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly  
 530 535 540  
 Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val  
 545 550 555 560  
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu  
 565 570 575  
 Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser  
 580 585 590  
 Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu  
 595 600 605  
 Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp  
 610 615 620  
 Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys  
 625 630 635 640  
 Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe  
 645 650 655  
 Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys  
 660 665 670  
 Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe  
 675 680 685  
 Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr  
 690 695 700  
 Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln  
 705 710 715 720  
 Pro Thr Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile  
 725 730 735  
 Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn  
 740 745 750  
 Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Ala Pro His Arg Gly  
 755 760 765  
 Gly Leu Pro Val  
 770

&lt;210&gt; 389

&lt;211&gt; 833

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 389

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
 1 5 10 15  
 Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile  
 20 25 30  
 Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln  
 35 40 45

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly  
 50 55 60  
 Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His  
 65 70 75 80  
 Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr  
 85 90 95  
 Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala  
 100 105 110  
 Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu  
 115 120 125  
 Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr  
 130 135 140  
 Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser  
 145 150 155 160  
 Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu  
 165 170 175  
 Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro  
 180 185 190  
 Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu  
 195 200 205  
 Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp  
 210 215 220  
 Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro  
 225 230 235 240  
 Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe  
 245 250 255  
 Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser  
 260 265 270  
 Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro  
 275 280 285  
 Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val  
 290 295 300  
 Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu  
 305 310 315 320  
 Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys  
 325 330 335  
 Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu  
 340 345 350  
 Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn  
 355 360 365  
 Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr  
 370 375 380  
 Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu  
 385 390 395 400  
 Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro  
 405 410 415  
 Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu  
 420 425 430  
 Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe  
 435 440 445  
 Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala  
 450 455 460  
 Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly  
 465 470 475 480  
 Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr  
 485 490 495  
 His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu  
 500 505 510

Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr  
 515 520 525  
 Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro  
 530 535 540  
 Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val  
 545 550 555 560  
 Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys  
 565 570 575  
 Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala  
 580 585 590  
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 595 600 605  
 Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln  
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 660 665 670  
 Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg  
 675 680 685  
 Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe  
 690 695 700  
 Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn  
 705 710 715 720  
 Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu  
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 Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu  
 740 745 750  
 Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn Glu  
 755 760 765  
 Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu Ile  
 770 775 780  
 Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val  
 785 790 795 800  
 Leu Val Thr Thr Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln  
 805 810 815  
 Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu  
 820 825 830  
 Gln

<210> 390  
 <211> 438  
 <212> PRT  
 <213> Homo sapiens

<400> 390  
 Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn  
 1 5 10 15  
 Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser  
 20 25 30  
 Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser  
 35 40 45  
 Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro  
 50 55 60

125

Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His  
 65 70 75 80  
 Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu  
 85 90 95  
 Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu  
 100 105 110  
 Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser  
 115 120 125  
 Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu  
 130 135 140  
 Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp  
 145 150 155 160  
 Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp  
 165 170 175  
 Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu  
 180 185 190  
 Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val  
 195 200 205  
 Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu  
 210 215 220  
 Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser  
 225 230 235 240  
 Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu  
 245 250 255  
 Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro  
 260 265 270  
 Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu  
 275 280 285  
 Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys  
 290 295 300  
 Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val  
 305 310 315 320  
 Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val  
 325 330 335  
 Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu  
 340 345 350  
 Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe  
 355 360 365  
 Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp  
 370 375 380  
 Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys  
 385 390 395 400  
 Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly  
 405 410 415  
 Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu  
 420 425 430  
 Asp Leu Glu Asp Leu Gln  
 435

&lt;210&gt; 391

&lt;211&gt; 2627

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 391

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caaggacaat gactgcttga attgagccct tgaggaatga agctttgaag gaaaagaata 2460
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<210> 392  
 <211> 309  
 <212> PRT  
 <213> Homo sapiens

<400> 392  
 His Ala Ser Ala His Ala Ser Gly Arg Gln Arg Gln Leu His Ser Ala  
 1 5 10 15  
 Ser Thr Gln Ile Arg Trp Glu Pro Ser Pro Ala Met Ala Ser Leu Gly  
 20 25 30  
 Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile Ile Leu Ala Gly  
 35 40 45  
 Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser Gly Arg His Ser Ile  
 50 55 60  
 Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile Gly Glu Asp Gly Ile

```

65          70          75          80
Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile Val Ile
      85          90          95
Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val His Glu Phe Lys Glu
      100        105        110
Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr
      115        120        125
Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu
      130        135        140
Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile
      145        150        155        160
Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala
      165        170        175
Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr
      180        185        190
Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp
      195        200        205
Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr
      210        215        220
Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val
      225        230        235        240
Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn
      245        250        255
Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val Thr Glu Ser Glu Ile
      260        265        270
Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser Lys Ala Ser Leu Cys
      275        280        285
Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu Leu Pro Leu Ser Pro
      290        295        300
Tyr Leu Met Leu Lys
305

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&lt;210&gt; 393

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 393

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Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
1      5      10      15
Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
      20      25      30
Gly Arg His Ser Ile Thr Val Thr Val Ala Ser Ala Gly Asn Ile
      35      40      45
Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
      50      55      60
Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
      65      70      75      80
His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
      85      90      95
Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
      100     105     110
Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
      115     120     125
Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
      130     135     140
Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn

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128

|                     |                     |                 |         |     |  |     |
|---------------------|---------------------|-----------------|---------|-----|--|-----|
| 145                 |                     | 150             |         | 155 |  | 160 |
| Ala Ser Ser Glu Thr | Leu Arg Cys Glu Ala | Pro Arg Trp Phe | Pro Gln |     |  |     |
|                     | 165                 | 170             | 175     |     |  |     |
| Pro Thr Val Val Trp | Ala Ser Gln Val Asp | Gln Gly Ala Asn | Phe Ser |     |  |     |
|                     | 180                 | 185             | 190     |     |  |     |
| Glu Val Ser Asn Thr | Ser Phe Glu Leu Asn | Ser Glu Asn Val | Thr Met |     |  |     |
|                     | 195                 | 200             | 205     |     |  |     |
| Lys Val Val Ser Val | Leu Tyr Asn Val Thr | Ile Asn Asn Thr | Tyr Ser |     |  |     |
|                     | 210                 | 215             | 220     |     |  |     |
| Cys Met Ile Glu Asn | Asp Ile Ala Lys Ala | Thr Gly Asp Ile | Lys Val |     |  |     |
|                     | 225                 | 230             | 235     |     |  | 240 |
| Thr Glu Ser Glu Ile | Lys Arg Arg Ser His | Leu Gln Leu Leu | Asn Ser |     |  |     |
|                     | 245                 | 250             | 255     |     |  |     |
| Lys Ala Ser Leu Cys | Val Ser Ser Phe Phe | Ala Ile Ser Trp | Ala Leu |     |  |     |
|                     | 260                 | 265             | 270     |     |  |     |
| Leu Pro Leu Ser Pro | Tyr Leu Met Leu     | Lys             |         |     |  |     |
|                     | 275                 | 280             |         |     |  |     |

<210> 394  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 394  
 Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile  
 1 5 10 15  
 Ile Ile Leu Ala  
 20

<210> 395  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 395  
 Ile Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile  
 1 5 10 15  
 Ser Gly Arg His  
 20

<210> 396  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 396  
 Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly  
 1 5 10 15  
 Asn Ile Gly Glu  
 20

<210> 397  
 <211> 20  
 <212> PRT

<213> Homo sapiens

<400> 397

Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp  
 1 5 10 15  
 Ile Lys Leu Ser  
 20

<210> 398

<211> 20

<212> PRT

<213> Homo sapiens

<400> 398

Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val  
 1 5 10 15  
 Leu Gly Leu Val  
 20

<210> 399

<211> 20

<212> PRT

<213> Homo sapiens

<400> 399

Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser  
 1 5 10 15  
 Glu Gln Asp Glu  
 20

<210> 400

<211> 20

<212> PRT

<213> Homo sapiens

<400> 400

Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala Asp  
 1 5 10 15  
 Gln Val Ile Val  
 20

<210> 401

<211> 20

<212> PRT

<213> Homo sapiens

<400> 401

Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val Gln  
 1 5 10 15  
 Leu Thr Asp Ala  
 20

<210> 402



130

<211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 402  
 Val Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser  
 1 5 10 15  
 Lys Gly Lys Gly Asn  
 20

<210> 403  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 403  
 Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe Ser  
 1 5 10 15  
 Met Pro Glu Val  
 20

<210> 404  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 404  
 Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr Leu  
 1 5 10 15  
 Arg Cys Glu Ala  
 20

<210> 405  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 405  
 Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp  
 1 5 10 15  
 Ala Ser Gln Val  
 20

<210> 406  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 406  
 Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn  
 1 5 10 15  
 Thr Ser Phe Glu  
 20

<210> 407  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 407  
 Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys Val Val  
 1 5 10 15  
 Ser Val Leu Tyr  
 20

<210> 408  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 408  
 Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys Met  
 1 5 10 15  
 Ile Glu Asn Asp  
 20

<210> 409  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 409  
 Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val Thr  
 1 5 10 15  
 Glu Ser Glu Ile  
 20

<210> 410  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 410  
 Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser  
 1 5 10 15  
 Lys Ala Ser Leu  
 20

<210> 411  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 411  
 Ser Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala  
 1 5 10 15  
 Leu Leu Pro Leu

20

<210> 412  
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 <212> PRT  
 <213> Homo sapiens

<400> 412  
 Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu Leu Pro Leu Ser Pro Tyr  
 1 5 10 15  
 Leu Met Leu Lys  
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<210> 413  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<400> 413  
 Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly  
 1 5 10 15  
 Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile  
 20 25 30  
 Lys Leu Ser  
 35

<210> 414  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<400> 414  
 Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser  
 1 5 10 15  
 Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln  
 20 25 30  
 Val Ile Val  
 35

<210> 415  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
 Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe Ser  
 1 5 10 15  
 Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr Leu Arg  
 20 25 30  
 Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp Ala Ser  
 35 40 45  
 Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr Ser Phe  
 50 55 60  
 Glu

65

<210> 416  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 416  
Lys Leu Ser Asp Ile Val Ile Gln Trp Leu  
1 5 10

<210> 417  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 417  
Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile  
1 5 10

<210> 418  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 418  
Leu Leu Asn Ser Lys Ala Ser Leu Cys Val  
1 5 10

<210> 419  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 419  
Ser Leu Cys Val Ser Ser Phe Phe Ala Ile  
1 5 10

<210> 420  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 420  
Val Leu Tyr Asn Val Thr Ile Asn Asn Thr  
1 5 10

<210> 421  
<211> 10  
<212> PRT  
<213> Homo sapiens

134

&lt;400&gt; 421

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Phe | Trp | Ser | Ile | Ile | Ser | Ile | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

&lt;210&gt; 422

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 422

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Pro | Leu | Ser | Pro | Tyr | Leu | Met | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

&lt;210&gt; 423

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 423

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Met | Ile | Glu | Asn | Asp | Ile | Ala | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

&lt;210&gt; 424

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 424

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Gly | Ala | Phe | Ser | Met | Pro | Glu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

&lt;210&gt; 425

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 425

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Leu | Leu | Pro | Leu | Ser | Pro | Tyr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

&lt;210&gt; 426

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 426

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Leu | Ala | Gly | Ala | Ile | Ala | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

&lt;210&gt; 427

&lt;211&gt; 10

&lt;212&gt; PRT

<213> Homo sapiens

<400> 427

Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys  
1 5 10

<210> 428

<211> 10

<212> PRT

<213> Homo sapiens

<400> 428

Ala Leu Leu Pro Leu Ser Pro Tyr Leu Met  
1 5 10

<210> 429

<211> 10

<212> PRT

<213> Homo sapiens

<400> 429

Gln Leu Leu Asn Ser Lys Ala Ser Leu Cys  
1 5 10

<210> 430

<211> 10

<212> PRT

<213> Homo sapiens

<400> 430

Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile  
1 5 10

<210> 431

<211> 10

<212> PRT

<213> Homo sapiens

<400> 431

Trp Leu Lys Glu Gly Val Leu Gly Leu Val  
1 5 10

<210> 432

<211> 10

<212> PRT

<213> Homo sapiens

<400> 432

Leu Gln Leu Leu Asn Ser Lys Ala Ser Leu  
1 5 10

<210> 433

136

<211> 10  
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<400> 433  
Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile  
1 5 10

<210> 434  
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<212> PRT  
<213> Homo sapiens

<400> 434  
Gly Ile Ser Gly Arg His Ser Ile Thr Val  
1 5 10

<210> 435  
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<213> Homo sapiens

<400> 435  
Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile  
1 5 10

<210> 436  
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<212> PRT  
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<400> 436  
Ala Leu Leu Pro Leu Ser Pro Tyr Leu  
1 5

<210> 437  
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<400> 437  
Ser Leu Cys Val Ser Ser Phe Phe Ala  
1 5

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<400> 438  
Ile Leu Phe Trp Ser Ile Ile Ser Ile  
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Gln Leu Leu Asn Ser Lys Ala Ser Leu  
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<400> 440  
Lys Val Val Ser Val Leu Tyr Asn Val  
1 5

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<400> 441  
Ile Leu Ala Gly Ala Ile Ala Leu Ile  
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<400> 442  
Trp Leu Lys Glu Gly Val Leu Gly Leu  
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<400> 443  
Ile Ile Leu Ala Gly Ala Ile Ala Leu  
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<400> 444  
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1 5

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<400> 445  
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<212> PRT  
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<400> 447  
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<212> PRT  
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<400> 449  
Val Ile Gln Trp Leu Lys Glu Gly Val  
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<210> 450  
<211> 9  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 450

Ala Ile Ser Trp Ala Leu Leu Pro Leu  
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&lt;210&gt; 451

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 451

Ser Leu Gly Gln Ile Leu Phe Trp Ser  
1 5

&lt;210&gt; 452

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 452

Ile Ala Leu Ile Ile Gly Phe Gly Ile  
1 5

&lt;210&gt; 453

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 453

Cys Thr Phe Glu Pro Asp Ile Lys Leu  
1 5

&lt;210&gt; 454

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 454

Ile Val Gly Asn Ala Ser Leu Arg Leu  
1 5

&lt;210&gt; 455

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 455

Gly Gln Ile Leu Phe Trp Ser Ile Ile  
1 5

&lt;210&gt; 456

&lt;211&gt; 3447

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 456

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<211> 3557

<212> DNA

<213> Homo sapiens

<400> 457

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 cctgatacct ccacaatgca cctggcaacc tcgagaactc cagcctccct gtctggacct 360  
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&lt;210&gt; 458

&lt;211&gt; 1148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 458

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Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
      20      25      30
Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
      35      40      45
Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
      50      55      60
Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
      65      70      75      80
Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
      85      90      95
Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
      100      105      110
Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile
      115      120      125
Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
      130      135      140
Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
      145      150      155      160
Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
      165      170      175
Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys
      180      185      190
Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
      195      200      205
Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
      210      215      220
Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg
      225      230      235      240
Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu
      245      250      255
Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser
      260      265      270
Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg
      275      280      285
Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
      290      295      300
Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr | Leu | Leu | Arg | Pro | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Asp | Gly | Thr | Ala | Thr | Gly | Val | Asp | Ala | Ile | Cys | Thr | His | His | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asp | Pro | Lys | Ser | Pro | Arg | Leu | Asp | Arg | Glu | Gln | Leu | Tyr | Trp | Glu | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Gln | Leu | Thr | His | Asn | Ile | Thr | Glu | Leu | Gly | His | Tyr | Ala | Leu | Asp |
|     | 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |
| Asn | Asp | Ser | Leu | Phe | Val | Asn | Gly | Phe | Thr | His | Arg | Ser | Ser | Val | Ser |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Thr | Ser | Thr | Pro | Gly | Thr | Pro | Thr | Val | Tyr | Leu | Gly | Ala | Ser | Lys |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Thr | Pro | Ala | Ser | Ile | Phe | Gly | Pro | Ser | Ala | Ala | Ser | His | Leu | Leu | Ile |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Thr | Asn | Leu | Arg | Tyr | Glu | Glu | Asn |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Met | Trp | Pro | Gly | Ser | Arg | Lys | Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gly | Leu | Leu | Arg | Pro | Leu | Phe | Lys | Asn | Thr | Ser | Val | Gly | Pro | Leu | Tyr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ser | Gly | Ser | Arg | Leu | Thr | Leu | Leu | Arg | Pro | Glu | Lys | Asp | Gly | Glu | Ala |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Thr | Gly | Val | Asp | Ala | Ile | Cys | Thr | His | Arg | Pro | Asp | Pro | Thr | Gly | Pro |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Gly | Leu | Asp | Arg | Glu | Gln | Leu | Tyr | Leu | Glu | Leu | Ser | Gln | Leu | Thr | His |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Ser | Ile | Thr | Glu | Leu | Gly | Pro | Tyr | Thr | Leu | Asp | Arg | Asp | Ser | Leu | Tyr |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Val | Asn | Gly | Phe | Thr | His | Arg | Ser | Ser | Val | Pro | Thr | Thr | Ser | Thr | Gly |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Val | Val | Ser | Glu | Glu | Pro | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Asn | Asn | Leu |
|     |     |     | 565 |     |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Arg | Tyr | Met | Ala | Asp | Met | Gly | Gln | Pro | Gly | Ser | Leu | Lys | Phe | Asn | Ile |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     |     | 590 |     |
| Thr | Asp | Asn | Val | Met | Lys | His | Leu | Leu | Ser | Pro | Leu | Phe | Gln | Arg | Ser |
|     | 595 |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ser | Leu | Gly | Ala | Arg | Tyr | Thr | Gly | Cys | Arg | Val | Ile | Ala | Leu | Arg | Ser |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Val | Lys | Asn | Gly | Ala | Glu | Thr | Arg | Val | Asp | Leu | Leu | Cys | Thr | Tyr | Leu |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Gln | Pro | Leu | Ser | Gly | Pro | Gly | Leu | Pro | Ile | Lys | Gln | Val | Phe | His | Glu |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Leu | Ser | Gln | Gln | Thr | His | Gly | Ile | Thr | Arg | Leu | Gly | Pro | Tyr | Ser | Leu |
|     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |     |
| Asp | Lys | Asp | Ser | Leu | Tyr | Leu | Asn | Gly | Tyr | Asn | Glu | Pro | Gly | Leu | Asp |
|     | 675 |     |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |
| Glu | Pro | Pro | Thr | Thr | Pro | Lys | Pro | Ala | Thr | Thr | Phe | Leu | Pro | Pro | Leu |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |
| Ser | Glu | Ala | Thr | Thr | Ala | Met | Gly | Tyr | His | Leu | Lys | Thr | Leu | Thr | Leu |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Asn | Phe | Thr | Ile | Ser | Asn | Leu | Gln | Tyr | Ser | Pro | Asp | Met | Gly | Lys | Gly |
|     |     |     | 725 |     |     |     |     |     | 730 |     |     |     |     | 735 |     |
| Ser | Ala | Thr | Phe | Asn | Ser | Thr | Glu | Gly | Val | Leu | Gln | His | Leu | Leu | Arg |
|     |     | 740 |     |     |     |     |     | 745 |     |     |     |     | 750 |     |     |
| Pro | Leu | Phe | Gln | Lys | Ser | Ser | Met | Gly | Pro | Phe | Tyr | Leu | Gly | Cys | Gln |
|     | 755 |     |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
| Leu | Ile | Ser | Leu | Arg | Pro | Glu | Lys | Asp | Gly | Ala | Ala | Thr | Gly | Val | Asp |

|   |      |      |      |      |
|---|------|------|------|------|
| 770   |      | 775  |      | 780  |
| Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile |      |      |      |      |
| 785   |      | 790  |      | 800  |
| Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln |      |      |      |      |
|   | 805  |      | 810  | 815  |
| Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr |      |      |      |      |
|   | 820  |      | 825  | 830  |
| Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His |      |      |      |      |
|   | 835  |      | 840  | 845  |
| Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr |      |      |      |      |
|   | 850  |      | 855  | 860  |
| Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys |      |      |      |      |
| 865   |      | 870  |      | 880  |
| Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu |      |      |      |      |
|   | 885  |      | 890  | 895  |
| Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn |      |      |      |      |
|   | 900  |      | 905  | 910  |
| Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn |      |      |      |      |
|   | 915  |      | 920  | 925  |
| Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His |      |      |      |      |
|   | 930  |      | 935  | 940  |
| Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser |      |      |      |      |
| 945   |      | 950  |      | 960  |
| Thr Gln His Phe Tyr Pro Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser |      |      |      |      |
|   | 965  |      | 970  | 975  |
| Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg |      |      |      |      |
|   | 980  |      | 985  | 990  |
| Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys |      |      |      |      |
|   | 995  |      | 1000 | 1005 |
| Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn |      |      |      |      |
|   | 1010 |      | 1015 | 1020 |
| Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala |      |      |      |      |
| 1025  |      | 1030 |      | 1040 |
| Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr |      |      |      |      |
|   | 1045 |      | 1050 | 1055 |
| Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val |      |      |      |      |
|   | 1060 |      | 1065 | 1070 |
| Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn |      |      |      |      |
|   | 1075 |      | 1080 | 1085 |
| Ser Asp Leu Pro Phe Trp Ala Val Ile Phe Ile Gly Leu Ala Gly Leu |      |      |      |      |
|   | 1090 |      | 1095 | 1100 |
| Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg |      |      |      |      |
| 1105  |      | 1110 |      | 1120 |
| Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Cys Pro Gly     |      |      |      |      |
|   | 1125 |      | 1130 | 1135 |
| Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln                 |      |      |      |      |
|   | 1140 |      | 1145 |      |

&lt;210&gt; 459

&lt;211&gt; 1156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 459

|   |
|---|
| Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser |
| 1 5 10 15   |
| Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Asp | Gly | Ala | Ala | Thr | Arg | Val | Asp | Ala | Val | Cys | Thr | His | Arg | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asp | Pro | Lys | Ser | Pro | Gly | Leu | Asp | Arg | Glu | Arg | Leu | Tyr | Trp | Lys | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gln | Leu | Thr | His | Gly | Ile | Thr | Glu | Leu | Gly | Pro | Tyr | Thr | Leu | Asp |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | His | Ser | Leu | Tyr | Val | Asn | Gly | Phe | Thr | His | Gln | Ser | Ser | Met | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Thr | Arg | Thr | Pro | Asp | Thr | Ser | Thr | Met | His | Leu | Ala | Thr | Ser | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Pro | Ala | Ser | Leu | Ser | Gly | Pro | Thr | Thr | Ala | Ser | Pro | Leu | Leu | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Phe | Thr | Ile | Asn | Phe | Thr | Ile | Thr | Asn | Leu | Arg | Tyr | Glu | Glu | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | His | His | Pro | Gly | Ser | Arg | Lys | Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu |
|     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Gln | Gly | Leu | Leu | Arg | Pro | Val | Phe | Lys | Asn | Thr | Ser | Val | Gly | Pro | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Ser | Gly | Cys | Arg | Leu | Thr | Leu | Leu | Arg | Pro | Lys | Lys | Asp | Gly | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Thr | Lys | Val | Asp | Ala | Ile | Cys | Thr | Tyr | Arg | Pro | Asp | Pro | Lys | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Gly | Leu | Asp | Arg | Glu | Gln | Leu | Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Ser | Ile | Thr | Glu | Leu | Gly | Pro | Tyr | Thr | Leu | Asp | Arg | Asp | Ser | Leu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Tyr | Val | Asn | Gly | Phe | Thr | Gln | Arg | Ser | Ser | Val | Pro | Thr | Thr | Ser | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Gly | Thr | Pro | Thr | Val | Asp | Leu | Gly | Thr | Ser | Gly | Thr | Pro | Val | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Pro | Gly | Pro | Ser | Ala | Ala | Ser | Pro | Leu | Leu | Val | Leu | Phe | Thr | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Phe | Thr | Ile | Thr | Asn | Leu | Arg | Tyr | Glu | Glu | Asn | Met | Gln | His | Pro |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Ser | Arg | Lys | Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Ser | Leu | Phe | Lys | Ser | Thr | Ser | Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | Leu | Thr | Leu | Leu | Arg | Pro | Glu | Lys | Asp | Gly | Thr | Ala | Thr | Gly | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asp | Ala | Ile | Cys | Thr | His | His | Pro | Asp | Pro | Lys | Ser | Pro | Arg | Leu | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Arg | Glu | Gln | Leu | Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr | His | Asn | Ile | Thr |
|     | 370 |     |     |     |     | 375 |     | </  |     |     |     |     |     |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |
| Arg | Pro | Glu | Lys | Asp | Gly | Glu | Ala | Thr | Gly | Val | Asp | Ala | Ile | Cys | Thr |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |
| His | Arg | Pro | Asp | Pro | Thr | Gly | Pro | Gly | Leu | Asp | Arg | Glu | Gln | Leu | Tyr |  |  |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |  |
| Leu | Glu | Leu | Ser | Gln | Leu | Thr | His | Ser | Ile | Thr | Glu | Leu | Gly | Pro | Tyr |  |  |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |
| Thr | Leu | Asp | Arg | Asp | Ser | Leu | Tyr | Val | Asn | Gly | Phe | Thr | His | Arg | Ser |  |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |  |
| Ser | Val | Pro | Thr | Thr | Ser | Thr | Gly | Val | Val | Ser | Glu | Glu | Pro | Phe | Thr |  |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |  |
| Leu | Asn | Phe | Thr | Ile | Asn | Asn | Leu | Arg | Tyr | Met | Ala | Asp | Met | Gly | Gln |  |  |
|     |     | 580 |     |     |     |     |     | 585 |     |     |     |     | 590 |     |     |  |  |
| Pro | Gly | Ser | Leu | Lys | Phe | Asn | Ile | Thr | Asp | Asn | Val | Met | Lys | His | Leu |  |  |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     |     | 605 |     |     |  |  |
| Leu | Ser | Pro | Leu | Phe | Gln | Arg | Ser | Ser | Leu | Gly | Ala | Arg | Tyr | Thr | Gly |  |  |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |  |  |
| Cys | Arg | Val | Ile | Ala | Leu | Arg | Ser | Val | Lys | Asn | Gly | Ala | Glu | Thr | Arg |  |  |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |  |  |
| Val | Asp | Leu | Leu | Cys | Thr | Tyr | Leu | Gln | Pro | Leu | Ser | Gly | Pro | Gly | Leu |  |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |  |  |
| Pro | Ile | Lys | Gln | Val | Phe | His | Glu | Leu | Ser | Gln | Gln | Thr | His | Gly | Ile |  |  |
|     |     | 660 |     |     |     |     |     | 665 |     |     |     |     |     | 670 |     |  |  |
| Thr | Arg | Leu | Gly | Pro | Tyr | Ser | Leu | Asp | Lys | Asp | Ser | Leu | Tyr | Leu | Asn |  |  |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |  |  |
| Gly | Tyr | Asn | Glu | Pro | Gly | Leu | Asp | Glu | Pro | Pro | Thr | Thr | Pro | Lys | Pro |  |  |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |  |  |
| Ala | Thr | Thr | Phe | Leu | Pro | Pro | Leu | Ser | Glu | Ala | Thr | Thr | Ala | Met | Gly |  |  |
| 705 |     |     |     | 710 |     |     |     |     |     | 715 |     |     |     |     | 720 |  |  |
| Tyr | His | Leu | Lys | Thr | Leu | Thr | Leu | Asn | Phe | Thr | Ile | Ser | Asn | Leu | Gln |  |  |
|     |     |     | 725 |     |     |     |     |     | 730 |     |     |     |     | 735 |     |  |  |
| Tyr | Ser | Pro | Asp | Met | Gly | Lys | Gly | Ser | Ala | Thr | Phe | Asn | Ser | Thr | Glu |  |  |
|     |     | 740 |     |     |     |     |     | 745 |     |     |     |     | 750 |     |     |  |  |
| Gly | Val | Leu | Gln | His | Leu | Leu | Arg | Pro | Leu | Phe | Gln | Lys | Ser | Ser | Met |  |  |
|     | 755 |     |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |  |  |
| Gly | Pro | Phe | Tyr | Leu | Gly | Cys | Gln | Leu | Ile | Ser | Leu | Arg | Pro | Glu | Lys |  |  |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |  |  |
| Asp | Gly | Ala | Ala | Thr | Gly | Val | Asp | Thr | Thr | Cys | Thr | Tyr | His | Pro | Asp |  |  |
| 785 |     |     |     | 790 |     |     |     |     |     | 795 |     |     |     |     | 800 |  |  |
| Pro | Val | Gly | Pro | Gly | Leu | Asp | Ile | Gln | Gln | Leu | Tyr | Trp | Glu | Leu | Ser |  |  |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |  |  |
| Gln | Leu | Thr | His | Gly | Val | Thr | Gln | Leu | Gly | Phe | Tyr | Val | Leu | Asp | Arg |  |  |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     |     | 830 |     |  |  |
| Asp | Ser | Leu | Phe | Ile | Asn | Gly | Tyr | Ala | Pro | Gln | Asn | Leu | Ser | Ile | Arg |  |  |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |  |  |
| Gly | Glu | Tyr | Gln | Ile | Asn | Phe | His | Ile | Val | Asn | Trp | Asn | Leu | Ser | Asn |  |  |
|     | 850 |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |  |  |
| Pro | Asp | Pro | Thr | Ser | Ser | Glu | Tyr | Ile | Thr | Leu | Leu | Arg | Asp | Ile | Gln |  |  |
| 865 |     |     |     | 870 |     |     |     |     |     | 875 |     |     |     |     | 880 |  |  |
| Asp | Lys | Val | Thr | Thr | Leu | Tyr | Lys | Gly | Ser | Gln | Leu | His | Asp | Thr | Phe |  |  |
|     |     |     |     | 885 |     |     |     |     | 890 |     |     |     |     | 895 |     |  |  |
| Arg | Phe | Cys | Leu | Val | Thr | Asn | Leu | Thr | Met | Asp | Ser | Val | Leu | Val | Thr |  |  |
|     |     | 900 |     |     |     |     |     | 905 |     |     |     |     | 910 |     |     |  |  |
| Val | Lys | Ala | Leu | Phe | Ser | Ser | Asn | Leu | Asp | Pro | Ser | Leu | Val | Glu | Gln |  |  |
|     |     | 915 |     |     |     |     |     | 920 |     |     |     |     | 925 |     |     |  |  |
| Val | Phe | Leu | Asp | Lys | Thr | Leu | Asn | Ala | Ser | Phe | His | Trp | Leu | Gly | Ser |  |  |
|     | 930 |     |     |     |     | 935 |     |     |     |     | 940 |     |     |     |     |  |  |
| Thr | Tyr | Gln | Leu | Val | Asp | Ile | His | Val | Thr | Glu | Met | Glu | Ser | Ser | Val |  |  |

945                      950                      955                      960  
 Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Pro Asn Phe  
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 Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr  
                                  980                      985                      990  
 Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln  
                                  995                      1000                      1005  
 Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val  
                                  1010                      1015                      1020  
 Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser  
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 Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile  
                                  1045                      1050                      1055  
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                                  1060                      1065                      1070  
 Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser Pro Asn  
                                  1075                      1080                      1085  
 Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val  
                                  1090                      1095                      1100  
 Ile Phe Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile  
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 Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr  
                                  1125                      1130                      1135  
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                                  1140                      1145                      1150  
 Glu Asp Leu Gln  
                                  1155

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 <212> PRT  
 <213> Homo sapiens

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                                  20                      25                      30  
 Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser  
                                  35                      40                      45  
 Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu  
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 Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp  
 65                      70                      75

<210> 461  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 461  
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 Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val  
                                  20                      25                      30  
 Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Glu | Arg | Leu | Tyr | Trp | Lys | Leu | Ser | Gln | Leu | Thr | His | Gly | Ile | Thr |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Leu | Gly | Pro | Tyr | Thr | Leu | Asp | Arg | His | Ser | Leu | Tyr | Val | Asn | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Thr | His | Gln | Ser | Ser | Met | Thr | Thr | Thr | Arg | Thr | Pro | Asp | Thr | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Met | His | Leu | Ala | Thr | Ser | Arg | Thr | Pro | Ala | Ser | Leu | Ser | Gly | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Thr | Ala | Ser | Pro | Leu | Leu | Val | Leu | Phe | Thr | Ile | Asn | Phe | Thr | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asn | Leu | Arg | Tyr | Glu | Glu | Asn | Met | His | His | Pro | Gly | Ser | Arg | Lys |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Arg | Pro | Val | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asn | Thr | Ser | Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Arg | Pro | Lys | Lys | Asp | Gly | Ala | Ala | Thr | Lys | Val | Asp | Ala | Ile | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Tyr | Arg | Pro | Asp | Pro | Lys | Ser | Pro | Gly | Leu | Asp | Arg | Glu | Gln | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr | His | Ser | Ile | Thr | Glu | Leu | Gly | Pro |
| 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Tyr | Thr | Leu | Asp | Arg | Asp | Ser | Leu | Tyr | Val | Asn | Gly | Phe | Thr | Gln | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Ser | Val | Pro | Thr | Thr | Ser | Ile | Pro | Gly | Thr | Pro | Thr | Val | Asp | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Thr | Ser | Gly | Thr | Pro | Val | Ser | Lys | Pro | Gly | Pro | Ser | Ala | Ala | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Leu | Leu | Val | Leu | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Thr | Asn | Leu | Arg |
|     |     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Tyr | Glu | Glu | Asn | Met | Gln | His | Pro | Gly | Ser | Arg | Lys | Phe | Asn | Thr | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Arg |     |     |     |     |     |     |     |
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&lt;210&gt; 462

&lt;211&gt; 2996

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 462

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&lt;210&gt; 463

&lt;211&gt; 3557

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 463

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&lt;210&gt; 464

&lt;211&gt; 2712

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 464

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&lt;210&gt; 465

&lt;211&gt; 1175

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 465

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&lt;210&gt; 466

&lt;211&gt; 1959

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 466

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&lt;210&gt; 467

&lt;211&gt; 1636

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 467

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<213> Homo sapiens

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<212> DNA  
<213> Homo sapiens

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<400> 469
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tggaaca 607

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<210> 470  
<211> 981  
<212> DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 470

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&lt;210&gt; 471

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 471

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&lt;210&gt; 472

&lt;211&gt; 1315

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 472

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ccaccgtctt gacccccaaa gccctggagt ggacagggag cagctatact gggagctgag 60
ccagctgacc aatggcatca aagagctggg cccctacacc tggacaggaa cagtctctat 120
gtcaatggtt taccatctcg gacctctgtg cccaccacca gcactcctgg gacctccaca 180
gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgaac tgctggccct 240
ctcctggtgc tgttcaccct caacttcacc atcaccaacc tgaagtatga ggaggacatg 300
catcgccctg gctccaggaa gttcaacacc actgagaggg tcctgcagac tctgcttggg 360
cctatgttca agaacaccag tgttggcctt ctgtactctg gctgcagact gaccttgctc 420
aggtccgaga aggatggagc agccactgga gtggatgcca tctgcacca ccgtcttgac 480

```

```

ccccaaagcc ctggagtggg cagggagcag ctatactggg agctgagcca gctgaccaat 540
ggcatcaaag agctggggccc ctacacbtctg gacaggaaca gtctctatgt caatggtttc 600
acccatttga tccctgtgcc caccagcagc actcctggga cctccacagt ggaccttggg 660
tcagggactc catcctccct ccccagcccc acaactgctg gccctctcct ggtgccgttc 720
accctcaact tcaccatcac caacctgaag tacgaggagg acatgcattg ccctggctcc 780
aggaagtcca acaccacaga gagagtcttg cagagtctgc ttgggtccat gttcaagaac 840
accagtgttg gccctctgta ctctggctgc agactgacct tgctcaggtc cgagaaggat 900
ggagcagcca ctggagtggg tgccatctgc accaccgtc ttgaccccaa aagcctggag 960
tggacagggg gcagctatac tgggagctga gccagctgac caatgccatc aaagagctgg 1020
gtccctacac cctggacagc aacagtcttc tatgtcaatg gtttcacca tcagacctct 1080
gcgccaaca ccagcactcc tgggacctcc acagtggacc ttgggacctc agggactcca 1140
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accatcacca acctgcagta cgaggaggac atgcatcacc caggctccag gaagttcaac 1260
accacggagc gggctctgca gggctctgctt ggtcccatgt tcaagaacac tacga 1315

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&lt;210&gt; 473

&lt;211&gt; 689

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 473

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acggcatcag gagagggcca gcagtcgtgg ggctggggct ggaggatgga gtccctgagg 60
ttccacatc cactgtggag gtcccaggag tgctgtgggt gggcatagag cttcgatggg 120
tgaaccatt gacatagaga ctgttccgtt ccagggtgta ggggccagc tcagtgatgc 180
cgtgggtcag ctgggtcagc tcccagtaca gctgctctct gttcagtcca gggctttgag 240
ggtcaggggtg gtgggtacag atggcatcca ctctgggtggc tgcttgttcc ttctctggcc 300
ttgagcaagg tcagtctgca gcctgagagc taacagaggt ccgataactg gtattcttga 360
acaagggcct agagcagaac cctgtaggac catcgccgtg gtatatgaac ttcctagagc 420
caggatttgc cacggccatc actcatactg caacttctgt atggcaaagt tgaggataaa 480
cggcaccagg agagggccag ccacttatgg gtctaggtag ggaggatgga gtttcagagg 540
ttctcgagat ccactgtgga ggtcccagga gtgctgggtg ttgacacaga gctctgatgg 600
gtgaaaccat tgacatagag actgttcctg tccagggtgt aggggccag ctcttcaatg 660
tcattggtca gtttgcttag ctcccagta 689

```

&lt;210&gt; 474

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 474

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gtggatatga gttgaatact cactgctggt ggtggacaca gagctctgat gggtgaaacc 60
tgcatagaga aggagggagg agagtgggta agagacaagg agaggtgggg gaccaaatgg 120
aggtcaatgc taccctggtg caatgaaccg agtttcatgg tacagggaca attgaagatt 180
ttctatcagc atcctcacat caggaaaagaa tgccctgagg gaacacagtc catgatggtg 240
aggaaaccat gaagtccaga ccttagtcat cccatgtaga gcacatgaca gaattttcaa 300
aggccaggca gggagtgtga cctctagtta gagattagag gctgccagc aagggggaag 360
agatttcaac cacatcacag ccactcacca ttgacataga gactgttcct gtccagggtg 420
taggggcca gctcttcaat gtcattggtc agtttgctta gctcccagta cagctgctcc 480
ctgttgagtc caggg 495

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&lt;210&gt; 475

&lt;211&gt; 192

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 475

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agtggccagg ctactaccag tcacacctag acctggagga tctgcaatga ctggaacttg 60
ccgtgacctg gggatagcct cttcatcaat ggctatgcac cccagaattt atcaatccgg 120

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156

ggcgagtacc agataaattt ccacattgtc aactggaacc tcagtaatcc agaccccaca 180  
tcctcagagt ac 192

<210> 476  
<211> 500  
<212> DNA  
<213> Homo sapiens

<400> 476  
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gtgttgaaact tcctggaacc aggggtgacgc atgtcctcct catactgcag gttggtgata 180  
gtgaagttga ggggtgaatgg caccaggaga gggccagggc tgtgtggcca gggagggagg 240  
ctggagtccc agaggtttcc aggtgcaactg cagagggtccc aggaatactg gtggttgga 300  
cagagctccg atgggtgaag ccattgacat agagactgtc cctgtccagg tgtaggggcc 360  
cagctctgta acgctgttgg tcagctggct cagctcccag tatagccgct ctctgtccag 420  
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atgtttctca ggtctgagca 500

<210> 477  
<211> 191  
<212> DNA  
<213> Homo sapiens

<400> 477  
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tcaagggacg catggaaact ttttatatta ttctctcttt aaatcctggt gcatatgttt 120  
agaagtaggc cttttgaaa tatataaagt tctccacttt tgaacatggt gtttctttcc 180  
cacctccacg a 191

<210> 478  
<211> 914  
<212> PRT  
<213> Homo sapiens

<400> 478  
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Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu  
20 25 30  
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser  
35 40 45  
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu  
50 55 60  
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser  
65 70 75 80  
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu  
85 90 95  
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala  
100 105 110  
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu  
115 120 125  
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu  
130 135 140  
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr  
145 150 155 160  
His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val  
165 170 175

Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala  
 180 185 190  
 Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn  
 195 200 205  
 Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr  
 210 215 220  
 Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr  
 225 230 235 240  
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro  
 245 250 255  
 Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg  
 260 265 270  
 Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu  
 275 280 285  
 Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu  
 290 295 300  
 Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val  
 305 310 315 320  
 Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn  
 325 330 335  
 Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly  
 340 345 350  
 Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser  
 355 360 365  
 Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg  
 370 375 380  
 Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp  
 385 390 395 400  
 Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile  
 405 410 415  
 Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg  
 420 425 430  
 Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr  
 435 440 445  
 Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr  
 450 455 460  
 Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His  
 465 470 475 480  
 Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser  
 485 490 495  
 Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val  
 500 505 510  
 Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro  
 515 520 525  
 Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly  
 530 535 540  
 Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val  
 545 550 555 560  
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu  
 565 570 575  
 Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser  
 580 585 590  
 Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu  
 595 600 605  
 Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp  
 610 615 620  
 Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys  
 625 630 635 640

Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe  
 645 650 655  
 Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys  
 660 665 670  
 Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe  
 675 680 685  
 Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr  
 690 695 700  
 Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln  
 705 710 715 720  
 Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile  
 725 730 735  
 Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn  
 740 745 750  
 Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe  
 755 760 765  
 Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr  
 770 775 780  
 Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys  
 785 790 795 800  
 Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu  
 805 810 815  
 Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr  
 820 825 830  
 Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn  
 835 840 845  
 Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu  
 850 855 860  
 Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly  
 865 870 875 880  
 Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val  
 885 890 895  
 Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp  
 900 905 910  
 Leu Gln

<210> 479  
 <211> 1148  
 <212> PRT  
 <213> Homo sapiens

<400> 479  
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 20 25 30  
 Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp  
 35 40 45  
 Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr  
 50 55 60  
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly  
 65 70 75 80  
 Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser  
 85 90 95  
 Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro  
 100 105 110

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Thr | Ala | Ser | Pro | Leu | Leu | Val | Leu | Phe | Thr | Ile | Asn | Phe | Thr | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Thr | Asn | Leu | Arg | Tyr | Glu | Glu | Asn | Met | His | His | Pro | Gly | Ser | Arg | Lys |  |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Arg | Pro | Val | Phe |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Lys | Asn | Thr | Ser | Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr | Leu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu | Arg | Pro | Lys | Lys | Asp | Gly | Ala | Ala | Thr | Lys | Val | Asp | Ala | Ile | Cys |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Thr | Tyr | Arg | Pro | Asp | Pro | Lys | Ser | Pro | Gly | Leu | Asp | Arg | Glu | Gln | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr | His | Ser | Ile | Thr | Glu | Leu | Gly | Pro |  |
| 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |
| Tyr | Thr | Leu | Asp | Arg | Asp | Ser | Leu | Tyr | Val | Asn | Gly | Phe | Thr | Gln | Arg |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Ser | Ser | Val | Pro | Thr | Thr | Ser | Ile | Pro | Gly | Thr | Pro | Thr | Val | Asp | Leu |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Gly | Thr | Ser | Gly | Thr | Pro | Val | Ser | Lys | Pro | Gly | Pro | Ser | Ala | Ala | Ser |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Pro | Leu | Leu | Val | Leu | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Thr | Asn | Leu | Arg |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Tyr | Glu | Glu | Asn | Met | Gln | His | Pro | Gly | Ser | Arg | Lys | Phe | Asn | Thr | Thr |  |
| 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |
| Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Arg | Ser | Leu | Phe | Lys | Ser | Thr | Ser |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr | Leu | Leu | Arg | Pro | Glu |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Lys | Asp | Gly | Thr | Ala | Thr | Gly | Val | Asp | Ala | Ile | Cys | Thr | His | His | Pro |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Asp | Pro | Lys | Ser | Pro | Arg | Leu | Asp | Arg | Glu | Gln | Leu | Tyr | Trp | Glu | Leu |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Ser | Gln | Leu | Thr | His | Asn | Ile | Thr | Glu | Leu | Gly | His | Tyr | Ala | Leu | Asp |  |
| 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |  |
| Asn | Asp | Ser | Leu | Phe | Val | Asn | Gly | Phe | Thr | His | Arg | Ser | Ser | Val | Ser |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Thr | Thr | Ser | Thr | Pro | Gly | Thr | Pro | Thr | Val | Tyr | Leu | Gly | Ala | Ser | Lys |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Thr | Pro | Ala | Ser | Ile | Phe | Gly | Pro | Ser | Ala | Ala | Ser | His | Leu | Leu | Ile |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Leu | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Thr | Asn | Leu | Arg | Tyr | Glu | Glu | Asn |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |
| Met | Trp | Pro | Gly | Ser | Arg | Lys | Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln |  |
| 450 |     |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |
| Gly | Leu | Leu | Arg | Pro | Leu | Phe | Lys | Asn | Thr | Ser | Val | Gly | Pro | Leu | Tyr |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| Ser | Gly | Ser | Arg | Leu | Thr | Leu | Leu | Arg | Pro | Glu | Lys | Asp | Gly | Glu | Ala |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |
| Thr | Gly | Val | Asp | Ala | Ile | Cys | Thr | His | Arg | Pro | Asp | Pro | Thr | Gly | Pro |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |
| Gly | Leu | Asp | Arg | Glu | Gln | Leu | Tyr | Leu | Glu | Leu | Ser | Gln | Leu | Thr | His |  |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |
| Ser | Ile | Thr | Glu | Leu | Gly | Pro | Tyr | Thr | Leu | Asp | Arg | Asp | Ser | Leu | Tyr |  |
| 530 |     |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |
| Val | Asn | Gly | Phe | Thr | His | Arg | Ser | Ser | Val | Pro | Thr | Thr | Ser | Thr | Gly |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |
| Val | Val | Ser | Glu | Glu | Pro | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Asn | Asn | Leu |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |

|      |     |      |     |     |      |      |      |     |     |      |      |      |     |     |      |  |  |
|------|-----|------|-----|-----|------|------|------|-----|-----|------|------|------|-----|-----|------|--|--|
| Arg  | Tyr | Met  | Ala | Asp | Met  | Gly  | Gln  | Pro | Gly | Ser  | Leu  | Lys  | Phe | Asn | Ile  |  |  |
|      |     |      | 580 |     |      |      |      | 585 |     |      |      |      | 590 |     |      |  |  |
| Thr  | Asp | Asn  | Val | Met | Lys  | His  | Leu  | Leu | Ser | Pro  | Leu  | Phe  | Gln | Arg | Ser  |  |  |
|      |     | 595  |     |     |      |      | 600  |     |     |      |      | 605  |     |     |      |  |  |
| Ser  | Leu | Gly  | Ala | Arg | Tyr  | Thr  | Gly  | Cys | Arg | Val  | Ile  | Ala  | Leu | Arg | Ser  |  |  |
|      |     | 610  |     |     |      | 615  |      |     |     |      | 620  |      |     |     |      |  |  |
| Val  | Lys | Asn  | Gly | Ala | Glu  | Thr  | Arg  | Val | Asp | Leu  | Leu  | Cys  | Thr | Tyr | Leu  |  |  |
| 625  |     |      |     |     | 630  |      |      |     |     | 635  |      |      |     |     | 640  |  |  |
| Gln  | Pro | Leu  | Ser | Gly | Pro  | Gly  | Leu  | Pro | Ile | Lys  | Gln  | Val  | Phe | His | Glu  |  |  |
|      |     |      |     | 645 |      |      |      |     | 650 |      |      |      |     | 655 |      |  |  |
| Leu  | Ser | Gln  | Gln | Thr | His  | Gly  | Ile  | Thr | Arg | Leu  | Gly  | Pro  | Tyr | Ser | Leu  |  |  |
|      |     |      |     | 660 |      |      |      | 665 |     |      |      |      | 670 |     |      |  |  |
| Asp  | Lys | Asp  | Ser | Leu | Tyr  | Leu  | Asn  | Gly | Tyr | Asn  | Glu  | Pro  | Gly | Leu | Asp  |  |  |
|      |     | 675  |     |     |      | 680  |      |     |     |      |      | 685  |     |     |      |  |  |
| Glu  | Pro | Pro  | Thr | Thr | Pro  | Lys  | Pro  | Ala | Thr | Thr  | Phe  | Leu  | Pro | Pro | Leu  |  |  |
|      |     | 690  |     |     |      | 695  |      |     |     |      | 700  |      |     |     |      |  |  |
| Ser  | Glu | Ala  | Thr | Thr | Ala  | Met  | Gly  | Tyr | His | Leu  | Lys  | Thr  | Leu | Thr | Leu  |  |  |
| 705  |     |      |     |     | 710  |      |      |     |     | 715  |      |      |     |     | 720  |  |  |
| Asn  | Phe | Thr  | Ile | Ser | Asn  | Leu  | Gln  | Tyr | Ser | Pro  | Asp  | Met  | Gly | Lys | Gly  |  |  |
|      |     |      |     | 725 |      |      |      |     | 730 |      |      |      | 735 |     |      |  |  |
| Ser  | Ala | Thr  | Phe | Asn | Ser  | Thr  | Glu  | Gly | Val | Leu  | Gln  | His  | Leu | Leu | Arg  |  |  |
|      |     |      | 740 |     |      |      |      | 745 |     |      |      |      | 750 |     |      |  |  |
| Pro  | Leu | Phe  | Gln | Lys | Ser  | Ser  | Met  | Gly | Pro | Phe  | Tyr  | Leu  | Gly | Cys | Gln  |  |  |
|      |     | 755  |     |     |      |      | 760  |     |     |      |      | 765  |     |     |      |  |  |
| Leu  | Ile | Ser  | Leu | Arg | Pro  | Glu  | Lys  | Asp | Gly | Ala  | Ala  | Thr  | Gly | Val | Asp  |  |  |
|      |     | 770  |     |     |      | 775  |      |     |     |      | 780  |      |     |     |      |  |  |
| Thr  | Thr | Cys  | Thr | Tyr | His  | Pro  | Asp  | Pro | Val | Gly  | Pro  | Gly  | Leu | Asp | Ile  |  |  |
| 785  |     |      |     |     | 790  |      |      |     |     | 795  |      |      |     |     | 800  |  |  |
| Gln  | Gln | Leu  | Tyr | Trp | Glu  | Leu  | Ser  | Gln | Leu | Thr  | His  | Gly  | Val | Thr | Gln  |  |  |
|      |     |      |     | 805 |      |      |      |     | 810 |      |      |      |     | 815 |      |  |  |
| Leu  | Gly | Phe  | Tyr | Val | Leu  | Asp  | Arg  | Asp | Ser | Leu  | Phe  | Ile  | Asn | Gly | Tyr  |  |  |
|      |     |      | 820 |     |      |      |      | 825 |     |      |      |      | 830 |     |      |  |  |
| Ala  | Pro | Gln  | Asn | Leu | Ser  | Ile  | Arg  | Gly | Glu | Tyr  | Gln  | Ile  | Asn | Phe | His  |  |  |
|      |     | 835  |     |     |      |      | 840  |     |     |      |      | 845  |     |     |      |  |  |
| Ile  | Val | Asn  | Trp | Asn | Leu  | Ser  | Asn  | Pro | Asp | Pro  | Thr  | Ser  | Ser | Glu | Tyr  |  |  |
|      |     | 850  |     |     |      | 855  |      |     |     |      | 860  |      |     |     |      |  |  |
| Ile  | Thr | Leu  | Leu | Arg | Asp  | Ile  | Gln  | Asp | Lys | Val  | Thr  | Thr  | Leu | Tyr | Lys  |  |  |
| 865  |     |      |     |     | 870  |      |      |     |     | 875  |      |      |     |     | 880  |  |  |
| Gly  | Ser | Gln  | Leu | His | Asp  | Thr  | Phe  | Arg | Phe | Cys  | Leu  | Val  | Thr | Asn | Leu  |  |  |
|      |     |      |     | 885 |      |      |      |     | 890 |      |      |      |     | 895 |      |  |  |
| Thr  | Met | Asp  | Ser | Val | Leu  | Val  | Thr  | Val | Lys | Ala  | Leu  | Phe  | Ser | Ser | Asn  |  |  |
|      |     |      | 900 |     |      |      |      | 905 |     |      |      |      | 910 |     |      |  |  |
| Leu  | Asp | Pro  | Ser | Leu | Val  | Glu  | Gln  | Val | Phe | Leu  | Asp  | Lys  | Thr | Leu | Asn  |  |  |
|      |     | 915  |     |     |      |      | 920  |     |     |      |      | 925  |     |     |      |  |  |
| Ala  | Ser | Phe  | His | Trp | Leu  | Gly  | Ser  | Thr | Tyr | Gln  | Leu  | Val  | Asp | Ile | His  |  |  |
|      |     |      |     |     |      | 935  |      |     |     | 940  |      |      |     |     |      |  |  |
| Val  | Thr | Glu  | Met | Glu | Ser  | Ser  | Val  | Tyr | Gln | Pro  | Thr  | Ser  | Ser | Ser | Ser  |  |  |
| 945  |     |      |     |     | 950  |      |      |     |     | 955  |      |      |     |     | 960  |  |  |
| Thr  | Gln | His  | Phe | Tyr | Pro  | Asn  | Phe  | Thr | Ile | Thr  | Asn  | Leu  | Pro | Tyr | Ser  |  |  |
|      |     |      |     | 965 |      |      |      |     | 970 |      |      |      |     | 975 |      |  |  |
| Gln  | Asp | Lys  | Ala | Gln | Pro  | Gly  | Thr  | Thr | Asn | Tyr  | Gln  | Arg  | Asn | Lys | Arg  |  |  |
|      |     |      | 980 |     |      |      |      | 985 |     |      |      |      | 990 |     |      |  |  |
| Asn  | Ile | Glu  | Asp | Ala | Leu  | Asn  | Gln  | Leu | Phe | Arg  | Asn  | Ser  | Ser | Ile | Lys  |  |  |
|      |     | 995  |     |     |      |      | 1000 |     |     |      |      | 1005 |     |     |      |  |  |
| Ser  | Tyr | Phe  | Ser | Asp | Cys  | Gln  | Val  | Ser | Thr | Phe  | Arg  | Ser  | Val | Pro | Asn  |  |  |
|      |     | 1010 |     |     |      | 1015 |      |     |     |      | 1020 |      |     |     |      |  |  |
| Arg  | His | His  | Thr | Gly | Val  | Asp  | Ser  | Leu | Cys | Asn  | Phe  | Ser  | Pro | Leu | Ala  |  |  |
| 1025 |     |      |     |     | 1030 |      |      |     |     | 1035 |      |      |     |     | 1040 |  |  |

161

Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr  
                   1045                  1050                  1055  
 Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val  
                   1060                  1065                  1070  
 Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn  
                   1075                  1080                  1085  
 Ser Asp Leu Pro Phe Trp Ala Val Ile Phe Ile Gly Leu Ala Gly Leu  
                   1090                  1095                  1100  
 Leu Gly Leu Ile Thr Cys Ser Ile Cys Gly Val Leu Val Thr Thr Arg  
                   1110                  1115                  1120  
 Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly  
                   1125                  1130                  1135  
 Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln  
                   1140                  1145

<210> 480  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 480  
 Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu  
   1                  5                  10                  15  
 Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu  
                   20                  25                  30  
 Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala  
                   35                  40                  45  
 Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser  
                   50                  55                  60  
 Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr  
                   65                  70                  75                  80  
 Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu  
                   85                  90                  95  
 Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr  
                   100                  105                  110  
 Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu  
                   115                  120                  125  
 Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn  
                   130                  135                  140  
 Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly  
                   145                  150                  155                  160  
 Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly  
                   165                  170                  175  
 Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg  
                   180                  185                  190  
 Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp  
                   195                  200                  205  
 Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Leu Glu Trp Thr Gly  
                   210                  215                  220  
 Ser Ser Tyr Thr Gly Ser  
                   225                  230

<210> 481  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens



&lt;400&gt; 481

```

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 1          5          10          15
Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
          20          25          30
Tyr Ser Gly Cys Arg Leu Thr Leu Arg Pro Glu Lys Asp Gly Thr
          35          40          45
Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser
          50          55          60
Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
          65          70          75          80
His Asn Ile Thr Glu Leu Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu
          85          90          95
Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr
          100          105          110
Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser
          115          120          125
Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu
          130          135          140
Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly
          145          150          155          160
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg
          165          170          175
Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
          180          185          190
Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp
          195          200          205
Ala Ile
          210

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&lt;210&gt; 482

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 482

```

Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
 1          5          10          15
Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
          20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
          35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
          50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Cys Ser
          65          70          75          80
Gly Pro Cys Ser Arg Ala Pro Val Leu Ala Leu Cys Thr Leu Ala Ala
          85          90          95
Asp

```

&lt;210&gt; 483

&lt;211&gt; 438

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 483

```

Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn
 1          5          10          15
Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser
 20          25          30
Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser
 35          40          45
Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro
 50          55          60
Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His
 65          70          75          80
Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu
 85          90          95
Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu
100          105          110
Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser
115          120          125
Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu
130          135          140
Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp
145          150          155          160
Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp
165          170          175
Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu
180          185          190
Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val
195          200          205
Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu
210          215          220
Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser
225          230          235          240
Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu
245          250          255
Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro
260          265          270
Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu
275          280          285
Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys
290          295          300
Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val
305          310          315          320
Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val
325          330          335
Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu
340          345          350
Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser
355          360          365
Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp
370          375          380
Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys
385          390          395          400
Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly
405          410          415
Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu
420          425          430
Asp Leu Glu Asp Leu Gln
435

```

<210> 484  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens

<400> 484

```

Met Thr Leu Lys Ser Trp Ala Pro Thr Pro Trp Thr Gly Thr Val Ser
 1          5          10          15
Met Ser Met Val Ser Pro Ile Arg Ala Leu Cys Pro Pro Pro Ala Leu
          20          25          30
Leu Gly Pro Pro Gln Trp Ile Ser Glu Pro Gln Trp Thr Pro Ser Ser
          35          40          45
Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe
          50          55          60
Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly
          65          70          75          80
His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
          85          90          95
Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser
          100          105          110
Gly Cys Arg Leu Thr Ser Leu Arg Ser Lys Lys Asp Gly Ala Ala Thr
          115          120          125
Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly
          130          135          140
Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly
          145          150          155          160
Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val
          165          170          175
Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser Thr Pro Gly
          180          185          190
Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Leu Pro
          195          200          205
Ala Thr Gln Ser Leu Ala Leu Ser
          210          215

```

<210> 485  
 <211> 268  
 <212> PRT  
 <213> Homo sapiens

<400> 485

```

Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr
 1          5          10          15
Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu
          20          25          30
Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu
          35          40          45
Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser
          50          55          60
Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
          65          70          75          80
Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp
          85          90          95
Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro
          100          105          110

```

165

Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys  
 115 120 125  
 Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn  
 130 135 140  
 Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr  
 145 150 155 160  
 Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Val Asp Ser  
 165 170 175  
 Ile Leu Pro Leu Gln Pro His Asn Tyr Gly Cys Trp Pro Ser Pro Gly  
 180 185 190  
 Thr Ile His Pro Gln Leu His His His Gln Pro Ala Val Trp Gly Gly  
 195 200 205  
 His Gly Ser Pro Trp Leu Gln Glu Val Gln His His Arg Glu Gly Pro  
 210 215 220  
 Ala Gly Ser Ala Trp Ser His Ile Gln Glu His Gln Cys Trp Pro Ser  
 225 230 235 240  
 Val Leu Trp Leu Gln Thr Asp Leu Ser Gln Val Gln Glu Gly Trp Ser  
 245 250 255  
 Ser His Trp Ser Gly Cys His Leu His Pro Ser Ser  
 260 265

&lt;210&gt; 486

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 486

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu  
 1 5 10 15  
 Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu  
 20 25 30  
 Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu  
 35 40 45  
 Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly  
 50 55 60  
 Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr  
 65 70 75 80  
 His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu  
 85 90 95  
 Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr  
 100 105 110  
 Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn  
 115 120 125  
 Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn  
 130 135 140  
 Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg  
 145 150 155 160  
 Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg  
 165 170 175  
 Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr  
 180 185 190  
 Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His  
 195 200 205  
 Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser  
 210 215 220  
 Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Pro  
 225 230 235 240

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Glu | Pro | Pro | Thr | Thr | Pro | Lys | Pro | Ala | Thr | Thr | Phe | Leu | Pro | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Ser | Glu | Ala | Thr | Thr | Ala | Met | Gly | Tyr | His | Leu | Lys | Thr | Leu | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Asn | Ser | His | Leu | Gln | Ser | Pro | Val | Phe | Thr | Arg | Tyr | Gly | Gln | Gly |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Leu | Lys | Val | His | Ser | Ile | His | Arg | Gly | Gly | Ser | Phe | Ser | Asn | Trp | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

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<210> 487
<211> 294
<212> PRT
<213> Homo sapiens
```

[illegible]

|       |     |
|-------|-----|
| <210> | 488 |
| <211> | 233 |

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 488

```

Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe
 1           5           10           15
His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu
          20           25           30
Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His
          35           40           45
Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys
          50           55           60
Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
65           70           75           80
Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe
          85           90           95
Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His
          100          105          110
Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val
          115          120          125
Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly
130          135          140
Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp
145          150          155          160
Gly Tyr Phe Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu
          165          170          175
Pro Phe Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu
          180          185          190
Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys
          195          200          205
Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln
210          215          220
Ser His Leu Asp Leu Glu Asp Leu Gln
225          230

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&lt;210&gt; 489

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 489

```

Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe
 1           5           10           15
His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu
          20           25           30
Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His
          35           40           45
Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys
          50           55           60
Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
65           70           75           80
Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe
          85           90           95
Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His
          100          105          110
Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val
          115          120          125

```

168

Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly  
 130 135 140  
 Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp  
 145 150 155 160  
 Gly Tyr Phe Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu  
 165 170 175  
 Pro Phe

<210> 490  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 490  
 Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu Ala Pro Gly Ser  
 1 5 10 15

<210> 491  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 491  
 Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr  
 1 5 10 15

<210> 492  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 492  
 Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro  
 1 5 10 15

<210> 493  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 493  
 Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu  
 1 5 10 15

<210> 494  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 494  
 Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr  
 1 5 10 15

<210> 495  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 495  
Leu Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly  
1 5 10 15

<210> 496  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 496  
Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Tyr Val Leu  
1 5 10 15

<210> 497  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 497  
Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile  
1 5 10 15

<210> 498  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 498  
Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu  
1 5 10 15

<210> 499  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 499  
Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser  
1 5 10 15

<210> 500  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 500



Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr  
1 5 10 15

<210> 501

<211> 15

<212> PRT

<213> Homo sapiens

<400> 501

Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr  
1 5 10 15

<210> 502

<211> 15

<212> PRT

<213> Homo sapiens

<400> 502

Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg  
1 5 10 15

<210> 503

<211> 15

<212> PRT

<213> Homo sapiens

<400> 503

Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly  
1 5 10 15

<210> 504

<211> 15

<212> PRT

<213> Homo sapiens

<400> 504

Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp  
1 5 10 15

<210> 505

<211> 15

<212> PRT

<213> Homo sapiens

<400> 505

Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln  
1 5 10 15

<210> 506

<211> 15

<212> PRT

<213> Homo sapiens

171

&lt;400&gt; 506

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Ile | Gln | Gln | Leu | Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

&lt;210&gt; 507

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 507

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ile | Val | Asn | Trp | Asn | Leu | Ser | Asn | Pro | Asp | Pro | Thr | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

&lt;210&gt; 508

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 508

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Thr | Ser | Ser | Glu | Tyr | Ile | Thr | Leu | Leu | Arg | Asp | Ile | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

&lt;210&gt; 509

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 509

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Asp | Ile | Gln | Asp | Lys | Val | Thr | Thr | Leu | Tyr | Lys | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

&lt;210&gt; 510

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 510

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Tyr | Lys | Gly | Ser | Gln | Leu | His | Asp | Thr | Phe | Arg | Phe | Cys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

&lt;210&gt; 511

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 511

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Ala | Gln | Pro | Gly | Thr | Thr | Asn | Tyr | Gln | Arg | Asn | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

&lt;210&gt; 512

&lt;211&gt; 450

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 <213> Homo sapiens

<400> 512  
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 ctggtgtgga caccacctgc acctaccacc ctgaccctgt gggccccggg ctggacatac 360  
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 tcctggacag ggatagcctc ttcatcaatg 450

<210> 513  
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 <212> DNA  
 <213> Homo sapiens

<400> 513  
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 ccctcaagtt caacatcaca gacaacgtca tgaagcacct gctcagtcct ttgttccaga 180  
 ggagcagcct ggggtgcacgg tacacagget gcagggcat cgcactaagg tctgtgaaga 240  
 acggtgctga gacacgggtg gacctcctct gcacctacct gcagcccctc agcggcccag 300  
 gtctgcctat caagcagggtg ttccatgagc tgagccagca gacctatggc atcaccgggc 360  
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<210> 514  
 <211> 465  
 <212> DNA  
 <213> Homo sapiens

<400> 514  
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 tactattcac cctcaacttc accatcacta acctgcggtg tgaggagaac atgtggcctg 180  
 gctccaggaa gttcaacact acagagaggg tcttcagggt cctgctaagg cccttgttca 240  
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 aagatgggga agccaccgga gtggatgcca tctgcacca cgcacctgac cccacaggcc 360  
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 agctgggccc ctacacactg gacagggaca gtctctatgt caatg 465

<210> 515  
 <211> 463  
 <212> DNA  
 <213> Homo sapiens

<400> 515  
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 tgctattcac tctcaacttc accatcacca acctgcggtg tgaggagaac atgcagcacc 180  
 ctggctccag gaagtccaac accacggaga gggctcttca gggcctggtc cctgttcaag 240  
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 aggtgggaca gagagcagct gtattgggag ctgagccagc tgaccacaa tatcactgag 420  
 ctgggcccct atgccctgga caacgacagc ctctttgtca atg 463

<210> 516

<211> 156  
<212> DNA  
<213> Homo sapiens

<400> 516  
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cctacaccct ggacagggac agtctctatg tcaatg 156

<210> 517  
<211> 450  
<212> DNA  
<213> Homo sapiens

<400> 517  
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acttcaccat ctccaatctc cagtattcac cagatatggg caagggctca gctacattca 180  
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gccccttcta cttgggttgc caactgatct ccctcaggcc tgagaaggat ggggcagcca 300  
ctggtgtgga caccacctgc acctaccacc ctgacctgt gggccccggg ctggacatac 360  
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<210> 518  
<211> 402  
<212> DNA  
<213> Homo sapiens

<400> 518  
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tcacactgaa cttcaccatc aacaacctgc gctacatggc ggacatgggc caaccggct 120  
ccctcaagtt caacatcaca gacaacgtca tgaagcacct gctcagtcct ttgttccaga 180  
ggagcagcct ggtgacagc tacacagget gcagggtcat cgcactaagg tctgtgaaga 240  
acggtgctga gacacgggtg gacctcctct gcacctacct gcagccctc agcggccag 300  
gtctgcctat caagcaggtg ttccatgagc tgagccagca gacctatggc atcaccggc 360  
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<210> 519  
<211> 465  
<212> DNA  
<213> Homo sapiens

<400> 519  
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tgggagcatc taagactcca gctcgatat ttggcccttc agctgccagc catctcctga 120  
tactattcac cttcaacttc accatcacta acctgcggtg tgaggagAAC atgtggcctg 180  
gctccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg cccttgttca 240  
agaacaccag tgttgccct ctgtactctg gctccaggct gaccttctc aggccagaga 300  
aagatgggga agccaccgga gtggatgcca tctgcacca ccgccctgac cccacaggcc 360  
ctgggctgga cagagagcag ctgtatttgg agctgagcca gctgaccac agcatcactg 420  
agctgggccc ctacacactg gacagggaca gtctctatgt caatg 465

<210> 520  
<211> 468  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 520

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gtttcacaca gcggagctct gtgcccacca ctagcattcc tgggaccccc acagtggacc 60
tggaacatc tgggactcca gtttctaacc ctgggccctc ggctgccagc cctctcctgg 120
tgctattcac tctcaacttc accatcacca acctgcggtg tgaggagAAC atgcagcacc 180
ctggctccag gaagtccaac accacggaga gggtccttca gggcctgctc aggtccctgt 240
tcaagagcac cagtgttggc cctctgtact ctggctgcag actgactttg ctcaggccctg 300
aaaaggatgg gacagccact ggagtggatg ccatctgcac ccaccaccct gaccccaaaa 360
gccctaggct ggacagagag cagctgtatt gggagctgag ccagctgacc cacaatatca 420
ctgagctggg ccactatgcc ctggacaacg acagcctctt tgtcaatg 468

```

&lt;210&gt; 521

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 521

```

gtttcaccca tcagagctct atgacgacca ccagaactcc tgatacctcc acaatgcacc 60
tggaacacct gagaaactcca gcctccctgt ctggacctac gaccgccagc cctctcctgg 120
tgctattcac aattaacttc accatcacta acctgcggtg tgaggagAAC atgcacacc 180
ctggctctag aaagtttaac accacggaga gagtccttca gggctctgctc aggcctgtgt 240
tcaagaacac cagtgttggc cctctgtact ctggctgcag actgaccttg ctcaggccca 300
agaaggatgg ggacgccacc aaagtggatg ccatctgcac ctaccgccct gatcccaaaa 360
gccctggact ggacagagag cagctatact gggagctgag ccagctaacc cacagcatca 420
ctgagctggg ccctacacc ctggacaggg acagtctcta tgtcaatg 468

```

&lt;210&gt; 522

&lt;211&gt; 262

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 522

```

gagaggggtcc ttcaggggtct gcttatgccc ttgttcaaga acaccagtgt cagctctctg 60
tactctgggt gcagactgac cttgctcagg cctgagaagg atggggcagc caccagagtg 120
gatgctgtct gcacccatcg tcctgacccc aaaagccctg gactggacag agagcggctg 180
tactggaagc tgagccagct gaccacggc atcactgagc tgggcccta caccctggac 240
aggcacagtc tctatgtcaa tg 262

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&lt;210&gt; 523

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 523

```

aggacatgcc tcaccctggc tccaggaagt tcaacaccac agagagggtc ctgcagggtc 60
tgcttgggtcc cttgttcaag aactccagtg tcggccctct gtactctggc tgcagactga 120
tctctctcag gtctgagaag gatggggcag ccactggagt ggatgccatc tgcacccacc 180
accttaaccc tcaaagcctg gactggacag ggagcagctg tactggcagc tgagccagat 240
gaccaatggc atcaaagagc tgggcccta caccctggac cggaacagtc tctacgtcaa 300
tg 302

```

&lt;210&gt; 524

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 524

```

gtttcaccca tcggagctct gggctcacca ccagcaactcc ttggacttcc acagttgacc 60
ttgaacctc agggactcca tccccgtcc ccagcccccac aactgttggc cctctcctgg 120

```

```

tgccattcac cctaaacttc accatcacca acctgcagta tgaggaggac atgcatcgcc 180
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tcaagaactc cagtgttggc cctctgtact ctggctgcag actgacctct ctcaggcccg 300
agaaggatgg ggcagcaact ggaatggatg ctgtctgcct ctaccaccct aatcccaaaa 360
gacctgggct ggacagagag cagctgtact gggagctaag ccagctgacc cacaacatca 420
ctgagctggg cccctacagc ctggacaggg acagtctcta tgtcaatg 468

```

&lt;210&gt; 525

&lt;211&gt; 470

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 525

```

gtttcaccca tcagaactct gtgcccacca ccagtactcc tgggacctcc acagtgtact 60
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taccattcac attcaacttt accatcacca acctgcatta tgaggaaaac atgcaacacc 180
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agaaggatgg ggcagcaact ggaatggatg ctgtctgtct ctaccgaccc taatcccatc 360
ggacctgggc tggacagaga gcagctgtac tgggagctga gccagctgac ccacgacatc 420
actgagctgg gccctacag cctggacag ggacagtctc tatgtcaatg 470

```

&lt;210&gt; 526

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 526

```

gtttcaccca tcagaactct gtgcccacca ccagtactcc tgggacctcc acagtgtact 60
gggcaaccac tgggactcca tctccttcc ccggccacac agagcctggc cctctcctga 120
taccattcac tttcaacttt accatcacca acctgcatta tgaggaaaac atgcaacacc 180
tggttccagg aagttaaca ccacggagag ggttctgcag ggtctgctca cggccttggt 240
caagaacacc agtgttggcc ctctgtactc tggctgcaga ctgaccttgc tcagacctga 300
gaagcaggag gcagccactg gagtggacac catctgcact caccgccttg accctctaaa 360
ccctggactg gacagagagc agctatactg ggagctgagc aaactgaccc gtggcatcat 420
cgagctgggc ccctacctcc tggacagagg cagtctctat gtcaatg 467

```

&lt;210&gt; 527

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 527

```

gtttcaccca tcggaacttt gtgcccacca ccagcactcc tgggacctcc acagtacacc 60
taggaacctc tgaaactcca tctccctac ctagaccat agtgccctggc cctctcctgg 120
tgccattcac cctcaacttc accatcacca acttgcagta tgaggaggcc atgacgacacc 180
ctggctccag gaagttcaat accacggaga gggtcctaca gggctctgctc aggcccttgt 240
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agaaggacaa ggcagccacc agagtggatg ccatctgtac ccaccaccct gacctcaaaa 360
gccctggact gaacagagag cagctgtact gggagctgag ccagctgacc cacggcatca 420
ctgagctggg cccctacacc ctggacaggg acagtctcta tgtcaatg 468

```

&lt;210&gt; 528

&lt;211&gt; 537

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 528

```

gtttcaccca tcagagcccc ataccaacca ccagcactcc tgatacctcc acaatgcacc 60
tgggaacctc gagaactcca gcctccctgt ctggacctac gaccgccagc cctctcctgg 120
tgctattcac aattaacttc accatcacta acctgcggtg tgaggagaac atgcatcacc 180
gctggctcta gaaagttaa caccacggag agagtccttc agggctctgt caggcctgtg 240
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ggcggtcatt ggtccagaca gggagcctgg agttctcgag gttgccagggt gcatgtc 537

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<210> 529  
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 <212> DNA  
 <213> Homo sapiens

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<400> 529
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gcgccccagg tctgcctatc aagcagggtg tccatgagct gagccagcag acccatggca 180
tcacccggct gggccctac tctctggaca aagacagcct ctaccttaac g 231

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<210> 530  
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 <212> DNA  
 <213> Homo sapiens

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<400> 530
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acttcacat ctccaatctc cagtattcac cagatatggg caagggtca gctacattca 180
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agcgatagct cttcat 376

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<210> 531  
 <211> 75  
 <212> DNA  
 <213> Homo sapiens

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<400> 531
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gtctctatgt caatg 75

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<210> 532  
 <211> 906  
 <212> DNA  
 <213> Homo sapiens

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<400> 532
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tgccgttcac cctcaacttt accatcacca atctgcagta tggggaggac atgcgtcacc 180
ctggctccag gaagttcaac accacagaga gggctctgca gggctctgtt ggctccttgt 240
tcaagaactc cagtgtcggc cctctgtact ctggctgcag actgatctct ctcaggctctg 300
agaaggatgg ggagccact ggagtggatg ccatctgcac ccaccacctt aaccctcaa 360
gcctggact ggacaggag cagctgtact ggcagctgag ccagagacca caacctcatt 420
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gtgcatcaaa gatgctgacc tcaactgtca tcagttcttg gacagacagc actacaactt 540
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ctgcagagac caacacaatg gttcccagga caactcccaa gttttcccat agtaagtcag 660
acaccacact cccagtagcc atcaccagtc ctggggccaga agccagttca gctgtttcaa 720
cgacaactat ctcaactgat atgtcagatc tgggtgacctc actggtccct agttctggga 780
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ccacgtggct cactcatcct gcagaaacca gaacaacggg ttctgggaca attcccaact 900
tttccc                                     906

```

&lt;210&gt; 533

&lt;211&gt; 404

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 533

```

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tgccgttcac cctcaacttt accatcacca atctgcagta tggggaggac atgcgtcacc 180
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tcaagaactc cagtgtcggc cctctgtact ctggctgcag actgatctct ctcaggctctg 300
agaaggatgg ggcagccact ggagtggatg ccatctgcac ccaccacctt aaccctcaaa 360
gccttggaact ggacagggag cagctgtact ggcagctgag ccag                                     404

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&lt;210&gt; 534

&lt;211&gt; 157

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 534

```

gcagccacca aagtggatgc catctgcacc taccgccctg atcccaaaag ccctggactg 60
gacagagagc agctatactg ggagctgagc cagctaacc ccagcatcac tgagctgggc 120
ccctacacc tggacagggg cagctctctat gtcaatg                                     157

```

&lt;210&gt; 535

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 535

```

gtttcacaca gcggagctct gtgcccacca ctagcattcc tgggaccccc acagtggacc 60
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gccctaggct ggacagagag cagctgtatt gggagctgag ccagctgacc cacaatatca 420
ctgagctggg cccctatgcc ctggacaacg acagcctctt tgtcaatg                                     468

```

&lt;210&gt; 536

&lt;211&gt; 334

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 536

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tactattcac cctcaacttc accatcacta acctgcggta tgaggagaac atgtggcctg 180
gtccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg cccttgttca 240

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aagatgggga agccaccgga gtggatgcca tctg 334

<210> 537  
<211> 127  
<212> DNA  
<213> Homo sapiens

<400> 537  
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<210> 538  
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<212> DNA  
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agaaggatgg agcagccact ggagtggatg ccatctgcac ccaccgtctt gacccccaaa 360  
gccctggagt ggacagggag cagctatact gggagctgag ccagctgacc aatggcatca 420  
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<212> DNA  
<213> Homo sapiens

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aggatggagc agccactgga gtggatgcca tctgcacca ccgtcttgac cccaaaagcc 360  
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gctgggtccc tacaccctgg acagcaacag tcttctatgt caatg 465

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<212> DNA  
<213> Homo sapiens

<400> 540  
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tgccattcac cctcaacttc accatcacca acctgcagta cgaggaggac atgcatcacc 180  
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tcaagaacac tacga 255

<210> 541  
<211> 390  
<212> DNA

<213> Homo sapiens

<400> 541

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actcatcacc aacctgcagt acgaggagga catgcgccac ctggttccag gaagttcaac 120
gcgcacagag agagaactgc agggctcgtgc tcaaacccta gatcaggaat agcagtctgg 180
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<210> 542

<211> 468

<212> DNA

<213> Homo sapiens

<400> 542

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gccctggact caacagggag cagctgtact gggagctaag caaactgacc aatgacattg 420
aagagctggg cccctacacc ctggacagga acagtctcta tgtcaatg 468
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<210> 543

<211> 475

<212> DNA

<213> Homo sapiens

<400> 543

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ctcctggtac cattcacctc caacttcacc atcaccaacc tgcagtatgg ggaggacatg 180
ggtcaccctg gctccaggaa gttcaacacc acagagaggg tcctgcaggg tctgcttggt 240
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cccaaaagcc ctggactcaa cagagagcgg ctgtactggg agctgagcca actgaccaat 420
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<210> 544

<211> 485

<212> DNA

<213> Homo sapiens

<400> 544

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cgtggttcca ggaacgatgt caacaccaca ggagaggggt ctgcagggtc ttcgctcacg 240
cccattgtta caagaacacc agtagttggc cctctgtact ctggctgcag aatgaccttg 300
ctcagacctg agaagcagga ggcaacacac tgggaatggac accatctgta tccaccagcg 360
ttagatccca tcaggacctg gactggacag agagcaggct atactgggag ctagagccag 420
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caatg 485
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<210> 545

<211> 141  
<212> DNA  
<213> Homo sapiens

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taccattcac cctcaactta c 141

<210> 546  
<211> 142  
<212> DNA  
<213> Homo sapiens

<400> 546  
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aaagacagcc tctaccttaa cg 142

<210> 547  
<211> 185  
<212> DNA  
<213> Homo sapiens

<400> 547  
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tcgccctgac cctgaagacc tcggactgga cagagagcga ctgtactggg agctgagcaa 120  
tctgacaaat ggcattccagg agctggggccc ctacaccctg gaccggaaca gtctctatgt 180  
caatg 185

<210> 548  
<211> 462  
<212> DNA  
<213> Homo sapiens

<400> 548  
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tgccgttcac cctcaacttc accatcacca acctgcagta cgaggaggac atgcgtcgca 180  
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atggggcagc cactggagtg gatgccatct gacccaccg ccttgacccc aaaagccctg 360  
gactcaacag ggagcagctg tactgggagc taagcaaact gaccaatgac attgaagagc 420  
tgggccccta caccctggac aggaacagtc tctatgtcaa tg 462

<210> 549  
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<213> Homo sapiens

<400> 549  
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accagtgttg gccctctgta ctctggctgc agactgacct ctctcaggtc tgagaaggat 240  
ggagcagcca ctggagtgga tgccatctgc atccatcatc ttgaccccaa aagccctgga 300  
ctcaacagag agcggctgta ctgggagctg agccaaactga ccaatggcat caaagagctg 360  
ggcccctaca ccctggacag gaacagtctc tatgtcaatg 400

<210> 550  
<211> 468  
<212> DNA  
<213> Homo sapiens

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agaaggatgg agcagtcact ggagtggatg ccatctgcac ccaccgtctt gacccccaaa 360  
gccctggagt ggacagggag cagctatact gggagctgag ccagctgacc aatggcatca 420  
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<210> 551  
<211> 366  
<212> DNA  
<213> Homo sapiens

<400> 551  
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ctctgcgtgg tcctatgttc aagaacacca gtgggtggcct tctgtactct ggctgcagac 180  
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accgtcttga ccccaaaagc cctggagtgg acagggagca gctatactgg gagctgagcc 300  
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<210> 552  
<211> 465  
<212> DNA  
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<400> 552  
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cattcacctc caacttcacc atcaccaacc tgcagtacga ggaggacatg catcacccag 180  
gctccaggaa gttcaacacc acggagcggg tctgagggg tctgcttggg cccatgttca 240  
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agaatggggc agccactgga atggatgcca tctgcagcca ccgtcttgac cccaaaagcc 360  
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<210> 553  
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<213> Homo sapiens

<400> 553  
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caccaacctg gagtacgagg aggacatgca ttgccctggc tccaggaagt tcaacaccac 180  
agagagagtc ctgcagagtc tgcttgggtc catgttcaag aacaccagtg ttggccctct 240  
gtactctggc tgcagactga ccttgtctcag gtccgagaag gatggagcag ccactggagt 300  
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<210> 554  
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 <213> Homo sapiens

<400> 554  
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 gtacgaggag gacatgcata acccaggctc cagggaagttc aacaccacgg agcgggtcct 180  
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 gagccagctg acccatggca tcaaa 385

<210> 555  
 <211> 173  
 <212> DNA  
 <213> Homo sapiens

<400> 555  
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<210> 556  
 <211> 468  
 <212> DNA  
 <213> Homo sapiens

<400> 556  
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 ctgagctggg cccctacagc ctggacaggc acagtctcta tgtcaatg 468

<210> 557  
 <211> 468  
 <212> DNA  
 <213> Homo sapiens

<400> 557  
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 gacctggact ggacagagag cggctatact gggagctgag ccagctgacc aacagcatca 420  
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<210> 558  
 <211> 468  
 <212> DNA

<213> Homo sapiens

<400> 558

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<210> 559

<211> 468

<212> DNA

<213> Homo sapiens

<400> 559

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<210> 560

<211> 468

<212> DNA

<213> Homo sapiens

<400> 560

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<210> 561

<211> 468

<212> DNA

<213> Homo sapiens

<400> 561

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<210> 562

<211> 407  
 <212> DNA  
 <213> Homo sapiens

<400> 562

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gactggacag agagcggctg tactggaagc tgagccagct gaccacggc atcactgagc 360
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<210> 563  
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 <212> DNA  
 <213> Homo sapiens .

<400> 563

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<210> 564  
 <211> 468  
 <212> DNA  
 <213> Homo sapiens

<400> 564

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gccctaggct ggacagagag cagctgtatt gggagctgag ccagctgacc cacaatatca 420
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<210> 565  
 <211> 465  
 <212> DNA  
 <213> Homo sapiens

<400> 565

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agctgggccc ctacacactg gacagggaca gtctctatgt caatg 465
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<210> 566  
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 <212> DNA  
 <213> Homo sapiens

<400> 566  
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 ccctcaagtt caacatcaca gacaacgtca tgaagcacct gctcagtcct ttgttcaga 180  
 ggagcagcct ggggtgcacgg tacacaggct gcagggtcat cgcactaagg tctgtgaaga 240  
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 gtctgcctat caagcaggtg ttccatgagc tgagccagca gacccatggc atcaccgggc 360  
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<210> 567  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<400> 567  
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agggatagcc tcttcatcaa tggctatgca cccagaatt tatcaatccg gggcgagtac 9600
cagataaatt tccacattgt caactggaac ctcagtaatc cagacccac atcctcagag 9660
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aa 10622

```

&lt;210&gt; 570

&lt;211&gt; 469

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

<222> 71, 92, 93, 120, 124, 168, 178, 218, 230, 300,  
321, 350, 387, 412, 414, 415, 422, 423, 451

&lt;223&gt; n = A, T, C or G

&lt;400&gt; 570

```

gtttcaccca tcggagctct gtgcccacca ccagcactcc tgggacctcc acagtggacc 60
tgggaacctc wgggactcca tcctccctcc cyrgcccccag agctgctggc cctctcctgr 120
tgcyattcac cctcaacttc accatcacca acctgcagta tgaggagrac atgcatrc 180
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agccctggac tggacagaga gcagctrtac tgggagctga gccagctgac cmayrgcatc 420
amwgagctgg gccctacac cctggacagg racagtctct atgtcaatg 469

```

&lt;210&gt; 571

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variant

&lt;222&gt; 69, 107, 110

&lt;223&gt; Xaa = Any amino acid

&lt;400&gt; 571

```

His Pro Gln Leu Glu Gln Gln Pro Gln Ser His Ser Trp Cys His Ser
          5                      10                      15

```

```

Pro Ser Thr Ser Thr His His Gln Pro Ala Val Arg Gly Gly His Ala
          20                      25                      30

```

190

Ala Pro Gly Ser Arg Lys Phe Asn Ala His Arg Glu Arg Thr Ala Gly  
                   35                  40                  45

Ser Cys Ser Asn Pro Arg Ser Gly Ile Ala Val Trp Asn Thr Ser Ile  
           50                  55                  60

Gln Ala Ala Asp Xaa Pro His Ser Gly Gln Arg Arg Ile Ala Gln Pro  
   65                  70                  75                  80

Arg Gln Trp Met Pro Ser Ala His Ile Ala Leu Thr Leu Lys Thr Ser  
                   85                  90                  95

Asp Trp Thr Glu Ser Asp Cys Thr Gly Ser Xaa Ala Ile Xaa Gln Met  
                  100                 105                 110

Ala Ser Arg Ser Trp Ala Pro Thr Pro Trp Thr Gly Thr Val Ser Met  
          115                 120                 125

Ser Met  
   130

<210> 572  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> variant  
 <222> 1,58,78,92,94  
 <223> Xaa = Any amino acid

<400> 572  
 Xaa Ile Pro Ser Ser Asn Ser Ser His Ser Pro Ile His Gly Ala Ile  
                   5                  10                  15

His Pro Gln Leu Gln Leu Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met  
           20                  25                  30

Arg His Leu Val Pro Gly Ser Ser Thr Arg Thr Glu Arg Glu Leu Gln  
          35                  40                  45

Gly Arg Ala Gln Thr Leu Asp Gln Glu Xaa Gln Ser Gly Ile Pro Leu  
   50                  55                  60

Phe Arg Leu Gln Thr Ser Leu Thr Gln Ala Arg Glu Gly Xaa Leu Ser  
   65                  70                  75                  80

His Gly Ser Gly Cys His Leu His Thr Ser Pro Xaa Pro Xaa Arg Pro  
          85                  90                  95

Arg Thr Gly Gln Arg Ala Thr Val Leu Gly Ala Glu Gln Ser Asp Lys  
          100                 105                 110

Trp His Pro Gly Ala Gly Pro Leu His Pro Gly Pro Glu Gln Ser Leu  
          115                 120                 125

Cys Gln

130

```
<210> 573
<211> 130
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> 1,54
<223> Xaa = Any amino acid
```

|   |     |
|---|-----|
| <400>   | 573 |
| Xaa Ser Pro Ala Arg Thr Ala Ala Thr Val Pro Phe Met Val Pro Phe<br>5                    10                    15                                    |     |
| Thr Leu Asn Phe Asn Ser Ser Pro Thr Cys Ser Thr Arg Arg Thr Cys<br>20                                25                    30                       |     |
| Gly Thr Trp Phe Gln Glu Val Gln Arg Ala Gln Arg Glu Asn Cys Arg<br>35                                40                    45                       |     |
| Val Val Leu Lys Pro Xaa Ile Arg Asn Ser Ser Leu Glu Tyr Leu Tyr<br>50                                55                    60                       |     |
| Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala<br>65                                70                    75                    80 |     |
| Thr Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu<br>85                                90                    95                       |     |
| Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn<br>100                                105                    110                    |     |
| Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr<br>115                                120                    125                    |     |
| Val Asn<br>130  |     |

```
<210> 574
<211> 156
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> 101  
<223> Xaa = Any amino acid
```

<400> 574  
Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr  
                  5                       10                       15  
  
Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser  
                20                       25                       30

Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr  
                   35                                  40                                  45  
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg  
           50                                  55                                  60  
 Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu  
       65                                  70                                  75                                  80  
 Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
                                   85                                  90                                  95  
 Leu Leu Arg Pro Xaa Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile  
                   100                                  105                                  110  
 Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln  
                   115                                  120                                  125  
 Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly  
           130                                  135                                  140  
 Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn  
       145                                  150                                  155

&lt;210&gt; 575

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variant

&lt;222&gt; 103

&lt;223&gt; Xaa = Any amino acid

&lt;400&gt; 575

Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr  
                                   5                                  10                                  15  
 Ser Thr Val Asp Leu Arg Thr Ser Val Thr Pro Ser Ser Leu Ser Ser  
                   20                                  25                                  30  
 Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn  
                   35                                  40                                  45  
 Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly  
           50                                  55                                  60  
 Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly  
       65                                  70                                  75                                  80  
 Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg  
                   85                                  90                                  95  
 Leu Thr Ser Leu Arg Ser Xaa Lys Asp Gly Ala Ala Thr Gly Val Asp  
           100                                  105                                  110

193

Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg  
 115 120 125

Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu  
 130 135 140

Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn  
 145 150 155

<210> 576

<211> 122

<212> PRT

<213> Homo sapiens

<400> 576

Ala Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr  
 5 10 15

Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe  
 20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Arg Gly Pro Met Phe Lys  
 35 40 45

Asn Thr Ser Gly Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu  
 50 55 60

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr  
 65 70 75 80

His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr  
 85 90 95

Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr  
 100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn  
 115 120

<210> 577

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 11,106,151

<223> Xaa = Any amino acid

<400> 577

Gly Phe Thr His Arg Thr Ser Val Pro Thr Xaa Ser Thr Pro Gly Thr  
 5 10 15

Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser  
 20 25 30



Pro Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr  
                   35                                  40                                  45  
 Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg  
           50                                  55                                  60  
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Leu Gly Pro Met  
       65                                  70                                  75                                  80  
 Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr  
                                   85                                  90                                  95  
 Leu Leu Arg Ser Glu Lys Asp Gly Ala Xaa Thr Gly Val Asp Ala Ile  
                   100                                  105                                  110  
 Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln  
           115                                  120                                  125  
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly  
       130                                  135                                  140  
 Pro Tyr Thr Leu Asp Arg Xaa Ser Leu Tyr Val Asn  
   145                                  150                                  155

<210> 578  
 <211> 155  
 <212> PRT  
 <213> Homo sapiens

<400> 578  
 Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr  
                                   5                                  10                                  15  
 Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro  
                   20                                  25                                  30  
 Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile  
           35                                  40                                  45  
 Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys  
       50                                  55                                  60  
 Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe  
       65                                  70                                  75                                  80  
 Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu  
                                   85                                  90                                  95  
 Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys  
           100                                  105                                  110  
 Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu  
           115                                  120                                  125  
 Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro  
       130                                  135                                  140

195

Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn  
 145 150 155

&lt;210&gt; 579

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variant

&lt;222&gt; 52,138

&lt;223&gt; Xaa = Any amino acid

&lt;400&gt; 579

Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr  
                   5                                  10                                  15

Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro  
                   20                                  25                                  30

Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile  
                   35                                  40                                  45

Thr Asn Leu Xaa Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys  
                   50                                  55                                  60

Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly Pro Met Phe  
                   65                                  70                                  75                                  80

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu  
                                   85                                  90                                  95

Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys  
                   100                                  105                                  110

Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu  
                   115                                  120                                  125

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Xaa Ile Lys Glu Leu Gly Pro  
                   130                                  135                                  140

Tyr Thr Leu Asp Ser Asn Ser Leu Tyr Val Asn  
 145 150 155

&lt;210&gt; 580

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variant

&lt;222&gt; 23

&lt;223&gt; Xaa = Any amino acid

&lt;400&gt; 580

Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser | Thr | Val | Asp | Leu | Gly | Xaa | Ser | Gly | Thr | Pro | Ser | Ser | Leu | Pro | Ser |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Pro | Thr | Ser | Ala | Gly | Pro | Leu | Leu | Val | Pro | Phe | Thr | Leu | Asn | Phe | Thr |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Ile | Thr | Asn | Leu | Gln | Tyr | Glu | Glu | Asp | Met | His | His | Pro | Gly | Ser | Arg |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Lys | Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Gly | Pro | Met |  |  |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Phe | Lys | Asn | Thr | Ser | Val | Gly | Leu | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Leu | Leu | Arg | Pro | Glu | Lys | Asn | Gly | Ala | Ala | Thr | Gly | Met | Asp | Ala | Ile |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Cys | Ser | His | Arg | Leu | Asp | Pro | Lys | Ser | Pro | Gly | Leu | Asn | Arg | Glu | Gln |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Leu | Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr | His | Gly | Ile | Lys | Glu | Leu | Gly |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Pro | Tyr | Thr | Leu | Asp | Arg | Asn | Ser | Leu | Tyr | Val | Asn |     |     |     |     |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |  |  |

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<210> 581
<211> 156
<212> PRT
<213> Homo sapiens
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|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 581 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly       | Phe | Thr | His | Arg | Ser | Ser | Val | Ala | Pro | Thr | Ser | Thr | Pro | Gly | Thr |
|           |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser       | Thr | Val | Asp | Leu | Gly | Thr | Ser | Gly | Thr | Pro | Ser | Ser | Leu | Pro | Ser |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro       | Thr | Thr | Ala | Val | Pro | Leu | Leu | Val | Pro | Phe | Thr | Leu | Asn | Phe | Thr |
|           |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ile       | Thr | Asn | Leu | Gln | Tyr | Gly | Glu | Asp | Met | Arg | His | Pro | Gly | Ser | Arg |
|           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys       | Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Gly | Pro | Leu |
| 65        |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe       | Lys | Asn | Ser | Ser | Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Ile |
|           |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser       | Leu | Arg | Ser | Glu | Lys | Asp | Gly | Ala | Ala | Thr | Gly | Val | Asp | Ala | Ile |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys       | Thr | His | His | Leu | Asn | Pro | Gln | Ser | Pro | Gly | Leu | Asp | Arg | Glu | Gln |

115 120 125  
 Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly  
 130 135 140

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn  
 145 150 155

<210> 582  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> variant  
 <222> 151  
 <223> Xaa = Any amino acid

<400> 582  
 Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr  
 5 10 15

Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser  
 20 25 30

Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr  
 35 40 45

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg  
 50 55 60

Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile  
 65 70 75 80

Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
 85 90 95

Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val  
 100 105 110

Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln  
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly  
 130 135 140

Pro Tyr Ser Leu Asp Arg Xaa Ser Leu Tyr Val Asn  
 145 150 155

<210> 583  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> variant

Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr  
5 10 15

Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly  
20 25 30

His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr  
35 40 45

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg  
50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu  
65 70 75 80

Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
85 90 95

Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Xaa Asp Thr Ile  
100 105 110

Cys Xaa His Arg Xaa Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Xaa  
115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Xaa Ile Thr Glu Leu Gly  
130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn  
145                      150                      155

<213> Homo sapiens

Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr  
5 10 15

Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly  
20 25 30

His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr  
35 40 45

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg  
50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu  
65 70 75 80

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
85 90 95

Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile  
 100 105 110

Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg  
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly  
 130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn  
 145 150 155

<210> 585

<211> 156

<212> PRT

<213> Homo sapiens

<400> 585

Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr  
 5 10 15

Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly  
 20 25 30

His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr  
 35 40 45

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg  
 50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu  
 65 70 75 80

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
 85 90 95

Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile  
 100 105 110

Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln  
 115 120 125

Leu Tyr Trp Glu Leu Ser Lys Leu Thr Cys Gly Ile Ile Glu Leu Gly  
 130 135 140

Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn  
 145 150 155

<210> 586

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

**<222> 151, 156**

<223> Xaa = Any amino acid

<400> 586

Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr Pro Gly Thr  
5 10 15

Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg  
20 25 30

Pro Ile Val Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr  
35 40 45

Ile Thr Asn Leu Gln Tyr Glu Glu Ala Met Arg His Pro Gly Ser Arg  
50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu  
65 70 75 80

Phe Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr  
85 90 95

Leu Leu Arg Pro Glu Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile  
100 105 110

Cys Thr His His Pro Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln  
115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly  
130 135 140

Pro Tyr Thr Leu Asp Arg Xaa Ser Leu Tyr Val Xaa  
145                      150                      155

<210> 587

<211> 156

<212> PRT

<213> Homo sapiens

<400> 587

Gly Phe Thr His Trp Ser Pro Ile Pro Thr Thr Ser Thr Pro Gly Thr  
5 10 15

Ser Ile Val Asn Leu Gly Thr Ser Gly Ile Pro Pro Ser Leu Pro Glu  
20 25 30

Thr Thr Ala Thr Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr  
35 40 45

Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly Ser Arg  
50 55 60

Lys Phe Asn Ile Thr Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu  
65 70 75 80

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
85 90 95

201

Leu Leu Arg Pro Glu Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile  
 100 105 110

Cys Thr His Arg Pro Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln  
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly  
 130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn  
 145 150 155

&lt;210&gt; 588

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 588

Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr  
 5 10 15

Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro Ser Ser Leu Pro Gly  
 20 25 30

Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn Phe Thr  
 35 40 45

Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg  
 50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu  
 65 70 75 80

Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr  
 85 90 95

Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val  
 100 105 110

Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg  
 115 120 125

Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly  
 130 135 140

Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn  
 145 150 155

&lt;210&gt; 589

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 589

Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr



202

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |  |
| Ser | Thr | Met | His | Leu | Ala | Thr | Ser | Arg | Thr | Pro | Ala | Ser | Leu | Ser | Gly |     |  |
| 20  |     |     |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Pro | Thr | Thr | Ala | Ser | Pro | Leu | Leu | Val | Leu | Phe | Thr | Ile | Asn | Phe | Thr |     |  |
| 35  |     |     |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Ile | Thr | Asn | Leu | Arg | Tyr | Glu | Glu | Asn | Met | His | His | Pro | Gly | Ser | Arg |     |  |
| 50  |     |     |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Lys | Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln | Gly | Leu | Leu | Arg | Pro | Val |     |  |
| 65  |     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |  |
| Phe | Lys | Asn | Thr | Ser | Val | Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr |     |  |
|     |     |     |     | 85  |     |     |     |     |     |     |     | 90  |     |     |     | 95  |  |
| Leu | Leu | Arg | Pro | Lys | Lys | Asp | Gly | Ala | Ala | Thr | Lys | Val | Asp | Ala | Ile |     |  |
|     |     |     |     | 100 |     |     |     |     |     |     |     | 105 |     |     |     | 110 |  |
| Cys | Thr | Tyr | Arg | Pro | Asp | Pro | Lys | Ser | Pro | Gly | Leu | Asp | Arg | Glu | Gln |     |  |
| 115 |     |     |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Leu | Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr | His | Ser | Ile | Thr | Glu | Leu | Gly |     |  |
| 130 |     |     |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Pro | Tyr | Thr | Leu | Asp | Arg | Asp | Ser | Leu | Tyr | Val | Asn |     |     |     |     |     |  |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     |     |     |  |

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<210> 590
<211> 156
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> 145
<223> Xaa = Any amino acid
```

```

<400> 590
Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr
      5                      10                      15

Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly
      20                      25                      30

Pro Ser Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr
      35                      40                      45

Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
      50                      55                      60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu
      65                      70                      75                      80

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
      85                      90                      95

```

Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile  
 100 105 110

Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln  
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly  
 130 135 140

Xaa Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn  
 145 150 155

<210> 591

<211> 155

<212> PRT

<213> Homo sapiens

<400> 591

Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr  
 5 10 15

Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly  
 20 25 30

Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr  
 35 40 45

Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys  
 50 55 60

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe  
 65 70 75 80

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu  
 85 90 95

Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys  
 100 105 110

Thr His Arg Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu  
 115 120 125

Tyr Leu Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro  
 130 135 140

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn  
 145 150 155

<210> 592

<211> 134

<212> PRT

<213> Homo sapiens

<400> 592

Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly Val Val

204

[illegible]

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<210> 593
<211> 150
<212> PRT
<213> Homo sapiens
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```
<220>  
<221> variant  
<222> 7  
<223> Xaa = Any amino acid
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|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 593 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Gly       | Tyr | Asn | Glu | Pro | Gly | Xaa | Asp | Glu | Pro | Pro | Thr | Thr | Pro | Lys | Pro |  |
|           |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala       | Thr | Thr | Phe | Leu | Pro | Pro | Leu | Ser | Glu | Ala | Thr | Thr | Ala | Met | Gly |  |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr       | His | Leu | Lys | Thr | Leu | Thr | Leu | Asn | Phe | Thr | Ile | Ser | Asn | Leu | Gln |  |
|           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr       | Ser | Pro | Asp | Met | Gly | Lys | Gly | Ser | Ala | Thr | Phe | Asn | Ser | Thr | Glu |  |
|           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly       | Val | Leu | Gln | His | Leu | Leu | Arg | Pro | Leu | Phe | Gln | Lys | Ser | Ser | Met |  |
| 65        |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gly       | Pro | Phe | Tyr | Leu | Gly | Cys | Gln | Leu | Ile | Ser | Leu | Arg | Pro | Glu | Lys |  |
|           |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp       | Gly | Ala | Ala | Thr | Gly | Val | Asp | Thr | Thr | Cys | Thr | Tyr | His | Pro | Asp |  |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |

Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser  
 115 120 125

Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg  
 130 135 140

Asp Ser Leu Phe Ile Asn  
 145 150

<210> 594

<211> 318

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 136,248,268

<223> Xaa = Any amino acid

<400> 594

Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn  
 5 10 15

Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser  
 20 25 30

Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu  
 35 40 45

Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr  
 50 55 60

Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser  
 65 70 75 80

Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr  
 85 90 95

Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp  
 100 105 110

Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser  
 115 120 125

Ser Ser Thr Gln His Phe Tyr Xaa Asn Phe Thr Ile Thr Asn Leu Pro  
 130 135 140

Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn  
 145 150 155 160

Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser  
 165 170 175

Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val  
 180 185 190

Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro  
 195 200 205

Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg  
 210 215 220

Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser  
 225 230 235 240

Ser Val Leu Val Asp Gly Tyr Xaa Pro Asn Arg Asn Glu Pro Leu Thr  
 245 250 255

Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Xaa Ile Gly Leu Ala  
 260 265 270

Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr  
 275 280 285

Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys  
 290 295 300

Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln  
 305 310 315

&lt;210&gt; 595

&lt;211&gt; 3451

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560, 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 595

Ile Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala  
 1 5 10 15

Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Thr Ala Val Asp Ala Ile  
 20 25 30

Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg  
 35 40 45

Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly  
 50 55 60

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His  
 65 70 75 80

Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp  
 85 90 95

Val Gly Thr Ser Gly Thr Pro Ser Ser Pro Ser Pro Thr Thr Ala  
 100 105 110

Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu  
 115 120 125

Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr  
 130 135 140

Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr  
 145 150 155 160

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Xaa | Lys | Asp | Gly | Ala | Ala | Thr | Gly | Val | Asp | Ala | Ile | Cys | Thr | His | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Asp | Pro | Lys | Ser | Pro | Gly | Leu | Asn | Arg | Glu | Gln | Leu | Tyr | Trp | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Ser | Lys | Leu | Thr | Asn | Asp | Ile | Glu | Glu | Leu | Gly | Pro | Tyr | Thr | Leu |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Arg | Asn | Ser | Leu | Tyr | Val | Asn | Gly | Phe | Thr | His | Gln | Ser | Ser | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Thr | Thr | Ser | Thr | Pro | Gly | Thr | Ser | Thr | Val | Asp | Leu | Arg | Thr | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Thr | Pro | Ser | Ser | Leu | Ser | Ser | Pro | Thr | Ile | Met | Ala | Ala | Gly | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Val | Pro | Phe | Thr | Leu | Asn | Phe | Thr | Ile | Thr | Asn | Leu | Gln | Tyr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Glu | Asp | Met | Gly | His | Pro | Gly | Ser | Arg | Lys | Phe | Asn | Thr | Thr | Glu |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Val | Leu | Gln | Gly | Leu | Leu | Gly | Pro | Ile | Phe | Lys | Asn | Thr | Ser | Val |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Pro | Leu | Tyr | Ser | Gly | Cys | Arg | Leu | Thr | Ser | Leu | Arg | Ser | Xaa | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Gly | Ala | Ala | Thr | Gly | Val | Asp | Ala | Ile | Cys | Ile | His | His | Leu | Asp |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Pro | Lys | Ser | Pro | Gly | Leu | Asn | Arg | Glu | Arg | Leu | Tyr | Trp | Glu | Leu | Ser |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gln | Leu | Thr | Asn | Gly | Ile | Lys | Glu | Leu | Gly | Pro | Tyr | Thr | Leu | Asp | Arg |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asn | Ser | Leu | Tyr | Val | Asn | Ala | Ala | Gly | Pro | Leu | Val | Leu | Phe | Thr |     |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     | 400 |     |
| Leu | Asn | Phe | Thr | Ile | Thr | Asn | Leu | Lys | Tyr | Glu | Glu | Asp | Met | His | Arg |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Pro | Gly | Ser | Arg | Lys | Phe | Asn | Thr | Thr | Glu | Arg | Val | Leu | Gln | Thr | Leu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Arg | Gly | Pro | Met | Phe | Lys | Asn | Thr | Ser | Gly | Gly | Leu | Leu | Tyr | Ser | Gly |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Cys | Arg | Leu | Thr | Leu | Leu | Arg | Ser | Glu | Lys | Asp | Gly | Ala | Ala | Thr | Gly |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Val | Asp | Ala | Ile | Cys | Thr | His | Arg | Leu | Asp | Pro | Lys | Ser | Pro | Gly | Val |
| 465 |     |     |     | 470 |     |     |     |     |     | 475 |     |     |     | 480 |     |
| Asp | Arg | Glu | Gln | Leu | Tyr | Trp | Glu | Leu | Ser | Gln | Leu | Thr | Asn | Gly | Ile |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Lys | Glu | Leu | Gly | Pro | Tyr | Thr | Leu | Asp | Arg | Asn | Ser | Leu | Tyr | Val | Asn |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Gly | Phe | Thr | His | Arg | Thr | Ser | Val | Pro | Thr | Xaa | Ser | Thr | Pro | Gly | Thr |
|     |     | 515 |     |     |     |     |     |     |     |     |     |     |     |     |     |

|      |      |      |      |     |      |      |      |      |      |      |     |      |      |      |      |
|------|------|------|------|-----|------|------|------|------|------|------|-----|------|------|------|------|
| 625  |      |      |      |     | 630  |      |      |      |      | 635  |     |      |      | 640  |      |
| Leu  | Tyr  | Trp  | Glu  | Leu | Ser  | Gln  | Leu  | Thr  | Asn  | Gly  | Ile | Lys  | Glu  | Leu  | Gly  |
|      |      |      |      | 645 |      |      |      |      | 650  |      |     |      |      | 655  |      |
| Pro  | Tyr  | Thr  | Leu  | Asp | Arg  | Xaa  | Ser  | Leu  | Tyr  | Val  | Asn | Gly  | Phe  | Thr  | His  |
|      |      |      | 660  |     |      |      |      | 665  |      |      |     |      | 670  |      |      |
| Trp  | Ile  | Pro  | Val  | Pro | Thr  | Ser  | Ser  | Thr  | Pro  | Gly  | Thr | Ser  | Thr  | Val  | Asp  |
|      |      | 675  |      |     |      | 680  |      |      |      |      |     | 685  |      |      |      |
| Leu  | Gly  | Ser  | Gly  | Thr | Pro  | Ser  | Ser  | Leu  | Pro  | Ser  | Pro | Thr  | Thr  | Ala  | Gly  |
|      | 690  |      |      |     |      | 695  |      |      |      | 700  |     |      |      |      |      |
| Pro  | Leu  | Leu  | Val  | Pro | Phe  | Thr  | Leu  | Asn  | Phe  | Thr  | Ile | Thr  | Asn  | Leu  | Gln  |
| 705  |      |      |      |     | 710  |      |      |      |      | 715  |     |      |      |      | 720  |
| Tyr  | Glu  | Glu  | Asp  | Met | His  | His  | Pro  | Gly  | Ser  | Arg  | Lys | Phe  | Asn  | Thr  | Thr  |
|      |      |      | 725  |     |      |      |      | 730  |      |      |     |      |      | 735  |      |
| Glu  | Arg  | Val  | Leu  | Gln | Gly  | Leu  | Leu  | Gly  | Pro  | Met  | Phe | Lys  | Asn  | Thr  | Ser  |
|      |      | 740  |      |     |      |      |      | 745  |      |      |     |      | 750  |      |      |
| Val  | Gly  | Leu  | Leu  | Tyr | Ser  | Gly  | Cys  | Arg  | Leu  | Thr  | Leu | Leu  | Arg  | Pro  | Glu  |
|      |      | 755  |      |     |      |      | 760  |      |      |      |     | 765  |      |      |      |
| Lys  | Asn  | Gly  | Ala  | Ala | Thr  | Gly  | Met  | Asp  | Ala  | Ile  | Cys | Ser  | His  | Arg  | Leu  |
|      | 770  |      |      |     |      | 775  |      |      |      | 780  |     |      |      |      |      |
| Asp  | Pro  | Lys  | Ser  | Pro | Gly  | Leu  | Asn  | Arg  | Glu  | Gln  | Leu | Tyr  | Trp  | Glu  | Leu  |
| 785  |      |      |      |     | 790  |      |      |      |      | 795  |     |      |      |      | 800  |
| Ser  | Gln  | Leu  | Thr  | His | Gly  | Ile  | Lys  | Glu  | Leu  | Gly  | Pro | Tyr  | Thr  | Leu  | Asp  |
|      |      |      | 805  |     |      |      |      |      | 810  |      |     |      |      | 815  |      |
| Arg  | His  | Ser  | Leu  | Tyr | Val  | Asn  | Gly  | Phe  | Thr  | His  | Trp | Ile  | Pro  | Val  | Pro  |
|      |      | 820  |      |     |      |      |      | 825  |      |      |     |      | 830  |      |      |
| Thr  | Ser  | Ser  | Thr  | Pro | Gly  | Thr  | Ser  | Thr  | Val  | Asp  | Leu | Gly  | Ser  | Gly  | Thr  |
|      |      | 835  |      |     |      |      | 840  |      |      |      |     | 845  |      |      |      |
| Pro  | Ser  | Ser  | Leu  | Pro | Ser  | Pro  | Thr  | Thr  | Ala  | Gly  | Pro | Leu  | Leu  | Val  | Pro  |
|      | 850  |      |      |     |      | 855  |      |      |      | 860  |     |      |      |      |      |
| Phe  | Thr  | Leu  | Asn  | Phe | Thr  | Ile  | Thr  | Asn  | Leu  | Xaa  | Tyr | Glu  | Glu  | Asp  | Met  |
| 865  |      |      |      |     | 870  |      |      |      |      | 875  |     |      |      |      | 880  |
| His  | Cys  | Pro  | Gly  | Ser | Arg  | Lys  | Phe  | Asn  | Thr  | Thr  | Glu | Arg  | Val  | Leu  | Gln  |
|      |      |      | 885  |     |      |      |      | 890  |      |      |     |      |      | 895  |      |
| Ser  | Leu  | Leu  | Gly  | Pro | Met  | Phe  | Lys  | Asn  | Thr  | Ser  | Val | Gly  | Pro  | Leu  | Tyr  |
|      |      | 900  |      |     |      |      |      | 905  |      |      |     |      | 910  |      |      |
| Ser  | Gly  | Cys  | Arg  | Leu | Thr  | Leu  | Leu  | Arg  | Ser  | Glu  | Lys | Asp  | Gly  | Ala  | Ala  |
|      |      | 915  |      |     |      |      |      | 920  |      |      |     | 925  |      |      |      |
| Thr  | Gly  | Val  | Asp  | Ala | Ile  | Cys  | Thr  | His  | Arg  | Leu  | Asp | Pro  | Lys  | Ser  | Pro  |
|      | 930  |      |      |     |      | 935  |      |      |      | 940  |     |      |      |      |      |
| Gly  | Val  | Asp  | Arg  | Glu | Gln  | Leu  | Tyr  | Trp  | Glu  | Leu  | Ser | Gln  | Leu  | Thr  | Asn  |
| 945  |      |      |      |     | 950  |      |      |      |      | 955  |     |      |      |      | 960  |
| Xaa  | Ile  | Lys  | Glu  | Leu | Gly  | Pro  | Tyr  | Thr  | Leu  | Asp  | Ser | Asn  | Ser  | Leu  | Tyr  |
|      |      |      | 965  |     |      |      |      |      | 970  |      |     |      |      | 975  |      |
| Val  | Asn  | Gly  | Phe  | Thr | His  | Gln  | Thr  | Ser  | Ala  | Pro  | Asn | Thr  | Ser  | Thr  | Pro  |
|      |      | 980  |      |     |      |      |      | 985  |      |      |     |      | 990  |      |      |
| Gly  | Thr  | Ser  | Thr  | Val | Asp  | Leu  | Gly  | Xaa  | Ser  | Gly  | Thr | Pro  | Ser  | Ser  | Leu  |
|      |      | 995  |      |     |      |      | 1000 |      |      |      |     | 1005 |      |      |      |
| Pro  | Ser  | Pro  | Thr  | Ser | Ala  | Gly  | Pro  | Leu  | Leu  | Val  | Pro | Phe  | Thr  | Leu  | Asn  |
|      | 1010 |      |      |     |      | 1015 |      |      |      | 1020 |     |      |      |      |      |
| Phe  | Thr  | Ile  | Thr  | Asn | Leu  | Gln  | Tyr  | Glu  | Glu  | Asp  | Met | His  | His  | Pro  | Gly  |
| 1025 |      |      |      |     | 1030 |      |      |      |      | 1035 |     |      |      |      | 1040 |
| Ser  | Arg  | Lys  | Phe  | Asn | Thr  | Thr  | Glu  | Arg  | Val  | Leu  | Gln | Gly  | Leu  | Leu  | Gly  |
|      |      |      | 1045 |     |      |      |      |      | 1050 |      |     |      |      | 1055 |      |
| Pro  | Met  | Phe  | Lys  | Asn | Thr  | Ser  | Val  | Gly  | Leu  | Leu  | Tyr | Ser  | Gly  | Cys  | Arg  |
|      |      | 1060 |      |     |      |      |      | 1065 |      |      |     |      | 1070 |      |      |
| Leu  | Thr  | Leu  | Leu  | Arg | Pro  | Glu  | Lys  | Asn  | Gly  | Ala  | Ala | Thr  | Gly  | Met  | Asp  |
|      | 1075 |      |      |     |      |      | 1080 |      |      |      |     | 1085 |      |      |      |
| Ala  | Ile  | Cys  | Ser  | His | Arg  | Leu  | Asp  | Pro  | Lys  | Ser  | Pro | Gly  | Leu  | Asn  | Arg  |

|   |   |      |
|---|---|------|
| 1090  | 1095  | 1100 |
| Glu Gln Leu Tyr Trp   | Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu |      |
| 1105  | 1110  | 1115 |
| Leu Gly Pro Tyr Thr   | Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe | 1120 |
|   | 1125  | 1130 |
| Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr |   | 1135 |
|   | 1140  | 1145 |
| Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr |   | 1150 |
|   | 1155  | 1160 |
| Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr |   | 1165 |
|   | 1170  | 1175 |
| Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe |   | 1180 |
| 1185  | 1190  | 1195 |
| Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys |   | 1200 |
|   | 1205  | 1210 |
| Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu |   | 1215 |
|   | 1220  | 1225 |
| Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr |   | 1230 |
|   | 1235  | 1240 |
| His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr |   | 1245 |
|   | 1250  | 1255 |
| Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr |   | 1260 |
| 1265  | 1270  | 1275 |
| Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser |   | 1280 |
|   | 1285  | 1290 |
| Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly |   | 1295 |
|   | 1300  | 1305 |
| Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro |   | 1310 |
|   | 1315  | 1320 |
| Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr |   | 1325 |
|   | 1330  | 1335 |
| Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu |   | 1340 |
| 1345  | 1350  | 1355 |
| Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val |   | 1360 |
|   | 1365  | 1370 |
| Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys |   | 1375 |
|   | 1380  | 1385 |
| Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn |   | 1390 |
|   | 1395  | 1400 |
| Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser |   | 1405 |
|   | 1410  | 1415 |
| Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg |   | 1420 |
| 1425  | 1430  | 1435 |
| Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr |   | 1440 |
|   | 1445  | 1450 |
| Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr |   | 1455 |
|   | 1460  | 1465 |
| Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro |   | 1470 |
|   | 1475  | 1480 |
| Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met |   | 1485 |
|   | 1490  | 1495 |
| Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln |   | 1500 |
| 1505  | 1510  | 1515 |
| Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr |   | 1520 |
|   | 1525  | 1530 |
| Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala |   | 1535 |
|   | 1540  | 1545 |
| Thr Gly Xaa Asp Thr Ile Cys Xaa His Arg Xaa Asp Pro Ile Gly Pro |   | 1550 |



1555                      1560                      1565  
 Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Gln Leu Thr His  
 1570                      1575                      1580  
 Xaa Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr  
 1585                      1590                      1595                      1600  
 Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro  
 1605                      1610                      1615  
 Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu  
 1620                      1625                      1630  
 Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn  
 1635                      1640                      1645  
 Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly  
 1650                      1655                      1660  
 Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys  
 1665                      1670                      1675                      1680  
 Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg  
 1685                      1690                      1695  
 Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp  
 1700                      1705                      1710  
 Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg  
 1715                      1720                      1725  
 Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu  
 1730                      1735                      1740  
 Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe  
 1745                      1750                      1755                      1760  
 Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala  
 1765                      1770                      1775  
 Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr  
 1780                      1785                      1790  
 Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr  
 1795                      1800                      1805  
 Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe  
 1810                      1815                      1820  
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys  
 1825                      1830                      1835                      1840  
 Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu  
 1845                      1850                      1855  
 Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr  
 1860                      1865                      1870  
 His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr  
 1875                      1880                      1885  
 Trp Glu Leu Ser Lys Leu Thr Cys Gly Ile Ile Glu Leu Gly Pro Tyr  
 1890                      1895                      1900  
 Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn  
 1905                      1910                      1915                      1920  
 Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly  
 1925                      1930                      1935  
 Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro  
 1940                      1945                      1950  
 Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr  
 1955                      1960                      1965  
 Glu Glu Ala Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu  
 1970                      1975                      1980  
 Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Ile  
 1985                      1990                      1995                      2000  
 Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys  
 2005                      2010                      2015  
 Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro Asp

|      |     |     |     |     |      |     |     |     |     |      |     |     |     |     |      |  |
|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|--|
| 2020 |     |     |     |     | 2025 |     |     |     |     | 2030 |     |     |     |     |      |  |
| Pro  | Gln | Ser | Pro | Gly | Leu  | Asn | Arg | Glu | Gln | Leu  | Tyr | Trp | Glu | Leu | Ser  |  |
| 2035 |     |     |     |     | 2040 |     |     |     |     | 2045 |     |     |     |     |      |  |
| Gln  | Leu | Thr | His | Gly | Ile  | Thr | Glu | Leu | Gly | Pro  | Tyr | Thr | Leu | Asp | Arg  |  |
| 2050 |     |     |     |     | 2055 |     |     |     |     | 2060 |     |     |     |     |      |  |
| Xaa  | Ser | Leu | Tyr | Val | Xaa  | Gly | Phe | Thr | His | Trp  | Ser | Pro | Ile | Pro | Thr  |  |
| 2065 |     |     |     |     | 2070 |     |     |     |     | 2075 |     |     |     |     | 2080 |  |
| Thr  | Ser | Thr | Pro | Gly | Thr  | Ser | Ile | Val | Asn | Leu  | Gly | Thr | Ser | Gly | Ile  |  |
| 2085 |     |     |     |     | 2090 |     |     |     |     | 2095 |     |     |     |     |      |  |
| Pro  | Pro | Ser | Leu | Pro | Glu  | Thr | Thr | Ala | Thr | Gly  | Pro | Leu | Leu | Val | Pro  |  |
| 2100 |     |     |     |     | 2105 |     |     |     |     | 2110 |     |     |     |     |      |  |
| Phe  | Thr | Leu | Asn | Phe | Thr  | Ile | Thr | Asn | Leu | Gln  | Tyr | Glu | Glu | Asn | Met  |  |
| 2115 |     |     |     |     | 2120 |     |     |     |     | 2125 |     |     |     |     |      |  |
| Gly  | His | Pro | Gly | Ser | Arg  | Lys | Phe | Asn | Ile | Thr  | Glu | Ser | Val | Leu | Gln  |  |
| 2130 |     |     |     |     | 2135 |     |     |     |     | 2140 |     |     |     |     |      |  |
| Gly  | Leu | Leu | Lys | Pro | Leu  | Phe | Lys | Ser | Thr | Ser  | Val | Gly | Pro | Leu | Tyr  |  |
| 2145 |     |     |     |     | 2150 |     |     |     |     | 2155 |     |     |     |     | 2160 |  |
| Ser  | Gly | Cys | Arg | Leu | Thr  | Leu | Leu | Arg | Pro | Glu  | Lys | Asp | Gly | Val | Ala  |  |
| 2165 |     |     |     |     | 2170 |     |     |     |     | 2175 |     |     |     |     |      |  |
| Thr  | Arg | Val | Asp | Ala | Ile  | Cys | Thr | His | Arg | Pro  | Asp | Pro | Lys | Ile | Pro  |  |
| 2180 |     |     |     |     | 2185 |     |     |     |     | 2190 |     |     |     |     |      |  |
| Gly  | Leu | Asp | Arg | Gln | Gln  | Leu | Tyr | Trp | Glu | Leu  | Ser | Gln | Leu | Thr | His  |  |
| 2195 |     |     |     |     | 2200 |     |     |     |     | 2205 |     |     |     |     |      |  |
| Ser  | Ile | Thr | Glu | Leu | Gly  | Pro | Tyr | Thr | Leu | Asp  | Arg | Asp | Ser | Leu | Tyr  |  |
| 2210 |     |     |     |     | 2215 |     |     |     |     | 2220 |     |     |     |     |      |  |
| Val  | Asn | Gly | Phe | Thr | Gln  | Arg | Ser | Ser | Val | Pro  | Thr | Thr | Ser | Thr | Pro  |  |
| 2225 |     |     |     |     | 2230 |     |     |     |     | 2235 |     |     |     |     | 2240 |  |
| Gly  | Thr | Phe | Thr | Val | Gln  | Pro | Glu | Thr | Ser | Glu  | Thr | Pro | Ser | Ser | Leu  |  |
| 2245 |     |     |     |     | 2250 |     |     |     |     | 2255 |     |     |     |     |      |  |
| Pro  | Gly | Pro | Thr | Ala | Thr  | Gly | Pro | Val | Leu | Leu  | Pro | Phe | Thr | Leu | Asn  |  |
| 2260 |     |     |     |     | 2265 |     |     |     |     | 2270 |     |     |     |     |      |  |
| Phe  | Thr | Ile | Ile | Asn | Leu  | Gln | Tyr | Glu | Glu | Asp  | Met | His | Arg | Pro | Gly  |  |
| 2275 |     |     |     |     | 2280 |     |     |     |     | 2285 |     |     |     |     |      |  |
| Ser  | Arg | Lys | Phe | Asn | Thr  | Thr | Glu | Arg | Val | Leu  | Gln | Gly | Leu | Leu | Met  |  |
| 2290 |     |     |     |     | 2295 |     |     |     |     | 2300 |     |     |     |     |      |  |
| Pro  | Leu | Phe | Lys | Asn | Thr  | Ser | Val | Ser | Ser | Leu  | Tyr | Ser | Gly | Cys | Arg  |  |
| 2305 |     |     |     |     | 2310 |     |     |     |     | 2315 |     |     |     |     | 2320 |  |
| Leu  | Thr | Leu | Leu | Arg | Pro  | Glu | Lys | Asp | Gly | Ala  | Ala | Thr | Arg | Val | Asp  |  |
| 2325 |     |     |     |     | 2330 |     |     |     |     | 2335 |     |     |     |     |      |  |
| Ala  | Val | Cys | Thr | His | Arg  | Pro | Asp | Pro | Lys | Ser  | Pro | Gly | Leu | Asp | Arg  |  |
| 2340 |     |     |     |     | 2345 |     |     |     |     | 2350 |     |     |     |     |      |  |
| Glu  | Arg | Leu | Tyr | Trp | Lys  | Leu | Ser | Gln | Leu | Thr  | His | Gly | Ile | Thr | Glu  |  |
| 2355 |     |     |     |     | 2360 |     |     |     |     | 2365 |     |     |     |     |      |  |
| Leu  | Gly | Pro | Tyr | Thr | Leu  | Asp | Arg | His | Ser | Leu  | Tyr | Val | Asn | Gly | Phe  |  |
| 2370 |     |     |     |     | 2375 |     |     |     |     | 2380 |     |     |     |     |      |  |
| Thr  | His | Gln | Ser | Ser | Met  | Thr | Thr | Thr | Arg | Thr  | Pro | Asp | Thr | Ser | Thr  |  |
| 2385 |     |     |     |     | 2390 |     |     |     |     | 2395 |     |     |     |     | 2400 |  |
| Met  | His | Leu | Ala | Thr | Ser  | Arg | Thr | Pro | Ala | Ser  | Leu | Ser | Gly | Pro | Thr  |  |
| 2405 |     |     |     |     | 2410 |     |     |     |     | 2415 |     |     |     |     |      |  |
| Thr  | Ala | Ser | Pro | Leu | Leu  | Val | Leu | Phe | Thr | Ile  | Asn | Phe | Thr | Ile | Thr  |  |
| 2420 |     |     |     |     | 2425 |     |     |     |     | 2430 |     |     |     |     |      |  |
| Asn  | Leu | Arg | Tyr | Glu | Glu  | Asn | Met | His | His | Pro  | Gly | Ser | Arg | Lys | Phe  |  |
| 2435 |     |     |     |     | 2440 |     |     |     |     | 2445 |     |     |     |     |      |  |
| Asn  | Thr | Thr | Glu | Arg | Val  | Leu | Gln | Gly | Leu | Leu  | Arg | Pro | Val | Phe | Lys  |  |
| 2450 |     |     |     |     | 2455 |     |     |     |     | 2460 |     |     |     |     |      |  |
| Asn  | Thr | Ser | Val | Gly | Pro  | Leu | Tyr | Ser | Gly | Cys  | Arg | Leu | Thr | Leu | Leu  |  |
| 2465 |     |     |     |     | 2470 |     |     |     |     | 2475 |     |     |     |     | 2480 |  |
| Arg  | Pro | Lys | Lys | Asp | Gly  | Ala | Ala | Thr | Lys | Val  | Asp | Ala | Ile | Cys | Thr  |  |

|      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |     |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|
|      |      |      |      | 2485 |      |      |      |      | 2490 |      |      |      |      | 2495 |     |
| Tyr  | Arg  | Pro  | Asp  | Pro  | Lys  | Ser  | Pro  | Gly  | Leu  | Asp  | Arg  | Glu  | Gln  | Leu  | Tyr |
|      |      |      | 2500 |      |      |      |      | 2505 |      |      |      |      | 2510 |      |     |
| Trp  | Glu  | Leu  | Ser  | Gln  | Leu  | Thr  | His  | Ser  | Ile  | Thr  | Glu  | Leu  | Gly  | Pro  | Tyr |
|      |      |      | 2515 |      |      |      |      | 2520 |      |      |      |      | 2525 |      |     |
| Thr  | Leu  | Asp  | Arg  | Asp  | Ser  | Leu  | Tyr  | Val  | Asn  | Gly  | Phe  | Thr  | Gln  | Arg  | Ser |
|      |      |      | 2530 |      |      |      |      | 2535 |      |      |      |      | 2540 |      |     |
| Ser  | Val  | Pro  | Thr  | Thr  | Ser  | Ile  | Pro  | Gly  | Thr  | Pro  | Thr  | Val  | Asp  | Leu  | Gly |
| 2545 |      |      |      |      | 2550 |      |      |      |      | 2555 |      |      |      | 2560 |     |
| Thr  | Ser  | Gly  | Thr  | Pro  | Val  | Ser  | Lys  | Pro  | Gly  | Pro  | Ser  | Ala  | Ala  | Ser  | Pro |
|      |      |      |      | 2565 |      |      |      |      | 2570 |      |      |      |      | 2575 |     |
| Leu  | Leu  | Val  | Leu  | Phe  | Thr  | Leu  | Asn  | Phe  | Thr  | Ile  | Thr  | Asn  | Leu  | Arg  | Tyr |
|      |      |      | 2580 |      |      |      |      | 2585 |      |      |      |      | 2590 |      |     |
| Glu  | Glu  | Asn  | Met  | Gln  | His  | Pro  | Gly  | Ser  | Arg  | Lys  | Phe  | Asn  | Thr  | Thr  | Glu |
|      |      | 2595 |      |      |      | 2600 |      |      |      |      |      | 2605 |      |      |     |
| Arg  | Val  | Leu  | Gln  | Gly  | Leu  | Leu  | Arg  | Ser  | Leu  | Phe  | Lys  | Ser  | Thr  | Ser  | Val |
|      | 2610 |      |      |      |      | 2615 |      |      |      |      | 2620 |      |      |      |     |
| Gly  | Pro  | Leu  | Tyr  | Ser  | Gly  | Cys  | Arg  | Leu  | Thr  | Leu  | Leu  | Arg  | Pro  | Glu  | Lys |
| 2625 |      |      |      | 2630 |      |      |      |      | 2635 |      |      |      |      | 2640 |     |
| Asp  | Gly  | Thr  | Ala  | Thr  | Gly  | Val  | Asp  | Ala  | Ile  | Cys  | Thr  | His  | His  | Pro  | Asp |
|      |      |      | 2645 |      |      |      |      | 2650 |      |      |      |      |      | 2655 |     |
| Pro  | Lys  | Ser  | Pro  | Arg  | Leu  | Asp  | Arg  | Glu  | Gln  | Leu  | Tyr  | Trp  | Glu  | Leu  | Ser |
|      |      | 2660 |      |      |      |      |      | 2665 |      |      |      |      | 2670 |      |     |
| Gln  | Leu  | Thr  | His  | Asn  | Ile  | Thr  | Glu  | Leu  | Gly  | Xaa  | Tyr  | Ala  | Leu  | Asp  | Asn |
|      | 2675 |      |      |      |      | 2680 |      |      |      |      |      | 2685 |      |      |     |
| Asp  | Ser  | Leu  | Phe  | Val  | Asn  | Gly  | Phe  | Thr  | His  | Arg  | Ser  | Ser  | Val  | Ser  | Thr |
|      | 2690 |      |      |      |      | 2695 |      |      |      |      | 2700 |      |      |      |     |
| Thr  | Ser  | Thr  | Pro  | Gly  | Thr  | Pro  | Thr  | Val  | Tyr  | Leu  | Gly  | Ala  | Ser  | Lys  | Thr |
| 2705 |      |      |      | 2710 |      |      |      |      | 2715 |      |      |      |      | 2720 |     |
| Pro  | Ala  | Ser  | Ile  | Phe  | Gly  | Pro  | Ser  | Ala  | Ala  | Ser  | His  | Leu  | Leu  | Ile  | Leu |
|      |      |      | 2725 |      |      |      |      |      | 2730 |      |      |      |      | 2735 |     |
| Phe  | Thr  | Leu  | Asn  | Phe  | Thr  | Ile  | Thr  | Asn  | Leu  | Arg  | Tyr  | Glu  | Glu  | Asn  | Met |
|      |      | 2740 |      |      |      |      |      | 2745 |      |      |      |      | 2750 |      |     |
| Trp  | Pro  | Gly  | Ser  | Arg  | Lys  | Phe  | Asn  | Thr  | Thr  | Glu  | Arg  | Val  | Leu  | Gln  | Gly |
|      | 2755 |      |      |      |      | 2760 |      |      |      |      |      | 2765 |      |      |     |
| Leu  | Leu  | Arg  | Pro  | Leu  | Phe  | Lys  | Asn  | Thr  | Ser  | Val  | Gly  | Pro  | Leu  | Tyr  | Ser |
|      | 2770 |      |      |      |      | 2775 |      |      |      |      | 2780 |      |      |      |     |
| Gly  | Cys  | Arg  | Leu  | Thr  | Leu  | Leu  | Arg  | Pro  | Glu  | Lys  | Asp  | Gly  | Glu  | Ala  | Thr |
| 2785 |      |      |      | 2790 |      |      |      |      | 2795 |      |      |      |      | 2800 |     |
| Gly  | Val  | Asp  | Ala  | Ile  | Cys  | Thr  | His  | Arg  | Pro  | Asp  | Pro  | Thr  | Gly  | Pro  | Gly |
|      |      |      | 2805 |      |      |      |      |      | 2810 |      |      |      |      | 2815 |     |
| Leu  | Asp  | Arg  | Glu  | Gln  | Leu  | Tyr  | Leu  | Glu  | Leu  | Ser  | Gln  | Leu  | Thr  | His  | Ser |
|      |      | 2820 |      |      |      |      |      | 2825 |      |      |      |      | 2830 |      |     |
| Ile  | Thr  | Glu  | Leu  | Gly  | Pro  | Tyr  | Thr  | Leu  | Asp  | Arg  | Asp  | Ser  | Leu  | Tyr  | Val |
|      | 2835 |      |      |      |      |      | 2840 |      |      |      |      | 2845 |      |      |     |
| Asn  | Gly  | Phe  | Thr  | His  | Arg  | Ser  | Ser  | Val  | Pro  | Thr  | Thr  | Ser  | Thr  | Gly  | Val |
|      | 2850 |      |      |      |      | 2855 |      |      |      |      | 2860 |      |      |      |     |
| Val  | Ser  | Glu  | Glu  | Pro  | Phe  | Thr  | Leu  | Asn  | Phe  | Thr  | Ile  | Asn  | Asn  | Leu  | Arg |
| 2865 |      |      |      | 2870 |      |      |      |      | 2875 |      |      |      |      | 2880 |     |
| Tyr  | Met  | Ala  | Asp  | Met  | Gly  | Gln  | Pro  | Gly  | Ser  | Leu  | Lys  | Phe  | Asn  | Ile  | Thr |
|      |      |      | 2885 |      |      |      |      |      | 2890 |      |      |      |      | 2895 |     |
| Asp  | Asn  | Val  | Met  | Lys  | His  | Leu  | Leu  | Ser  | Pro  | Leu  | Phe  | Gln  | Arg  | Ser  | Ser |
|      |      | 2900 |      |      |      |      |      | 2905 |      |      |      |      | 2910 |      |     |
| Leu  | Gly  | Ala  | Arg  | Tyr  | Thr  | Gly  | Cys  | Arg  | Val  | Ile  | Ala  | Leu  | Arg  | Ser  | Val |
|      | 2915 |      |      |      |      |      | 2920 |      |      |      |      |      | 2925 |      |     |
| Lys  | Asn  | Gly  | Ala  | Glu  | Thr  | Arg  | Val  | Asp  | Leu  | Leu  | Cys  | Thr  | Tyr  | Leu  | Gln |
| 2930 |      |      |      |      |      | 2935 |      |      |      |      | 2940 |      |      |      |     |
| Pro  | Leu  | Ser  | Gly  | Pro  | Gly  | Leu  | Pro  | Ile  | Lys  | Gln  | Val  | Phe  | His  | Glu  | Leu |

|                 |                             |                     |             |      |  |      |
|-----------------|-----------------------------|---------------------|-------------|------|--|------|
| 2945            |                             | 2950                |             | 2955 |  | 2960 |
| Ser Gln Gln Thr | His Gly Ile Thr Arg         | Leu Gly Pro Tyr Ser | Leu Asp     |      |  |      |
|                 | 2965                        | 2970                | 2975        |      |  |      |
| Lys Asp Ser Leu | Tyr Leu Asn Gly Tyr Asn     | Glu Pro Gly Xaa Asp | Glu         |      |  |      |
|                 | 2980                        | 2985                | 2990        |      |  |      |
| Pro Pro Thr Thr | Pro Lys Pro Ala Thr Thr     | Phe Leu Pro Pro     | Leu Ser     |      |  |      |
|                 | 2995                        | 3000                | 3005        |      |  |      |
| Glu Ala Thr Thr | Ala Met Gly Tyr His         | Leu Lys Thr Leu     | Thr Leu Asn |      |  |      |
|                 | 3010                        | 3015                | 3020        |      |  |      |
| Phe Thr Ile Ser | Asn Leu Gln Tyr Ser Pro     | Asp Met Gly Lys Gly | Ser         |      |  |      |
|                 | 3025                        | 3030                | 3035        |      |  | 3040 |
| Ala Thr Phe Asn | Ser Thr Glu Gly Val Leu     | Gln His Leu Leu     | Arg Pro     |      |  |      |
|                 | 3045                        | 3050                | 3055        |      |  |      |
| Leu Phe Gln Lys | Ser Ser Met Gly Pro Phe     | Tyr Leu Gly Cys     | Gln Leu     |      |  |      |
|                 | 3060                        | 3065                | 3070        |      |  |      |
| Ile Ser Leu Arg | Pro Glu Lys Asp Gly Ala     | Ala Thr Gly Val     | Asp Thr     |      |  |      |
|                 | 3075                        | 3080                | 3085        |      |  |      |
| Thr Cys Thr Tyr | His Pro Asp Pro Val Gly     | Pro Gly Leu Asp     | Ile Gln     |      |  |      |
|                 | 3090                        | 3095                | 3100        |      |  |      |
| Gln Leu Tyr Trp | Glu Leu Ser Gln Leu Thr     | His Gly Val Thr     | Gln Leu     |      |  |      |
|                 | 3105                        | 3110                | 3115        |      |  | 3120 |
| Gly Phe Tyr Val | Leu Asp Arg Asp Ser Leu     | Phe Ile Asn Gly Tyr | Ala         |      |  |      |
|                 | 3125                        | 3130                | 3135        |      |  |      |
| Pro Gln Asn Leu | Ser Ile Arg Gly Glu Tyr     | Gln Ile Asn Phe     | His Ile     |      |  |      |
|                 | 3140                        | 3145                | 3150        |      |  |      |
| Val Asn Trp Asn | Leu Ser Asn Pro Asp Pro Thr | Ser Ser Glu Tyr     | Ile         |      |  |      |
|                 | 3155                        | 3160                | 3165        |      |  |      |
| Thr Leu Leu Arg | Asp Ile Gln Asp Lys Val Thr | Thr Leu Tyr Lys     | Gly         |      |  |      |
|                 | 3170                        | 3175                | 3180        |      |  |      |
| Ser Gln Leu His | Asp Thr Phe Arg Phe Cys     | Leu Val Thr Asn     | Leu Thr     |      |  |      |
|                 | 3185                        | 3190                | 3195        |      |  | 3200 |
| Met Asp Ser Val | Leu Val Thr Val Lys Ala     | Leu Phe Ser Ser     | Asn Leu     |      |  |      |
|                 | 3205                        | 3210                | 3215        |      |  |      |
| Asp Pro Ser Leu | Val Glu Gln Val Phe Leu     | Asp Lys Thr Leu     | Asn Ala     |      |  |      |
|                 | 3220                        | 3225                | 3230        |      |  |      |
| Ser Phe His Trp | Leu Gly Ser Thr Tyr Gln     | Leu Val Asp Ile     | His Val     |      |  |      |
|                 | 3235                        | 3240                | 3245        |      |  |      |
| Thr Glu Met Glu | Ser Ser Val Tyr Gln Pro Thr | Ser Ser Ser Thr     |             |      |  |      |
|                 | 3250                        | 3255                | 3260        |      |  |      |
| Gln His Phe Tyr | Xaa Asn Phe Thr Ile Thr     | Asn Leu Pro Tyr     | Ser Gln     |      |  |      |
|                 | 3265                        | 3270                | 3275        |      |  | 3280 |
| Asp Lys Ala Gln | Pro Gly Thr Thr Asn Tyr     | Gln Arg Asn Lys     | Arg Asn     |      |  |      |
|                 | 3285                        | 3290                | 3295        |      |  |      |
| Ile Glu Asp Ala | Leu Asn Gln Leu Phe Arg     | Asn Ser Ser Ile     | Lys Ser     |      |  |      |
|                 | 3300                        | 3305                | 3310        |      |  |      |
| Tyr Phe Ser Asp | Cys Gln Val Ser Thr Phe     | Arg Ser Val Pro     | Asn Arg     |      |  |      |
|                 | 3315                        | 3320                | 3325        |      |  |      |
| His His Thr Gly | Val Asp Ser Leu Cys Asn Phe | Ser Pro Leu Ala     | Arg         |      |  |      |
|                 | 3330                        | 3335                | 3340        |      |  |      |
| Arg Val Asp Arg | Val Ala Ile Tyr Glu Glu     | Phe Leu Arg Met     | Thr Arg     |      |  |      |
|                 | 3345                        | 3350                | 3355        |      |  | 3360 |
| Asn Gly Thr Gln | Leu Gln Asn Phe Thr Leu     | Asp Arg Ser Ser     | Val Leu     |      |  |      |
|                 | 3365                        | 3370                | 3375        |      |  |      |
| Val Asp Gly Tyr | Xaa Pro Asn Arg Asn Glu     | Pro Leu Thr Gly     | Asn Ser     |      |  |      |
|                 | 3380                        | 3385                | 3390        |      |  |      |
| Asp Leu Pro Phe | Trp Ala Val Ile Xaa Ile     | Gly Leu Ala Gly     | Leu Leu     |      |  |      |
|                 | 3395                        | 3400                | 3405        |      |  |      |
| Gly Leu Ile Thr | Cys Leu Ile Cys Gly         | Val Leu Val Thr     | Thr Arg Arg |      |  |      |

3410                      3415                      3420  
 Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr  
 3425                      3430                      3435                      3440  
 Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln  
                          3445                      3450

<210> 596  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

<400> 596

Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr  
                                  5                      10                      15  
 Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser  
                                  20                      25                      30  
 Pro Thr Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr  
                                  35                      40                      45  
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg  
                                  50                      55                      60  
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu  
                                  65                      70                      75                      80  
 Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
                                  85                      90                      95  
 Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile  
                                  100                      105                      110  
 Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln  
                                  115                      120                      125  
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly  
                                  130                      135                      140  
 Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn  
 145                      150                      155